

Val Ala Thr Leu Thr Tyr Ala Tyr Ser Asp Ser Thr Ala Val Val Gly
 20 25 30

Pro Leu Ala Pro Ala Ala Glu Pro His Ser Trp Asp Leu Cys Glu His
 35 40 45

His Ala Glu Arg Ile Thr Ala Pro Leu Gly Trp Glu Met Leu Arg Val
 50 55 60

Asn Asp Ile Lys Val Asp Asp Asp Glu Asp Leu Thr Ala Leu Ala Gln
 65 70 75 80

Ala Val Arg Glu Ala Gly Arg Thr Val Ser Gly Leu Val Pro Glu Asp
 85 90 95

Glu Val Gly Gly Asn His Pro Val Asn Arg Ser Ala Arg Ile Ala Glu
 100 105 110

Gln Lys Val His Arg Arg Gly His Leu Tyr Val Val Pro Asp Gln Asp
 115 120 125

Glu Ser
 130

<210> 525

<211> 614

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(591)

<223> RXC01372

<400> 525

cag gac acc ttc gtc ctt ccc acc ttg ccc acg gcc gca ggc ttg tcg 48
 Gln Asp Thr Phe Val Leu Pro Thr Leu Pro Thr Ala Ala Gly Leu Ser
 1 5 10 15

cct gcc cgc atc gtg gcg tcg ata agc act ctt tta gat ctt tta gaa 96
 Pro Ala Arg Ile Val Ala Ser Ile Ser Thr Leu Leu Asp Leu Leu Glu
 20 25 30

gca gac ccc agc att att tcc gac cgc ttg gaa cac ctc gcc gac tgc 144
 Ala Asp Pro Ser Ile Ile Ser Asp Arg Leu Glu His Leu Ala Asp Cys
 35 40 45

att gat gag gaa gtg gaa tcg cta tcg ccg gaa cgt gac gaa cta gtc 192
 Ile Asp Glu Glu Val Glu Ser Leu Ser Pro Glu Arg Asp Glu Leu Val
 50 55 60

aat ccc ggc cga aaa ctg cgc gca tac gta gat cac gca cgg atc gtg 240
 Asn Pro Gly Arg Lys Leu Arg Ala Tyr Val Asp His Ala Arg Ile Val
 65 70 75 80

cat acc ggc cga act gat gtg gga ctc gcg att gcc aac gtt atc gcc 288
 His Thr Gly Arg Thr Asp Val Gly Leu Ala Ile Ala Asn Val Ile Ala
 85 90 95

cca atc tgg acc cga cga ggc ctg gta tca gcc gtg ctg gat ttt ccc 336

Pro Ile Trp Thr Arg Arg Gly Leu Val Ser Ala Val Leu Asp Phe Pro
 100 105 110

gag ctc atg gaa tca ttg ccg gaa ctc cgc gga ccc gag cca att acc 384
 Glu Leu Met Glu Ser Leu Pro Glu Leu Arg Gly Pro Glu Pro Ile Thr
 115 120 125

gac gat ata ttc cat gac cca ttc ata gat gac gaa ccc ggg gtg gta 432
 Asp Asp Ile Phe His Asp Pro Phe Ile Asp Asp Glu Pro Gly Val Val
 130 135 140

ccg ttt agg gct gtt gtc tgg gcc gaa gag gaa ccc gga atc ccc gat 480
 Pro Phe Arg Ala Val Val Trp Ala Glu Glu Pro Gly Ile Pro Asp
 145 150 155 160

gcc atg gcg caa agc tgc gac gga cct agc aaa ggg gcg ctg aca caa 528
 Ala Met Ala Gln Ser Cys Asp Gly Pro Ser Lys Gly Ala Leu Thr Gln
 165 170 175

gca ctg cgt ttg ctg gtg cgc gga cag tca gcc acg acc tat tcc att 576
 Ala Leu Arg Leu Leu Val Arg Gly Gln Ser Ala Thr Thr Tyr Ser Ile
 180 185 190

gaa gaa aag gac ttg taaatggagc tattggaagg ctc 614
 Glu Glu Lys Asp Leu
 195

<210> 526

<211> 197

<212> PRT

<213> Corynebacterium glutamicum

<400> 526

Gln Asp Thr Phe Val Leu Pro Thr Leu Pro Thr Ala Ala Gly Leu Ser
 1 5 10 15

Pro Ala Arg Ile Val Ala Ser Ile Ser Thr Leu Leu Asp Leu Leu Glu
 20 25 30

Ala Asp Pro Ser Ile Ile Ser Asp Arg Leu Glu His Leu Ala Asp Cys
 35 40 45

Ile Asp Glu Glu Val Glu Ser Leu Ser Pro Glu Arg Asp Glu Leu Val
 50 55 60

Asn Pro Gly Arg Lys Leu Arg Ala Tyr Val Asp His Ala Arg Ile Val
 65 70 75 80

His Thr Gly Arg Thr Asp Val Gly Leu Ala Ile Ala Asn Val Ile Ala
 85 90 95

Pro Ile Trp Thr Arg Arg Gly Leu Val Ser Ala Val Leu Asp Phe Pro
 100 105 110

Glu Leu Met Glu Ser Leu Pro Glu Leu Arg Gly Pro Glu Pro Ile Thr
 115 120 125

Asp Asp Ile Phe His Asp Pro Phe Ile Asp Asp Glu Pro Gly Val Val
 130 135 140

Pro Phe Arg Ala Val Val Trp Ala Glu Glu Glu Pro Gly Ile Pro Asp
 145 150 155 160

Ala Met Ala Gln Ser Cys Asp Gly Pro Ser Lys Gly Ala Leu Thr Gln
 165 170 175

Ala Leu Arg Leu Leu Val Arg Gly Gln Ser Ala Thr Thr Tyr Ser Ile
 180 185 190

Glu Glu Lys Asp Leu
 195

<210> 527
 <211> 669
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(646)
 <223> RXC01659

<400> 527
 ttgatgcgcg ccgcggtgag cagcctgccg atccagagcg tgaagaatct gatgatttag 60

tcgagattga taccgtctct ggattccgcc tgctcagtac gtg gcg ggg gtt gcg 115
 Val Ala Gly Val Ala
 1 5

cag cgt ttt gtc gac gag cgc att cac gtc ggt ttg gat tcc atg cca 163
 Gln Arg Phe Val Asp Glu Arg Ile His Val Gly Leu Asp Ser Met Pro
 10 15 20

gaa gct gtg act gct gtg tgg atg gaa tct gat tgg gtg ttg gcg gaa 211
 Glu Ala Val Thr Ala Val Trp Met Glu Ser Asp Trp Val Leu Ala Glu
 25 30 35

acc atc aag ggt tcc acg cct tcc gat tgg gaa gag att ttg cgg ccg 259
 Thr Ile Lys Gly Ser Thr Pro Ser Asp Trp Glu Glu Ile Leu Arg Pro
 40 45 50

ttg gcg ctg ctc acg gac gcg tct ttc acg ttg cca cct cgt tcc acg 307
 Leu Ala Leu Leu Thr Asp Ala Ser Phe Thr Leu Pro Pro Arg Ser Thr
 55 60 65

cgt gcg caa acc ttg gat ttg aag cat ttg gaa cca agc cgt ctg aag 355
 Arg Ala Gln Thr Leu Asp Leu Lys His Leu Glu Pro Ser Arg Leu Lys
 70 75 80 85

ccg gag cag cca gaa aag cca gcg ttt act ccc aat gct tcg gaa gaa 403
 Pro Glu Gln Pro Glu Lys Pro Ala Phe Thr Pro Asn Ala Ser Glu Glu
 90 95 100

gat ttg tct cag ccg ttg gtg atc cgc ccc gag gag ccg ttg cag atg 451
 Asp Leu Ser Gln Pro Leu Val Ile Arg Pro Glu Glu Pro Leu Gln Met
 105 110 115

ccg gtt cgc ggt gtg cag gaa agc cgc gga gtg gtc gag cca cgg tca 499
 Pro Val Arg Gly Val Gln Glu Ser Arg Gly Val Val Glu Pro Arg Ser
 120 125 130

ttg ggt gcg gat gat gtg gag tcg att gcg gag ggc gat cca gag cgt 547
 Leu Gly Ala Asp Asp Val Glu Ser Ile Ala Glu Gly Asp Pro Glu Arg
 135 140 145

ccg agc gat ctt tat ggc acg cgt gtg ctg cgt gat ctc aat ggt cag 595
 Pro Ser Asp Leu Tyr Gly Thr Arg Val Leu Arg Asp Leu Asn Gly Gln
 150 155 160 165

tcc agt att ttc caa gat tcc acc gac gcg gat gag cca cca aaa aag 643
 Ser Ser Ile Phe Gln Asp Ser Thr Asp Ala Asp Glu Pro Pro Lys Lys
 170 175 180

tgg tagaaaactg gtgttttttcg gcc 669
 Trp

<210> 528

<211> 182

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 528

Val Ala Gly Val Ala Gln Arg Phe Val Asp Glu Arg Ile His Val Gly
 1 5 10 15

Leu Asp Ser Met Pro Glu Ala Val Thr Ala Val Trp Met Glu Ser Asp
 20 25 30

Trp Val Leu Ala Glu Thr Ile Lys Gly Ser Thr Pro Ser Asp Trp Glu
 35 40 45

Glu Ile Leu Arg Pro Leu Ala Leu Leu Thr Asp Ala Ser Phe Thr Leu
 50 55 60

Pro Pro Arg Ser Thr Arg Ala Gln Thr Leu Asp Leu Lys His Leu Glu
 65 70 75 80

Pro Ser Arg Leu Lys Pro Glu Gln Pro Glu Lys Pro Ala Phe Thr Pro
 85 90 95

Asn Ala Ser Glu Glu Asp Leu Ser Gln Pro Leu Val Ile Arg Pro Glu
 100 105 110

Glu Pro Leu Gln Met Pro Val Arg Gly Val Gln Glu Ser Arg Gly Val
 115 120 125

Val Glu Pro Arg Ser Leu Gly Ala Asp Asp Val Glu Ser Ile Ala Glu
 130 135 140

Gly Asp Pro Glu Arg Pro Ser Asp Leu Tyr Gly Thr Arg Val Leu Arg
 145 150 155 160

Asp Leu Asn Gly Gln Ser Ser Ile Phe Gln Asp Ser Thr Asp Ala Asp
 165 170 175

Glu Pro Pro Lys Lys Trp
 180

<210> 529
 <211> 981
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(958)
 <223> RXC01663

<400> 529

```
tatttttgctg gttggtcaca gtggagcgct aacccccgaga atcctatcga ggcctaaaat 60

cgtggccttga gtacgcactg ccagtaagggt gtgtgatgtg atg gaa ata agt gtc      115
                               Met Glu Ile Ser Val
                               1                      5

ttg atc atc gcc gca ctg atc ttg gtg gca ggc atc gta ctg tgg cgc      163
Leu Ile Ile Ala Ala Leu Ile Leu Val Ala Gly Ile Val Leu Trp Arg
                               10                      15                      20

gcg gac tcg tct aaa cag gca gct aaa aag gct gaa tca cct gtg ggc      211
Ala Asp Ser Ser Lys Gln Ala Ala Lys Lys Ala Glu Ser Pro Val Gly
                               25                      30                      35

tca gtc gca cct gcg ccc gtg ctg gtt gaa gaa gag ccg gac cct gag      259
Ser Val Ala Pro Ala Pro Val Leu Val Glu Glu Glu Pro Asp Pro Glu
                               40                      45                      50

ttt gag cca gaa ctg gac cct gaa cca gaa gcg caa cca gaa cca gag      307
Phe Glu Pro Glu Leu Asp Pro Glu Pro Glu Ala Gln Pro Glu Pro Glu
                               55                      60                      65

ctg gaa gtt gcg cct aga ttt gcg cca gaa cca gtt caa gat ctt gag      355
Leu Glu Val Ala Pro Arg Phe Ala Pro Glu Pro Val Gln Asp Leu Glu
                               70                      75                      80                      85

ccg gat cag gct gag gac att tat ttt gat gat tcc cct gaa ctc gat      403
Pro Asp Gln Ala Glu Asp Ile Tyr Phe Asp Asp Ser Pro Glu Leu Asp
                               90                      95                      100

gct gat gtt gaa aat gcc ttg gct gag ctt act gag gta gaa gac tac      451
Ala Asp Val Glu Asn Ala Leu Ala Glu Leu Thr Glu Val Glu Asp Tyr
                               105                      110                      115

ccg gaa gag cca gtg cag tct gag caa cct caa gcc cct gcc acg gcg      499
Pro Glu Glu Pro Val Gln Ser Glu Gln Pro Gln Ala Pro Ala Thr Ala
                               120                      125                      130

gag gta gct gcg gac gag gag caa cgg ggc gtc gat aag cat tcg ttt      547
Glu Val Ala Ala Asp Glu Glu Gln Arg Gly Val Asp Lys His Ser Phe
                               135                      140                      145

ttg agc tct ttg cct ggt tcg cag cgc cgg gag cgc cga aac tgg gcg      595
Leu Ser Ser Leu Pro Gly Ser Gln Arg Arg Glu Arg Arg Asn Trp Ala
                               150                      155                      160                      165

gcg aag cac cac ttc gat ttc atc aag gaa gat gcc ttt ttg acc gat      643
Ala Lys His His Phe Asp Phe Ile Lys Glu Asp Ala Phe Leu Thr Asp
                               170                      175                      180
```

gaa tgg tca agg ggt gcg gca tcg act ggt gcc gtt gca cgt gat gtg 691
 Glu Trp Ser Arg Gly Ala Ala Ser Thr Gly Ala Val Ala Arg Asp Val
 185 190 195

gtc agt ggc atg gct gaa gga tat gaa acg cat ctg gtg gat ttg gcg 739
 Val Ser Gly Met Ala Glu Gly Tyr Glu Thr His Leu Val Asp Leu Ala
 200 205 210

ggc gtg ccc gtg atg gcg atg cgc cgt gga att acc tct gac gtg gtc 787
 Gly Val Pro Val Met Ala Met Arg Arg Gly Ile Thr Ser Asp Val Val
 215 220 225

att gat gcg cgc cgc ggt gag cag cct gcc gat cca gag cgt gaa gaa 835
 Ile Asp Ala Arg Arg Gly Glu Gln Pro Ala Asp Pro Glu Arg Glu Glu
 230 235 240 245

tct gat gat tta gtc gag att gat acc gtc tct gga ttc cgc ctg ctc 883
 Ser Asp Asp Leu Val Glu Ile Asp Thr Val Ser Gly Phe Arg Leu Leu
 250 255 260

agt acg tgg cgg ggg ttg cgc agc gtt ttg tcg acg agc gca ttc acg 931
 Ser Thr Trp Arg Gly Leu Arg Ser Val Leu Ser Thr Ser Ala Phe Thr
 265 270 275

tcg gtt tgg att cca tgc cag aag ctg tgactgctgt gtggatggaa 978
 Ser Val Trp Ile Pro Cys Gln Lys Leu
 280 285

tct 981

<210> 530

<211> 286

<212> PRT

<213> Corynebacterium glutamicum

<400> 530

Met Glu Ile Ser Val Leu Ile Ile Ala Ala Leu Ile Leu Val Ala Gly
 1 5 10 15

Ile Val Leu Trp Arg Ala Asp Ser Ser Lys Gln Ala Ala Lys Lys Ala
 20 25 30

Glu Ser Pro Val Gly Ser Val Ala Pro Ala Pro Val Leu Val Glu Glu
 35 40 45

Glu Pro Asp Pro Glu Phe Glu Pro Glu Leu Asp Pro Glu Pro Glu Ala
 50 55 60

Gln Pro Glu Pro Glu Leu Glu Val Ala Pro Arg Phe Ala Pro Glu Pro
 65 70 75 80

Val Gln Asp Leu Glu Pro Asp Gln Ala Glu Asp Ile Tyr Phe Asp Asp
 85 90 95

Ser Pro Glu Leu Asp Ala Asp Val Glu Asn Ala Leu Ala Glu Leu Thr
 100 105 110

Glu Val Glu Asp Tyr Pro Glu Glu Pro Val Gln Ser Glu Gln Pro Gln
 115 120 125

Ala Pro Ala Thr Ala Glu Val Ala Ala Asp Glu Glu Gln Arg Gly Val
 130 135 140

Asp Lys His Ser Phe Leu Ser Ser Leu Pro Gly Ser Gln Arg Arg Glu
 145 150 155 160

Arg Arg Asn Trp Ala Ala Lys His His Phe Asp Phe Ile Lys Glu Asp
 165 170 175

Ala Phe Leu Thr Asp Glu Trp Ser Arg Gly Ala Ala Ser Thr Gly Ala
 180 185 190

Val Ala Arg Asp Val Val Ser Gly Met Ala Glu Gly Tyr Glu Thr His
 195 200 205

Leu Val Asp Leu Ala Gly Val Pro Val Met Ala Met Arg Arg Gly Ile
 210 215 220

Thr Ser Asp Val Val Ile Asp Ala Arg Arg Gly Glu Gln Pro Ala Asp
 225 230 235 240

Pro Glu Arg Glu Glu Ser Asp Asp Leu Val Glu Ile Asp Thr Val Ser
 245 250 255

Gly Phe Arg Leu Leu Ser Thr Trp Arg Gly Leu Arg Ser Val Leu Ser
 260 265 270

Thr Ser Ala Phe Thr Ser Val Trp Ile Pro Cys Gln Lys Leu
 275 280 285

<210> 531
 <211> 1545
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1522)
 <223> RXC01693

<400> 531
 aggagactgg ctggattatt ggctgggttt cttgggaaat cgtcatgggc attaatccta 60

gtcccaacaa ttgccagaac ccgaacacta ggcttgaacc atg aat act gca cct 115
 Met Asn Thr Ala Pro
 1 5

ttc aaa ctc gaa gct gac ttc gca tca gcc ctg ccc acc atg gca gcc 163
 Phe Lys Leu Glu Ala Asp Phe Ala Ser Ala Leu Pro Thr Met Ala Ala
 10 15 20

ccc tgg caa ggt gag gaa gcc ccc aac cct gag ctc gtg att tta aat 211
 Pro Trp Gln Gly Glu Glu Ala Pro Asn Pro Glu Leu Val Ile Leu Asn
 25 30 35

gac gac ctc gcc tac agc ctc ggg ctt gat ccg aca tgg ctt cgc aca 259
 Asp Asp Leu Ala Tyr Ser Leu Gly Leu Asp Pro Thr Trp Leu Arg Thr
 40 45 50

cct gag ggc gtt caa ttt ctt ctc gga ctc aac ccc gag ccc tta aca 307

Pro	Glu	Gly	Val	Gln	Phe	Leu	Leu	Gly	Leu	Asn	Pro	Glu	Pro	Leu	Thr		
55						60					65						
aaa	gca	gtt	gcg	cag	gcc	tat	tcc	ggc	cac	caa	ttc	gga	cag	ttt	gtg	355	
Lys	Ala	Val	Ala	Gln	Ala	Tyr	Ser	Gly	His	Gln	Phe	Gly	Gln	Phe	Val		
70					75					80					85		
gca	agc	ctt	ggt	gat	ggc	cga	gcg	ctt	ctt	ctc	ggc	gaa	gcc	cgc	tca	403	
Ala	Ser	Leu	Gly	Asp	Gly	Arg	Ala	Leu	Leu	Leu	Gly	Glu	Ala	Arg	Ser		
				90					95					100			
gct	gac	ggc	gta	ctg	cat	gat	atc	cac	ctc	aaa	gga	tct	gga	cga	acc	451	
Ala	Asp	Gly	Val	Leu	His	Asp	Ile	His	Leu	Lys	Gly	Ser	Gly	Arg	Thr		
			105					110					115				
caa	ttc	tcc	cga	gga	gcc	gat	gga	cgc	gcc	gtc	ctt	ggc	ccc	gtc	tta	499	
Gln	Phe	Ser	Arg	Gly	Ala	Asp	Gly	Arg	Ala	Val	Leu	Gly	Pro	Val	Leu		
		120					125					130					
cgc	gaa	tac	atc	atc	tcc	gaa	gcg	atg	cat	gca	ctt	ggt	gtt	ccc	acc	547	
Arg	Glu	Tyr	Ile	Ile	Ser	Glu	Ala	Met	His	Ala	Leu	Gly	Val	Pro	Thr		
	135					140					145						
acc	agg	tca	ctt	gca	gta	att	agc	acc	ggt	agg	aaa	atc	caa	cga	gga	595	
Thr	Arg	Ser	Leu	Ala	Val	Ile	Ser	Thr	Gly	Arg	Lys	Ile	Gln	Arg	Gly		
150					155					160					165		
agc	gta	gcc	cca	ggc	gca	gtc	ctt	gtt	cga	gta	gca	acc	agc	ctc	att	643	
Ser	Val	Ala	Pro	Gly	Ala	Val	Leu	Val	Arg	Val	Ala	Thr	Ser	Leu	Ile		
				170					175					180			
cga	gtc	gga	tcc	ttc	caa	tac	tcc	aac	atc	tct	ggt	ggc	atc	gaa	cta	691	
Arg	Val	Gly	Ser	Phe	Gln	Tyr	Ser	Asn	Ile	Ser	Gly	Gly	Ile	Glu	Leu		
			185					190					195				
tct	caa	cac	ctg	gcg	aac	tat	acg	atc	acc	agg	cat	ttc	cct	tcg	ttg	739	
Ser	Gln	His	Leu	Ala	Asn	Tyr	Thr	Ile	Thr	Arg	His	Phe	Pro	Ser	Leu		
		200					205					210					
gta	gct	gaa	cta	tcc	gca	cca	acc	ccc	gca	act	tat	gta	tca	ctg	ttt	787	
Val	Ala	Glu	Leu	Ser	Ala	Pro	Thr	Pro	Ala	Thr	Tyr	Val	Ser	Leu	Phe		
	215					220					225						
aaa	gcg	att	ctt	cag	cgc	caa	gca	gac	acc	gtt	gga	aaa	tgg	acc	agg	835	
Lys	Ala	Ile	Leu	Gln	Arg	Gln	Ala	Asp	Thr	Val	Gly	Lys	Trp	Thr	Arg		
230					235					240					245		
ctg	ggt	ttc	gtt	cac	gga	gcc	ctc	aac	aca	gac	aac	acg	ttg	ata	tcc	883	
Leu	Gly	Phe	Val	His	Gly	Ala	Leu	Asn	Thr	Asp	Asn	Thr	Leu	Ile	Ser		
				250					255					260			
gga	gaa	act	gtt	gac	tac	ggc	cca	tgc	gct	ttc	atg	gag	cgc	tac	cgt	931	
Gly	Glu	Thr	Val	Asp	Tyr	Gly	Pro	Cys	Ala	Phe	Met	Glu	Arg	Tyr	Arg		
			265					270					275				
ggc	gac	gcg	aaa	ttt	agc	tcc	atc	gac	act	tat	ggt	cgc	tac	aaa	ttt	979	
Gly	Asp	Ala	Lys	Phe	Ser	Ser	Ile	Asp	Thr	Tyr	Gly	Arg	Tyr	Lys	Phe		
		280					285					290					
gaa	aac	caa	cct	atg	atc	ctc	gga	tgg	aac	atg	gcc	cgc	ctc	gta	gaa	1027	
Glu	Asn	Gln	Pro	Met	Ile	Leu	Gly	Trp	Asn	Met	Ala	Arg	Leu	Val	Glu		

295	300	305	
acc ctc ctc cca ctc ctg ggc gcc aca cca gac gaa ggc atg aca gca			1075
Thr Leu Leu Pro Leu Leu Gly Ala Thr Pro Asp Glu Gly Met Thr Ala			
310	315	320	325
gcc caa gaa gct ctc gta gaa ttc gat gac ctc tgc gaa caa gca atc			1123
Ala Gln Glu Ala Leu Val Glu Phe Asp Asp Leu Cys Glu Gln Ala Ile			
	330	335	340
cga aaa gaa ttc gcc act gca ctg ggc ctt gac gag tca gac acc ggc			1171
Arg Lys Glu Phe Ala Thr Ala Leu Gly Leu Asp Glu Ser Asp Thr Gly			
	345	350	355
acg gta gag cag ttc cgt gaa ctg ctc tac ctc cat aac ccc gac atc			1219
Thr Val Glu Gln Phe Arg Glu Leu Leu Tyr Leu His Asn Pro Asp Ile			
	360	365	370
acc acg ctg ctg cgc gca ctc acc gac aac acc gca cca ccg agt ggc			1267
Thr Thr Leu Leu Arg Ala Leu Thr Asp Asn Thr Ala Pro Pro Ser Gly			
	375	380	385
ttt gaa gca ttc gtt cac gac tgg aaa acc caa gac cca gat atc gaa			1315
Phe Glu Ala Phe Val His Asp Trp Lys Thr Gln Asp Pro Asp Ile Glu			
390	395	400	405
gca atg cga gca gta aat cca ctt ttc att cca cgc aat cac ctc gtg			1363
Ala Met Arg Ala Val Asn Pro Leu Phe Ile Pro Arg Asn His Leu Val			
	410	415	420
gaa gct gct ctc gca gac gca gtt gaa ggg aat cta gaa aag ttc cac			1411
Glu Ala Ala Leu Ala Asp Ala Val Glu Gly Asn Leu Glu Lys Phe His			
	425	430	435
gaa ctc ctc gct gct gtc acc aat cct ttt gat cca act gcg ggc ccc			1459
Glu Leu Leu Ala Ala Val Thr Asn Pro Phe Asp Pro Thr Ala Gly Pro			
	440	445	450
gat gaa cta cgc ctg cca agc gaa gaa gga ttt gaa gaa gac tac atg			1507
Asp Glu Leu Arg Leu Pro Ser Glu Glu Gly Phe Glu Glu Asp Tyr Met			
	455	460	465
acc ttc tgc ggt acc taggacagat ggtggggcag acg			1545
Thr Phe Cys Gly Thr			
470			

<210> 532

<211> 474

<212> PRT

<213> Corynebacterium glutamicum

<400> 532

Met	Asn	Thr	Ala	Pro	Phe	Lys	Leu	Glu	Ala	Asp	Phe	Ala	Ser	Ala	Leu
1				5					10				15		

Pro	Thr	Met	Ala	Ala	Pro	Trp	Gln	Gly	Glu	Glu	Ala	Pro	Asn	Pro	Glu
			20					25					30		

Leu	Val	Ile	Leu	Asn	Asp	Asp	Leu	Ala	Tyr	Ser	Leu	Gly	Leu	Asp	Pro
		35					40					45			

Thr Trp Leu Arg Thr Pro Glu Gly Val Gln Phe Leu Leu Gly Leu Asn
 50 55 60
 Pro Glu Pro Leu Thr Lys Ala Val Ala Gln Ala Tyr Ser Gly His Gln
 65 70 75 80
 Phe Gly Gln Phe Val Ala Ser Leu Gly Asp Gly Arg Ala Leu Leu Leu
 85 90 95
 Gly Glu Ala Arg Ser Ala Asp Gly Val Leu His Asp Ile His Leu Lys
 100 105 110
 Gly Ser Gly Arg Thr Gln Phe Ser Arg Gly Ala Asp Gly Arg Ala Val
 115 120 125
 Leu Gly Pro Val Leu Arg Glu Tyr Ile Ile Ser Glu Ala Met His Ala
 130 135 140
 Leu Gly Val Pro Thr Thr Arg Ser Leu Ala Val Ile Ser Thr Gly Arg
 145 150 155 160
 Lys Ile Gln Arg Gly Ser Val Ala Pro Gly Ala Val Leu Val Arg Val
 165 170 175
 Ala Thr Ser Leu Ile Arg Val Gly Ser Phe Gln Tyr Ser Asn Ile Ser
 180 185 190
 Gly Gly Ile Glu Leu Ser Gln His Leu Ala Asn Tyr Thr Ile Thr Arg
 195 200 205
 His Phe Pro Ser Leu Val Ala Glu Leu Ser Ala Pro Thr Pro Ala Thr
 210 215 220
 Tyr Val Ser Leu Phe Lys Ala Ile Leu Gln Arg Gln Ala Asp Thr Val
 225 230 235 240
 Gly Lys Trp Thr Arg Leu Gly Phe Val His Gly Ala Leu Asn Thr Asp
 245 250 255
 Asn Thr Leu Ile Ser Gly Glu Thr Val Asp Tyr Gly Pro Cys Ala Phe
 260 265 270
 Met Glu Arg Tyr Arg Gly Asp Ala Lys Phe Ser Ser Ile Asp Thr Tyr
 275 280 285
 Gly Arg Tyr Lys Phe Glu Asn Gln Pro Met Ile Leu Gly Trp Asn Met
 290 295 300
 Ala Arg Leu Val Glu Thr Leu Leu Pro Leu Leu Gly Ala Thr Pro Asp
 305 310 315 320
 Glu Gly Met Thr Ala Ala Gln Glu Ala Leu Val Glu Phe Asp Asp Leu
 325 330 335
 Cys Glu Gln Ala Ile Arg Lys Glu Phe Ala Thr Ala Leu Gly Leu Asp
 340 345 350
 Glu Ser Asp Thr Gly Thr Val Glu Gln Phe Arg Glu Leu Leu Tyr Leu
 355 360 365

His Asn Pro Asp Ile Thr Thr Leu Leu Arg Ala Leu Thr Asp Asn Thr
 370 375 380

Ala Pro Pro Ser Gly Phe Glu Ala Phe Val His Asp Trp Lys Thr Gln
 385 390 395 400

Asp Pro Asp Ile Glu Ala Met Arg Ala Val Asn Pro Leu Phe Ile Pro
 405 410 415

Arg Asn His Leu Val Glu Ala Ala Leu Ala Asp Ala Val Glu Gly Asn
 420 425 430

Leu Glu Lys Phe His Glu Leu Leu Ala Ala Val Thr Asn Pro Phe Asp
 435 440 445

Pro Thr Ala Gly Pro Asp Glu Leu Arg Leu Pro Ser Glu Glu Gly Phe
 450 455 460

Glu Glu Asp Tyr Met Thr Phe Cys Gly Thr
 465 470

<210> 533
 <211> 1236
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1213)
 <223> RXC01703

<400> 533
 gttagacaaa tgggtaaaca gagctgacct agcgggaatcc gccatcaacg aaaggcattc 60

cgcgagggtt tggggctctgc ctcgaacaaa tcttgggttt gtg gca tgg cca tcc 115
 Val Ala Trp Pro Ser
 1 5

aac gcc aaa gaa aaa ctg ttt atc cac tgg cac tac tgg tgg caa gcg 163
 Asn Ala Lys Glu Lys Leu Phe Ile His Trp His Tyr Trp Trp Gln Ala
 10 15 20

cat tat cta gac tgc ctg gtg gat gct gct cgt cga cgc acc aca aag 211
 His Tyr Leu Asp Cys Leu Val Asp Ala Ala Arg Arg Arg Thr Thr Lys
 25 30 35

gcc cgt cgc gac cgc atc agg gac acc atc cgc ggc att tcg gtg cgc 259
 Ala Arg Arg Asp Arg Ile Arg Asp Thr Ile Arg Gly Ile Ser Val Arg
 40 45 50

aat gtg ggc aag ctg acc tcg aat cgt tat tac gac gac aaa gct tgg 307
 Asn Val Gly Lys Leu Thr Ser Asn Arg Tyr Tyr Asp Asp Lys Ala Trp
 55 60 65

ctg gcc ctt gct ctt ggg cgt gcc gga aaa gtg cga aag gtg cgc aca 355
 Leu Ala Leu Ala Leu Gly Arg Ala Gly Lys Val Arg Lys Val Arg Thr
 70 75 80 85

cca aaa tca ttg ccc tcg ttg gaa caa aac atc gtc gat ggc att gat 403
 Pro Lys Ser Leu Pro Ser Leu Glu Gln Asn Ile Val Asp Gly Ile Asp

90						95						100						
tcc	ctt	act	ggg	gtg	ctg	ccg	tgg	cgt	tcc	ggc	gaa	acc	ttc	tac	aac	451		
Ser	Leu	Thr	Gly	Val	Leu	Pro	Trp	Arg	Ser	Gly	Glu	Thr	Phe	Tyr	Asn			
			105					110					115					
gtt	ccc	tcc	aac	ggg	cct	gct	gcg	atc	atg	atg	gcc	cgc	acc	gac	cgt	499		
Val	Pro	Ser	Asn	Gly	Pro	Ala	Ala	Ile	Met	Met	Ala	Arg	Thr	Asp	Arg			
		120					125					130						
ttg	gac	gag	got	atg	aaa	atc	acc	gat	tgg	att	ttt	gac	aac	ctg	atc	547		
Leu	Asp	Glu	Ala	Met	Lys	Ile	Thr	Asp	Trp	Ile	Phe	Asp	Asn	Leu	Ile			
	135					140					145							
gat	ggc	gac	ggc	ctt	gtg	atg	gac	gga	ttg	cgc	atg	cgc	atg	cac	gga	595		
Asp	Gly	Asp	Gly	Leu	Val	Met	Asp	Gly	Leu	Arg	Met	Arg	Met	His	Gly			
150					155					160					165			
cct	gag	ctt	gtc	cgt	tcc	atc	cac	ccg	tat	tgc	caa	ggg	gtc	gcc	att	643		
Pro	Glu	Leu	Val	Arg	Ser	Ile	His	Pro	Tyr	Cys	Gln	Gly	Val	Ala	Ile			
			170						175					180				
ggg	gcg	tgt	ttg	gaa	att	gct	ctc	aaa	ctg	cgt	gag	cgc	gca	ggc	ttg	691		
Gly	Ala	Cys	Leu	Glu	Ile	Ala	Leu	Lys	Leu	Arg	Glu	Arg	Ala	Gly	Leu			
			185					190					195					
acc	act	act	gtg	gtg	gat	cac	tgg	tcg	gat	gcc	gat	aag	gca	gaa	gac	739		
Thr	Thr	Thr	Val	Val	Asp	His	Trp	Ser	Asp	Ala	Asp	Lys	Ala	Glu	Asp			
		200					205					210						
tcc	ctc	aaa	tac	ttt	gca	cac	atc	cac	gct	gtg	gtt	cag	gct	gtg	tcg	787		
Ser	Leu	Lys	Tyr	Phe	Ala	His	Ile	His	Ala	Val	Val	Gln	Ala	Val	Ser			
	215					220					225							
cgg	aag	atg	acc	aac	ttc	cac	ggc	gtt	att	gat	tgg	gac	acc	ggg	gac	835		
Arg	Lys	Met	Thr	Asn	Phe	His	Gly	Val	Ile	Asp	Trp	Asp	Thr	Gly	Asp			
230					235					240					245			
ggc	gac	ggc	ggg	ttg	ttc	aag	ggc	att	ttg	gtc	cgc	tat	tta	gct	gat	883		
Gly	Asp	Gly	Gly	Leu	Phe	Lys	Gly	Ile	Leu	Val	Arg	Tyr	Leu	Ala	Asp			
			250					255						260				
gtg	gcc	atc	cgc	ctg	cct	gac	gat	tca	cca	acc	aac	cgg	gaa	acc	aaa	931		
Val	Ala	Ile	Arg	Leu	Pro	Asp	Asp	Ser	Pro	Thr	Asn	Arg	Glu	Thr	Lys			
			265					270					275					
aag	att	gca	gca	cgc	ctg	gta	ctg	gaa	tcg	gcg	gaa	agc	gta	tgg	aac	979		
Lys	Ile	Ala	Ala	Arg	Leu	Val	Leu	Glu	Ser	Ala	Glu	Ser	Val	Trp	Asn			
		280					285					290						
cac	cga	ttg	gaa	gtt	gat	ggc	ctt	ccg	gta	ttc	gcc	aca	gac	tgg	aca	1027		
His	Arg	Leu	Glu	Val	Asp</													

caa ttg tcc ggt tgg atg ctc atg gaa gca gca gcg aaa gtg gcc gaa 1171
 Gln Leu Ser Gly Trp Met Leu Met Glu Ala Ala Ala Lys Val Ala Glu
 345 350 355

gaa ctg gaa aac aac ggc aat agt tac acc ggt cgc tcc cga 1213
 Glu Leu Glu Asn Asn Gly Asn Ser Tyr Thr Gly Arg Ser Arg
 360 365 370

tagccccgat agtgtatgtg ctg 1236

<210> 534

<211> 371

<212> PRT

<213> Corynebacterium glutamicum

<400> 534

Val Ala Trp Pro Ser Asn Ala Lys Glu Lys Leu Phe Ile His Trp His
 1 5 10 15

Tyr Trp Trp Gln Ala His Tyr Leu Asp Cys Leu Val Asp Ala Ala Arg
 20 25 30

Arg Arg Thr Thr Lys Ala Arg Arg Asp Arg Ile Arg Asp Thr Ile Arg
 35 40 45

Gly Ile Ser Val Arg Asn Val Gly Lys Leu Thr Ser Asn Arg Tyr Tyr
 50 55 60

Asp Asp Lys Ala Trp Leu Ala Leu Ala Leu Gly Arg Ala Gly Lys Val
 65 70 75 80

Arg Lys Val Arg Thr Pro Lys Ser Leu Pro Ser Leu Glu Gln Asn Ile
 85 90 95

Val Asp Gly Ile Asp Ser Leu Thr Gly Val Leu Pro Trp Arg Ser Gly
 100 105 110

Glu Thr Phe Tyr Asn Val Pro Ser Asn Gly Pro Ala Ala Ile Met Met
 115 120 125

Ala Arg Thr Asp Arg Leu Asp Glu Ala Met Lys Ile Thr Asp Trp Ile
 130 135 140

Phe Asp Asn Leu Ile Asp Gly Asp Gly Leu Val Met Asp Gly Leu Arg
 145 150 155 160

Met Arg Met His Gly Pro Glu Leu Val Arg Ser Ile His Pro Tyr Cys
 165 170 175

Gln Gly Val Ala Ile Gly Ala Cys Leu Glu Ile Ala Leu Lys Leu Arg
 180 185 190

Glu Arg Ala Gly Leu Thr Thr Thr Val Val Asp His Trp Ser Asp Ala
 195 200 205

Asp Lys Ala Glu Asp Ser Leu Lys Tyr Phe Ala His Ile His Ala Val
 210 215 220

Val Gln Ala Val Ser Arg Lys Met Thr Asn Phe His Gly Val Ile Asp

225 230 235 240
 Trp Asp Thr Gly Asp Gly Asp Gly Gly Leu Phe Lys Gly Ile Leu Val
 245 250 255
 Arg Tyr Leu Ala Asp Val Ala Ile Arg Leu Pro Asp Asp Ser Pro Thr
 260 265 270
 Asn Arg Glu Thr Lys Lys Ile Ala Ala Arg Leu Val Leu Glu Ser Ala
 275 280 285
 Glu Ser Val Trp Asn His Arg Leu Glu Val Asp Gly Leu Pro Val Phe
 290 295 300
 Ala Thr Asp Trp Thr Thr Asp Ala Arg Leu Pro Gln Asn Phe Gly Leu
 305 310 315 320
 Ser Ser Ser Ser Leu Ser Asp Leu Val Ser Val Val Arg Val Asp Glu
 325 330 335
 Arg Asp Leu Ser Val Gln Leu Ser Gly Trp Met Leu Met Glu Ala Ala
 340 345 350
 Ala Lys Val Ala Glu Glu Leu Glu Asn Asn Gly Asn Ser Tyr Thr Gly
 355 360 365
 Arg Ser Arg
 370

<210> 535
 <211> 800
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(777)
 <223> RXC02254

<400> 535
 atc gcc gtt gcc gaa gaa ggc gga ttg tgg gaa aac ctc ctg cag cac 48
 Ile Ala Val Ala Glu Glu Gly Gly Leu Trp Glu Asn Leu Leu Gln His
 1 5 10 15
 cgc ttc ggt gga cat ggt gcg cta gct ggt cac gcc ttg gga aac ctc 96
 Arg Phe Gly Gly His Gly Ala Leu Ala Gly His Ala Leu Gly Asn Leu
 20 25 30
 gtg atc gcg gcg ttg acc gac att ttg ggc acc tcc cag cat gcg ctt 144
 Val Ile Ala Ala Leu Thr Asp Ile Leu Gly Thr Ser Gln His Ala Leu
 35 40 45
 gat caa atc gct caa ctc gct gga gcc aaa gga cgc atc atc ccg gta 192
 Asp Gln Ile Ala Gln Leu Ala Gly Ala Lys Gly Arg Ile Ile Pro Val
 50 55 60
 tgt gct gaa cct ttg gat ctt gaa gcg gaa gta tca ggt cta gac tct 240
 Cys Ala Glu Pro Leu Asp Leu Glu Ala Glu Val Ser Gly Leu Asp Ser
 65 70 75 80

gat gct cga gtc atg cgt caa gtt cgt ggt caa gtg gcg gta gct gca 288
Asp Ala Arg Val Met Arg Gln Val Arg Gly Gln Val Ala Val Ala Ala
85 90 95

acc ccc ggg cag gtg cga cgc gtt cga atc att ccg gac aat cca gaa 336
Thr Pro Gly Gln Val Arg Arg Val Arg Ile Ile Pro Asp Asn Pro Glu
100 105 110

ccg aac ccc gct gcc atc gag gcc att ctc gat gca gat ttg gtc acc 384
Pro Asn Pro Ala Ala Ile Glu Ala Ile Leu Asp Ala Asp Leu Val Thr
115 120 125

ctt ggc cca ggt tcc tgg ttc tcc tct gtg att cca cac att ttg gtc 432
Leu Gly Pro Gly Ser Trp Phe Ser Ser Val Ile Pro His Ile Leu Val
130 135 140

cca ggg atc gtt gat gcc ttg gcg cag aca aaa gca acc aaa acc gtg 480
Pro Gly Ile Val Asp Ala Leu Ala Gln Thr Lys Ala Thr Lys Thr Val
145 150 155 160

gtg tta aac ctg acg tcc gag cca ggg gag acc gcg gga ttc tct gca 528
Val Leu Asn Leu Thr Ser Glu Pro Gly Glu Thr Ala Gly Phe Ser Ala
165 170 175

gaa cga cac atc cat gtg ctc cgc cag cat gct cga aac ctt cag gtt 576
Glu Arg His Ile His Val Leu Arg Gln His Ala Arg Asn Leu Gln Val
180 185 190

gac caa gtc att gtc gat gcc aag aca ctg tcc tca caa acc gaa cgc 624
Asp Gln Val Ile Val Asp Ala Lys Thr Leu Ser Ser Gln Thr Glu Arg
195 200 205

aat cat gta gaa cga gct gct cgc acc ctt ggt gca gaa gtc tcc ttc 672
Asn His Val Glu Arg Ala Ala Arg Thr Leu Gly Ala Glu Val Ser Phe
210 215 220

cat gat gtc cag gct gaa gat ggc cgt ggt cga ttc acc agt att cac 720
His Asp Val Gln Ala Glu Asp Gly Arg Gly Arg Phe Thr Ser Ile His
225 230 235 240

gat cca gca aag ctg tgt gca gcg ttg ctg gca agt ttt gct gga gca 768
Asp Pro Ala Lys Leu Cys Ala Ala Leu Leu Ala Ser Phe Ala Gly Ala
245 250 255

cga aag cgt taaggagtag gcgtgtcact gac 800
Arg Lys Arg

<210> 536

<211> 259

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 536

Ile Ala Val Ala Glu Glu Gly Gly Leu Trp Glu Asn Leu Leu Gln His
1 5 10 15

Arg Phe Gly Gly His Gly Ala Leu Ala Gly His Ala Leu Gly Asn Leu
20 25 30

```
<400> 537
gtgtgcagcg ttgctggcaa gttttgctgg agcacgaaag cgттаaggag taggcgtgtc 60
actgacgagt gatatcaaac aagaattggc gcagggtccat gtg gcc aaa aac agt 115
Val Ala Lys Asn Ser
```

	1	5	
gtt cgt gct gcg gaa gtg tct gca att tta agg ttt gct ggt gag atg			163
Val Arg Ala Ala Glu Val Ser Ala Ile Leu Arg Phe Ala Gly Glu Met			
	10	15	20
caa gct gtc ggc ggc aag ctg gtc atc gaa gca aat ttg gac agc atg			211
Gln Ala Val Gly Lys Leu Val Ile Glu Ala Asn Leu Asp Ser Met			
	25	30	35
caa gtc ggt atg agg ctt cag gag ttt atc caa ggt ttg tac aac tct			259
Gln Val Gly Met Arg Leu Gln Glu Phe Ile Gln Gly Leu Tyr Asn Ser			
	40	45	50
cga gtc gat gtg cac acc gtg aac ccg act gtg agc agg aaa acg cca			307
Arg Val Asp Val His Thr Val Asn Pro Thr Val Ser Arg Lys Thr Pro			
	55	60	65
cgg tat ttg gtg cgc atc att gac aat gcc gat gaa att gcg cga cgc			355
Arg Tyr Leu Val Arg Ile Ile Asp Asn Ala Asp Glu Ile Ala Arg Arg			
	70	75	80
acc gga ctg gtc acc agg tct gga cat gtg gtt aaa ggt cta gcg cct			403
Thr Gly Leu Val Thr Arg Ser Gly His Val Val Lys Gly Leu Ala Pro			
	90	95	100
tct gtg gtc agc gga aca atc agt gac gct gaa gct gca tgg cgc ggt			451
Ser Val Val Ser Gly Thr Ile Ser Asp Ala Glu Ala Ala Trp Arg Gly			
	105	110	115
gcg ttt cta gcc aat gga tct tta agt gat cca ggt cgt tcc tct tcg			499
Ala Phe Leu Ala Asn Gly Ser Leu Ser Asp Pro Gly Arg Ser Ser Ser			
	120	125	130
ttg gag gtg ttg tgt cct ggt caa gaa tca gca ttg gca ctg gtt gga			547
Leu Glu Val Leu Cys Pro Gly Gln Glu Ser Ala Leu Ala Leu Val Gly			
	135	140	145
tgt gcg cga aga att ggg atc gcg gcg aaa acg aaa gat tct cga gga			595
Cys Ala Arg Arg Ile Gly Ile Ala Ala Lys Thr Lys Asp Ser Arg Gly			
	150	155	160
ttt gat cgc gtc aat gtt cgt gat gcg gaa gca att ggg gca ctg ctc			643
Phe Asp Arg Val Asn Val Arg Asp Ala Glu Ala Ile Gly Ala Leu Leu			
	170	175	180
act cga atg ggt gcc cag aaa act cgc atg ttg tgg gaa gaa aaa cgc			691
Thr Arg Met Gly Ala Gln Lys Thr Arg Met Leu Trp Glu Glu Lys Arg			
	185	190	195
atc aag cgg gaa agt cga act ccg caa acc ggg ttg gcc aac ttc gac			739
Ile Lys Arg Glu Ser Arg Thr Pro Gln Thr Gly Leu Ala Asn Phe Asp			
	200	205	210
gat gcc aat ctg cgc agg tca gcc cga gca gca gtt gcc gct gca gcg			787
Asp Ala Asn Leu Arg Arg Ser Ala Arg Ala Ala Val Ala Ala Ala Ala			
	215	220	225
agg gta gaa cgc gcc atg aag att ctt ggt gat gat gtt cct gag cat			835
Arg Val Glu Arg Ala Met Lys Ile Leu Gly Asp Asp Val Pro Glu His			
	230	235	240
			245

ttg gct gag gct gga cag ctg cgt gtg cag cac cgt cag gca tcg ttg 883
 Leu Ala Glu Ala Gly Gln Leu Arg Val Gln His Arg Gln Ala Ser Leu
 250 255 260
 gag gag ttg ggc cgg ttg gct gat cct caa atg acc aag gat gct gtg 931
 Glu Glu Leu Gly Arg Leu Ala Asp Pro Gln Met Thr Lys Asp Ala Val
 265 270 275
 gcc ggt cgt att cgt cgt ctt ttg acg atg gca gat aag cgc gcc gaa 979
 Ala Gly Arg Ile Arg Arg Leu Leu Thr Met Ala Asp Lys Arg Ala Glu
 280 285 290
 gat ctg aag att cct gat aca aat tct gtt gtg acg gaa gat ttg ttg 1027
 Asp Leu Lys Ile Pro Asp Thr Asn Ser Val Val Thr Glu Asp Leu Leu
 295 300 305
 gaa gaa att tagatgattg aagcctaaaa acg 1059
 Glu Glu Ile
 310

<210> 538

<211> 312

<212> PRT

<213> Corynebacterium glutamicum

<400> 538

Val Ala Lys Asn Ser Val Arg Ala Ala Glu Val Ser Ala Ile Leu Arg
 1 5 10 15
 Phe Ala Gly Glu Met Gln Ala Val Gly Gly Lys Leu Val Ile Glu Ala
 20 25 30
 Asn Leu Asp Ser Met Gln Val Gly Met Arg Leu Gln Glu Phe Ile Gln
 35 40 45
 Gly Leu Tyr Asn Ser Arg Val Asp Val His Thr Val Asn Pro Thr Val
 50 55 60
 Ser Arg Lys Thr Pro Arg Tyr Leu Val Arg Ile Ile Asp Asn Ala Asp
 65 70 75 80
 Glu Ile Ala Arg Arg Thr Gly Leu Val Thr Arg Ser Gly His Val Val
 85 90 95
 Lys Gly Leu Ala Pro Ser Val Val Ser Gly Thr Ile Ser Asp Ala Glu
 100 105 110
 Ala Ala Trp Arg Gly Ala Phe Leu Ala Asn Gly Ser Leu Ser Asp Pro
 115 120 125
 Gly Arg Ser Ser Ser Leu Glu Val Leu Cys Pro Gly Gln Glu Ser Ala
 130 135 140
 Leu Ala Leu Val Gly Cys Ala Arg Arg Ile Gly Ile Ala Ala Lys Thr
 145 150 155 160
 Lys Asp Ser Arg Gly Phe Asp Arg Val Asn Val Arg Asp Ala Glu Ala
 165 170 175

Ile Gly Ala Leu Leu Thr Arg Met Gly Ala Gln Lys Thr Arg Met Leu
 180 185 190

Trp Glu Glu Lys Arg Ile Lys Arg Glu Ser Arg Thr Pro Gln Thr Gly
 195 200 205

Leu Ala Asn Phe Asp Asp Ala Asn Leu Arg Arg Ser Ala Arg Ala Ala
 210 215 220

Val Ala Ala Ala Ala Arg Val Glu Arg Ala Met Lys Ile Leu Gly Asp
 225 230 235 240

Asp Val Pro Glu His Leu Ala Glu Ala Gly Gln Leu Arg Val Gln His
 245 250 255

Arg Gln Ala Ser Leu Glu Glu Leu Gly Arg Leu Ala Asp Pro Gln Met
 260 265 270

Thr Lys Asp Ala Val Ala Gly Arg Ile Arg Arg Leu Leu Thr Met Ala
 275 280 285

Asp Lys Arg Ala Glu Asp Leu Lys Ile Pro Asp Thr Asn Ser Val Val
 290 295 300

Thr Glu Asp Leu Leu Glu Glu Ile
 305 310

<210> 539
 <211> 681
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(658)
 <223> RXC02435

<400> 539
 tcatgaatgt agaacggatt tatcgacaag cgccagcaag tacgttgatc tctttagcca 60

tcatcgctgt gtacgcagtg cggccattca atcgagatca gtg aca gac aac ctg 115
 Val Thr Asp Asn Leu
 1 5

ggt tca acc agt atc ggt gac gcg tgg att ctg tac gca ccg ctg atg 163
 Gly Ser Thr Ser Ile Gly Asp Ala Trp Ile Leu Tyr Ala Pro Leu Met
 10 15 20

gat gat ggt ggc ttt ggt cca ctg cgt gcc atc gga gga atg ttc ctg 211
 Asp Asp Gly Gly Phe Gly Pro Leu Arg Ala Ile Gly Gly Met Phe Leu
 25 30 35

cac att ggc ccc ggg cac atg ctg ttg aac ctt gtg ttg ttg tgg ttg 259
 His Ile Gly Pro Gly His Met Leu Leu Asn Leu Val Leu Leu Trp Leu
 40 45 50

ctg gga aga gaa att gaa cga gac ttc ggt tct gcg ctt ttc act gcg 307
 Leu Gly Arg Glu Ile Glu Arg Asp Phe Gly Ser Ala Leu Phe Thr Ala
 55 60 65

atg tac ttt gtg ggc ggt att ggt gcg tct gca gct gtc atc tgg atg 355
 Met Tyr Phe Val Gly Gly Ile Gly Ala Ser Ala Ala Val Ile Trp Met
 70 75 80 85
 gat ccc tat tca ccg aca gca ggt gct tcc ggc gcc att tac gcc atg 403
 Asp Pro Tyr Ser Pro Thr Ala Gly Ala Ser Gly Ala Ile Tyr Ala Met
 90 95 100
 atg gct att ttg gtg ggg ctt ttt gtg tta aga agc gcg gat atc cga 451
 Met Ala Ile Leu Val Gly Leu Phe Val Leu Arg Ser Ala Asp Ile Arg
 105 110 115
 gca ccc ttg atc ctt atc gcc atc aac atc gcc tat acc ttg atg tcc 499
 Ala Pro Leu Ile Leu Ile Ala Ile Asn Ile Ala Tyr Thr Leu Met Ser
 120 125 130
 acc aat gtt tct ctg tgg gga cac ctt gga ggt ttg atc act gga gct 547
 Thr Asn Val Ser Leu Trp Gly His Leu Gly Gly Leu Ile Thr Gly Ala
 135 140 145
 tta att act tgg cca atg gtt aaa gcg aaa act caa aga aca cgg tgg 595
 Leu Ile Thr Trp Pro Met Val Lys Ala Lys Thr Gln Arg Thr Arg Trp
 150 155 160 165
 att atc gtg ctc att ggt ttt gct gta gtt gtg gct gct gtc att cta 643
 Ile Ile Val Leu Ile Gly Phe Ala Val Val Ala Ala Val Ile Leu
 170 175 180
 gga att gac cgg gtg tagacacatt ccgccattg ccc 681
 Gly Ile Asp Arg Val
 185

<210> 540

<211> 186

<212> PRT

<213> Corynebacterium glutamicum

<400> 540

Val Thr Asp Asn Leu Gly Ser Thr Ser Ile Gly Asp Ala Trp Ile Leu
 1 5 10 15
 Tyr Ala Pro Leu Met Asp Asp Gly Gly Phe Gly Pro Leu Arg Ala Ile
 20 25 30
 Gly Gly Met Phe Leu His Ile Gly Pro Gly His Met Leu Leu Asn Leu
 35 40 45
 Val Leu Leu Trp Leu Leu Gly Arg Glu Ile Glu Arg Asp Phe Gly Ser
 50 55 60
 Ala Leu Phe Thr Ala Met Tyr Phe Val Gly Gly Ile Gly Ala Ser Ala
 65 70 75 80
 Ala Val Ile Trp Met Asp Pro Tyr Ser Pro Thr Ala Gly Ala Ser Gly
 85 90 95
 Ala Ile Tyr Ala Met Met Ala Ile Leu Val Gly Leu Phe Val Leu Arg
 100 105 110
 Ser Ala Asp Ile Arg Ala Pro Leu Ile Leu Ile Ala Ile Asn Ile Ala

115	120	125
Tyr Thr Leu Met Ser Thr Asn Val Ser Leu Trp Gly His Leu Gly Gly		
130	135	140
Leu Ile Thr Gly Ala Leu Ile Thr Trp Pro Met Val Lys Ala Lys Thr		
145	150	155
		160
Gln Arg Thr Arg Trp Ile Ile Val Leu Ile Gly Phe Ala Val Val Val		
	165	170
		175
Ala Ala Val Ile Leu Gly Ile Asp Arg Val		
180	185	

<210> 541
 <211> 681
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(658)
 <223> FRXA02435

<400> 541
 tcatgaatgt agaacggatt tatcgacaag cgccagcaag tacgttgatc tcttttagcca 60
 tcatcgctgt gtacgcagtg cggccattca atcgagatca gtg aca gac aac ctg 115
 Val Thr Asp Asn Leu
 1 5
 ggt tca acc agt atc ggt gac gcg tgg att ctg tac gca ccg ctg atg 163
 Gly Ser Thr Ser Ile Gly Asp Ala Trp Ile Leu Tyr Ala Pro Leu Met
 10 15 20
 gat gat ggt ggc ttt ggt cca ctg cgt gcc atc gga gga atg ttc ctg 211
 Asp Asp Gly Gly Phe Gly Pro Leu Arg Ala Ile Gly Gly Met Phe Leu
 25 30 35
 cac att ggc ccc ggg cac atg ctg ttg aac ctt gtg ttg ttg tgg ttg 259
 His Ile Gly Pro Gly His Met Leu Leu Asn Leu Val Leu Leu Trp Leu
 40 45 50
 ctg gga aga gaa att gaa cga gac ttc ggt tct gcg ctt ttc act gcg 307
 Leu Gly Arg Glu Ile Glu Arg Asp Phe Gly Ser Ala Leu Phe Thr Ala
 55 60 65
 atg tac ttt gtg ggc ggt att ggt gcg tct gca gct gtc atc tgg atg 355
 Met Tyr Phe Val Gly Gly Ile Gly Ala Ser Ala Ala Val Ile Trp Met
 70 75 80 85
 gat ccc tat tca ccg aca gca ggt gct tcc ggc gcc att tac gcc atg 403
 Asp Pro Tyr Ser Pro Thr Ala Gly Ala Ser Gly Ala Ile Tyr Ala Met
 90 95 100
 atg gct att ttg gtg ggg ctt ttt gtg tta aga agc gcg gat atc cga 451
 Met Ala Ile Leu Val Gly Leu Phe Val Leu Arg Ser Ala Asp Ile Arg
 105 110 115
 gca ccc ttg atc ctt atc gcc atc aac atc gcc tat acc ttg atg tcc 499

Ala Pro Leu Ile Leu Ile Ala Ile Asn Ile Ala Tyr Thr Leu Met Ser
 120 125 130

acc aat gtt tct ctg tgg gga cac ctt gga ggt ttg atc act gga gct 547
 Thr Asn Val Ser Leu Trp Gly His Leu Gly Gly Leu Ile Thr Gly Ala
 135 140 145

tta att act tgg cca atg gtt aaa gcg aaa act caa aga aca cgg tgg 595
 Leu Ile Thr Trp Pro Met Val Lys Ala Lys Thr Gln Arg Thr Arg Trp
 150 155 160 165

att atc gtg ctc att ggt ttt gct gta gtt gtg gct gct gtc att cta 643
 Ile Ile Val Leu Ile Gly Phe Ala Val Val Val Ala Ala Val Ile Leu
 170 175 180

gga att gac cgg gtg tagacacatt ccgcccattg ccc 681
 Gly Ile Asp Arg Val
 185

<210> 542

<211> 186

<212> PRT

<213> Corynebacterium glutamicum

<400> 542

Val Thr Asp Asn Leu Gly Ser Thr Ser Ile Gly Asp Ala Trp Ile Leu
 1 5 10 15

Tyr Ala Pro Leu Met Asp Asp Gly Gly Phe Gly Pro Leu Arg Ala Ile
 20 25 30

Gly Gly Met Phe Leu His Ile Gly Pro Gly His Met Leu Leu Asn Leu
 35 40 45

Val Leu Leu Trp Leu Leu Gly Arg Glu Ile Glu Arg Asp Phe Gly Ser
 50 55 60

Ala Leu Phe Thr Ala Met Tyr Phe Val Gly Gly Ile Gly Ala Ser Ala
 65 70 75 80

Ala Val Ile Trp Met Asp Pro Tyr Ser Pro Thr Ala Gly Ala Ser Gly
 85 90 95

Ala Ile Tyr Ala Met Met Ala Ile Leu Val Gly Leu Phe Val Leu Arg
 100 105 110

Ser Ala Asp Ile Arg Ala Pro Leu Ile Leu Ile Ala Ile Asn Ile Ala
 115 120 125

Tyr Thr Leu Met Ser Thr Asn Val Ser Leu Trp Gly His Leu Gly Gly
 130 135 140

Leu Ile Thr Gly Ala Leu Ile Thr Trp Pro Met Val Lys Ala Lys Thr
 145 150 155 160

Gln Arg Thr Arg Trp Ile Ile Val Leu Ile Gly Phe Ala Val Val Val
 165 170 175

Ala Ala Val Ile Leu Gly Ile Asp Arg Val
 180 185

<210> 543
 <211> 1141
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1111)
 <223> RXC03216

<400> 543

```

gctgtatcac agtcagctgc agcaggtggc gaaaccgttg cggteccagc ggctgctctg 60

atccctgcaa acaactagaa actattcaga aagcatcacc atg aaa ctc ggt ctc 115
                               Met Lys Leu Gly Leu
                               1 5

tac aac gcg atc ttc cac gac cgc acc ctg cca gaa gcg ctc gca gcc 163
Tyr Asn Ala Ile Phe His Asp Arg Thr Leu Pro Glu Ala Leu Ala Ala
          10          15          20

atc aaa gct gca ggt ctc acc gga att gaa ctc aac acc ggc gga ttt 211
Ile Lys Ala Ala Gly Leu Thr Gly Ile Glu Leu Asn Thr Gly Gly Phe
          25          30          35

ttg cct gca acc cac atc ccg acc atc gat gac atc ctg gtc agc gat 259
Leu Pro Ala Thr His Ile Pro Thr Ile Asp Asp Ile Leu Val Ser Asp
          40          45          50

gat gcc cgc gat gaa ttc ctc ggg att ttc gaa ggc acc ggc gtc gac 307
Asp Ala Arg Asp Glu Phe Leu Gly Ile Phe Glu Gly Thr Gly Val Asp
          55          60          65

atc tac ggc ctt aac tgc aac ggc aac ccg ctt cac ccc aac aag gcg 355
Ile Tyr Gly Leu Asn Cys Asn Gly Asn Pro Leu His Pro Asn Lys Ala
          70          75          80          85

atc ggg gac aag cat gcc gaa gac att cga cgt tcc atc cgc ctc gca 403
Ile Gly Asp Lys His Ala Glu Asp Ile Arg Arg Ser Ile Arg Leu Ala
          90          95          100

gag cgc ctc ggc caa aac cgt gtg gtc acc atg tct ggt ctt cct ggt 451
Glu Arg Leu Gly Gln Asn Arg Val Val Thr Met Ser Gly Leu Pro Gly
          105          110          115

ggc gaa cca ggc gcg aag tac acc aac tgg gtt gtc aac gcg tgg aac 499
Gly Glu Pro Gly Ala Lys Tyr Thr Asn Trp Val Val Asn Ala Trp Asn
          120          125          130

tcc gca gcc ttg gat gtc ctt gat tac caa tgg gat atc gca gct gaa 547
Ser Ala Ala Leu Asp Val Leu Asp Tyr Gln Trp Asp Ile Ala Ala Glu
          135          140          145

ttc tgg cgc gag acc gac cgc ttc gcc gca gat cac ggc gtg aaa gtg 595
Phe Trp Arg Glu Thr Asp Arg Phe Ala Ala Asp His Gly Val Lys Val
          150          155          160          165

gct ctt gag ctg cac cca cag aac atc gtg ttc aac tcc gct gac gtg 643
Ala Leu Glu Leu His Pro Gln Asn Ile Val Phe Asn Ser Ala Asp Val

```

	170	175	180	
cat aag ctc atc gat ctc acc ggc gcc acc cac gtg ggc gtc gaa ctg				691
His Lys Leu Ile Asp Leu Thr Gly Ala Thr His Val Gly Val Glu Leu				
	185	190	195	
gat gca tca cac ctg ttc tgg cag cag atg gac cca atc gct gtg att				739
Asp Ala Ser His Leu Phe Trp Gln Gln Met Asp Pro Ile Ala Val Ile				
	200	205	210	
gat cac ctc ggc gag ctc atc ttc cac gcc gcc gcc aaa gac gtg cga				787
Asp His Leu Gly Glu Leu Ile Phe His Ala Ala Ala Lys Asp Val Arg				
	215	220	225	
gtt aat aag gaa tgg gct cag ctc aac ggt gtg ctg gac aac agc ttc				835
Val Asn Lys Glu Trp Ala Gln Leu Asn Gly Val Leu Asp Asn Ser Phe				
	230	235	240	245
cga cgc ctt gac cca tcc gaa aac cgc acc aac ttg ggc ggc gac gag				883
Arg Arg Leu Asp Pro Ser Glu Asn Arg Thr Asn Leu Gly Gly Asp Glu				
	250	255	260	
tgg gcg aat gaa tgg cca aag aac tct gct tgg gat ttc gtt gct ctg				931
Trp Ala Asn Glu Trp Pro Lys Asn Ser Ala Trp Asp Phe Val Ala Leu				
	265	270	275	
ggc cgc ggt cat gac gtt gct tac tgg acc gaa ttc ctc cgc gca ctt				979
Gly Arg Gly His Asp Val Ala Tyr Trp Thr Glu Phe Leu Arg Ala Leu				
	280	285	290	
cac cgc gtc gat cca aac atg ctg gtc aac atc gaa cac gag gat gtt				1027
His Arg Val Asp Pro Asn Met Leu Val Asn Ile Glu His Glu Asp Val				
	295	300	305	
tca ctc ggt cgc gaa gaa ggc gtc aac gaa gcc gct aag gtg ctg atc				1075
Ser Leu Gly Arg Glu Glu Gly Val Asn Glu Ala Ala Lys Val Leu Ile				
	310	315	320	325
gag gcc aac aag gca ctc gaa gag tcc ctg gtt tct taaaaaaact				1121
Glu Ala Asn Lys Ala Leu Glu Glu Ser Leu Val Ser				
	330	335		
acgcctgccc cgcaacgctt				1141

<210> 544

<211> 337

<212> PRT

<213> Corynebacterium glutamicum

<400> 544

Met	Lys	Leu	Gly	Leu	Tyr	Asn	Ala	Ile	Phe	His	Asp	Arg	Thr	Leu	Pro
1				5					10					15	

Glu	Ala	Leu	Ala	Ala	Ile	Lys	Ala	Ala	Gly	Leu	Thr	Gly	Ile	Glu	Leu
				20				25					30		

Asn	Thr	Gly	Gly	Phe	Leu	Pro	Ala	Thr	His	Ile	Pro	Thr	Ile	Asp	Asp
		35					40					45			

Ile	Leu	Val	Ser	Asp	Asp	Ala	Arg	Asp	Glu	Phe	Leu	Gly	Ile	Phe	Glu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50	55	60
Gly Thr Gly Val Asp Ile Tyr Gly Leu Asn Cys Asn Gly Asn Pro Leu 65 70 75 80		
His Pro Asn Lys Ala Ile Gly Asp Lys His Ala Glu Asp Ile Arg Arg 85 90 95		
Ser Ile Arg Leu Ala Glu Arg Leu Gly Gln Asn Arg Val Val Thr Met 100 105 110		
Ser Gly Leu Pro Gly Gly Glu Pro Gly Ala Lys Tyr Thr Asn Trp Val 115 120 125		
Val Asn Ala Trp Asn Ser Ala Ala Leu Asp Val Leu Asp Tyr Gln Trp 130 135 140		
Asp Ile Ala Ala Glu Phe Trp Arg Glu Thr Asp Arg Phe Ala Ala Asp 145 150 155 160		
His Gly Val Lys Val Ala Leu Glu Leu His Pro Gln Asn Ile Val Phe 165 170 175		
Asn Ser Ala Asp Val His Lys Leu Ile Asp Leu Thr Gly Ala Thr His 180 185 190		
Val Gly Val Glu Leu Asp Ala Ser His Leu Phe Trp Gln Gln Met Asp 195 200 205		
Pro Ile Ala Val Ile Asp His Leu Gly Glu Leu Ile Phe His Ala Ala 210 215 220		
Ala Lys Asp Val Arg Val Asn Lys Glu Trp Ala Gln Leu Asn Gly Val 225 230 235 240		
Leu Asp Asn Ser Phe Arg Arg Leu Asp Pro Ser Glu Asn Arg Thr Asn 245 250 255		
Leu Gly Gly Asp Glu Trp Ala Asn Glu Trp Pro Lys Asn Ser Ala Trp 260 265 270		
Asp Phe Val Ala Leu Gly Arg Gly His Asp Val Ala Tyr Trp Thr Glu 275 280 285		
Phe Leu Arg Ala Leu His Arg Val Asp Pro Asn Met Leu Val Asn Ile 290 295 300		
Glu His Glu Asp Val Ser Leu Gly Arg Glu Glu Gly Val Asn Glu Ala 305 310 315 320		
Ala Lys Val Leu Ile Glu Ala Asn Lys Ala Leu Glu Glu Ser Leu Val 325 330 335		
Ser		

<210> 545

<211> 1416

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1393)

<223> RXA02175

<400> 545

```

tgacatgcgc ttggcgcac ccagttggta agaataaacg ggactacttc cgtaatccgg 60

aagagttttt ttccgaacaa atatgtttga aagggatatc gtg gct act gat aac 115
                               Val Ala Thr Asp Asn
                               1 5

aac aag gct gtc ctg cac tac ccc ggt ggc gag ttc gaa atg gac atc 163
Asn Lys Ala Val Leu His Tyr Pro Gly Gly Glu Phe Glu Met Asp Ile
                               10 15 20

atc gag gct tct gag ggt aac aac ggt gtt gtc ctg ggc aag atg ctg 211
Ile Glu Ala Ser Glu Gly Asn Asn Gly Val Val Leu Gly Lys Met Leu
                               25 30 35

tct gag act gga ctg atc act ttt gac cca ggt tat gtg agc act ggc 259
Ser Glu Thr Gly Leu Ile Thr Phe Asp Pro Gly Tyr Val Ser Thr Gly
                               40 45 50

tcc acc gag tcg aag atc acc tac atc gat ggc gat gcg gga atc ctg 307
Ser Thr Glu Ser Lys Ile Thr Tyr Ile Asp Gly Asp Ala Gly Ile Leu
                               55 60 65

cgt tac cgc ggc tat gac atc gct gat ctg gct gag aat gcc acc ttc 355
Arg Tyr Arg Gly Tyr Asp Ile Ala Asp Leu Ala Glu Asn Ala Thr Phe
                               70 75 80 85

aac gag gtt tct tac cta ctt atc aac ggt gag cta cca acc cca gat 403
Asn Glu Val Ser Tyr Leu Leu Ile Asn Gly Glu Leu Pro Thr Pro Asp
                               90 95 100

gag ctt cac aag ttt aac gac gag att cgc cac cac acc ctt ctg gac 451
Glu Leu His Lys Phe Asn Asp Glu Ile Arg His His Thr Leu Leu Asp
                               105 110 115

gag gac ttc aag tcc cag ttc aac gtg ttc cca cgc gac gct cac cca 499
Glu Asp Phe Lys Ser Gln Phe Asn Val Phe Pro Arg Asp Ala His Pro
                               120 125 130

atg gca acc ttg gct tcc tcg gtt aac att ttg tct acc tac tac cag 547
Met Ala Thr Leu Ala Ser Ser Val Asn Ile Leu Ser Thr Tyr Tyr Gln
                               135 140 145

gac cag ctg aac cca ctc gat gag gca cag ctt gat aag gca acc gtt 595
Asp Gln Leu Asn Pro Leu Asp Glu Ala Gln Leu Asp Lys Ala Thr Val
                               150 155 160 165

cgc ctc atg gca aag gtt cca atg ctg gct gcg tac gca cac cgc gca 643
Arg Leu Met Ala Lys Val Pro Met Leu Ala Ala Tyr Ala His Arg Ala
                               170 175 180

cgc aag ggt gct cct tac atg tac cca gac aac tcc ctc aat gcg cgt 691
Arg Lys Gly Ala Pro Tyr Met Tyr Pro Asp Asn Ser Leu Asn Ala Arg
                               185 190 195

```

gag aac ttc ctg cgc atg atg ttc ggt tac cca acc gag cca tac gag	739
Glu Asn Phe Leu Arg Met Met Phe Gly Tyr Pro Thr Glu Pro Tyr Glu	
200 205 210	
atc gac cca atc atg gtc aag gct ctg gac aag ctg ctc atc ctg cac	787
Ile Asp Pro Ile Met Val Lys Ala Leu Asp Lys Leu Leu Ile Leu His	
215 220 225	
gct gac cac gag cag aac tgc tcc acc tcc acc gtt cgt atg atc ggt	835
Ala Asp His Glu Gln Asn Cys Ser Thr Ser Thr Val Arg Met Ile Gly	
230 235 240 245	
tcc gca cag gcc aac atg ttt gtc tcc atc gct ggt ggc atc aac gct	883
Ser Ala Gln Ala Asn Met Phe Val Ser Ile Ala Gly Gly Ile Asn Ala	
250 255 260	
ctg tcc ggc cca ctg cac ggt ggc gca aac cag gct gtt ctg gag atg	931
Leu Ser Gly Pro Leu His Gly Gly Ala Asn Gln Ala Val Leu Glu Met	
265 270 275	
ctc gaa gac atc aag agc aac cac ggt ggc gac gca acc gag ttc atg	979
Leu Glu Asp Ile Lys Ser Asn His Gly Gly Asp Ala Thr Glu Phe Met	
280 285 290	
aac aag gtc aag aac aag gaa gac ggc gtc cgc ctc atg ggc ttc gga	1027
Asn Lys Val Lys Asn Lys Glu Asp Gly Val Arg Leu Met Gly Phe Gly	
295 300 305	
cac cgc gtt tac aag aac tac gat cca cgt gca gca atc gtc aag gag	1075
His Arg Val Tyr Lys Asn Tyr Asp Pro Arg Ala Ala Ile Val Lys Glu	
310 315 320 325	
acc gca cac gag atc ctc gag cac ctc ggt ggc gac gat ctt ctg gat	1123
Thr Ala His Glu Ile Leu Glu His Leu Gly Gly Asp Asp Leu Leu Asp	
330 335 340	
ctg gca atc aag ctg gaa gaa att gca ctg gct gat gat tac ttc atc	1171
Leu Ala Ile Lys Leu Glu Glu Ile Ala Leu Ala Asp Asp Tyr Phe Ile	
345 350 355	
tcc cgc aag ctc tac ccg aac gta gac ttc tac acc ggc ctg atc tac	1219
Ser Arg Lys Leu Tyr Pro Asn Val Asp Phe Tyr Thr Gly Leu Ile Tyr	
360 365 370	
cgc gca atg ggc ttc cca act gac ttc ttc acc gta ttg ttc gca atc	1267
Arg Ala Met Gly Phe Pro Thr Asp Phe Phe Thr Val Leu Phe Ala Ile	
375 380 385	
ggt cgt ctg cca gga tgg atc gct cac tac cgc gag cag ctc ggt gca	1315
Gly Arg Leu Pro Gly Trp Ile Ala His Tyr Arg Glu Gln Leu Gly Ala	
390 395 400 405	
gca ggc aac aag atc aac cgc cca cgc cag gtc tac acc ggc aac gaa	1363
Ala Gly Asn Lys Ile Asn Arg Pro Arg Gln Val Tyr Thr Gly Asn Glu	
410 415 420	
tcc cgc aag ttg gtt cct cgc gag gag cgc taaatttagc ggatgattct	1413
Ser Arg Lys Leu Val Pro Arg Glu Glu Arg	
425 430	
cgt	1416

<210> 546
 <211> 431
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 546

```

Val Ala Thr Asp Asn Asn Lys Ala Val Leu His Tyr Pro Gly Gly Glu
  1              5              10              15

Phe Glu Met Asp Ile Ile Glu Ala Ser Glu Gly Asn Asn Gly Val Val
      20              25              30

Leu Gly Lys Met Leu Ser Glu Thr Gly Leu Ile Thr Phe Asp Pro Gly
      35              40              45

Tyr Val Ser Thr Gly Ser Thr Glu Ser Lys Ile Thr Tyr Ile Asp Gly
      50              55              60

Asp Ala Gly Ile Leu Arg Tyr Arg Gly Tyr Asp Ile Ala Asp Leu Ala
      65              70              75              80

Glu Asn Ala Thr Phe Asn Glu Val Ser Tyr Leu Leu Ile Asn Gly Glu
      85              90              95

Leu Pro Thr Pro Asp Glu Leu His Lys Phe Asn Asp Glu Ile Arg His
      100             105             110

His Thr Leu Leu Asp Glu Asp Phe Lys Ser Gln Phe Asn Val Phe Pro
      115             120             125

Arg Asp Ala His Pro Met Ala Thr Leu Ala Ser Ser Val Asn Ile Leu
      130             135             140

Ser Thr Tyr Tyr Gln Asp Gln Leu Asn Pro Leu Asp Glu Ala Gln Leu
      145             150             155             160

Asp Lys Ala Thr Val Arg Leu Met Ala Lys Val Pro Met Leu Ala Ala
      165             170             175

Tyr Ala His Arg Ala Arg Lys Gly Ala Pro Tyr Met Tyr Pro Asp Asn
      180             185             190

Ser Leu Asn Ala Arg Glu Asn Phe Leu Arg Met Met Phe Gly Tyr Pro
      195             200             205

Thr Glu Pro Tyr Glu Ile Asp Pro Ile Met Val Lys Ala Leu Asp Lys
      210             215             220

Leu Leu Ile Leu His Ala Asp His Glu Gln Asn Cys Ser Thr Ser Thr
      225             230             235             240

Val Arg Met Ile Gly Ser Ala Gln Ala Asn Met Phe Val Ser Ile Ala
      245             250             255

Gly Gly Ile Asn Ala Leu Ser Gly Pro Leu His Gly Gly Ala Asn Gln
      260             265             270

Ala Val Leu Glu Met Leu Glu Asp Ile Lys Ser Asn His Gly Gly Asp
      275             280             285
  
```

Ala Thr Glu Phe Met Asn Lys Val Lys Asn Lys Glu Asp Gly Val Arg
290 295 300

Leu Met Gly Phe Gly His Arg Val Tyr Lys Asn Tyr Asp Pro Arg Ala
305 310 315 320

Ala Ile Val Lys Glu Thr Ala His Glu Ile Leu Glu His Leu Gly Gly
325 330 335

Asp Asp Leu Leu Asp Leu Ala Ile Lys Leu Glu Glu Ile Ala Leu Ala
340 345 350

Asp Asp Tyr Phe Ile Ser Arg Lys Leu Tyr Pro Asn Val Asp Phe Tyr
355 360 365

Thr Gly Leu Ile Tyr Arg Ala Met Gly Phe Pro Thr Asp Phe Phe Thr
370 375 380

Val Leu Phe Ala Ile Gly Arg Leu Pro Gly Trp Ile Ala His Tyr Arg
385 390 395 400

Glu Gln Leu Gly Ala Ala Gly Asn Lys Ile Asn Arg Pro Arg Gln Val
405 410 415

Tyr Thr Gly Asn Glu Ser Arg Lys Leu Val Pro Arg Glu Glu Arg
420 425 430

<210> 547

<211> 942

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(919)

<223> RXA02621

<400> 547

atgtacctga ctggtgcgcg acacttcgct cactaaagtt tttaaagatt tcgcttgaag 60

gcagaccata aggtctgcct ttctgcgtat taatgagtac atg tct gaa ctt att 115
Met Ser Glu Leu Ile
1 5

tgt gga cca gct att ctc ttc gca cca gct gga cgt gct gag atc att 163
Cys Gly Pro Ala Ile Leu Phe Ala Pro Ala Gly Arg Ala Glu Ile Ile
10 15 20

cca aaa gca gca tcg aag gcc gat atg gtc atc att gat ttg gaa gat 211
Pro Lys Ala Ala Ser Lys Ala Asp Met Val Ile Ile Asp Leu Glu Asp
25 30 35

ggg gca ggg gag gta gac cgt gag gtc gcc tac agg aac att aga gaa 259
Gly Ala Gly Glu Val Asp Arg Glu Val Ala Tyr Arg Asn Ile Arg Glu
40 45 50

tcg ggg ttg gat cct aaa cga acc att gtg aga acc gta ggg ccg agc 307
Ser Gly Leu Asp Pro Lys Arg Thr Ile Val Arg Thr Val Gly Pro Ser
55 60 65

gat cca cac ttt ttg gct gac gtg gag atg gtg aag tcc acg gat ttc 355
 Asp Pro His Phe Leu Ala Asp Val Glu Met Val Lys Ser Thr Asp Phe
 70 75 80 85

 aca ctt gtt atg gtt cct aaa ctt ctt ggc agc gtg cct gag gaa tta 403
 Thr Leu Val Met Val Pro Lys Leu Leu Gly Ser Val Pro Glu Glu Leu
 90 95 100

 gat ggc ctc aac att atc gcc atg att gaa acc cct cag gct gca acc 451
 Asp Gly Leu Asn Ile Ile Ala Met Ile Glu Thr Pro Gln Ala Ala Thr
 105 110 115

 agc att cct cag att gct gcg gac cct aaa gtc gtt gga atg ttc tgg 499
 Ser Ile Pro Gln Ile Ala Ala Asp Pro Lys Val Val Gly Met Phe Trp
 120 125 130

 ggc gcg gag gat ctc aca cac ctc ttg gga ggc act cat tct agg ttc 547
 Gly Ala Glu Asp Leu Thr His Leu Leu Gly Gly Thr His Ser Arg Phe
 135 140 145

 ttg ggt gat gag tcc aat gaa ggc tcc tac cga gac acc atg agg ctt 595
 Leu Gly Asp Glu Ser Asn Glu Gly Ser Tyr Arg Asp Thr Met Arg Leu
 150 155 160 165

 aca cgc gcc ctg atg cac ctc cac gcg gcg gcg aat ggg aag ttc acc 643
 Thr Arg Ala Leu Met His Leu His Ala Ala Asn Gly Lys Phe Thr
 170 175 180

 att gat gcc atc cat gcg gat ttc cac gat gaa gag ggc ctc tat tta 691
 Ile Asp Ala Ile His Ala Asp Phe His Asp Glu Glu Gly Leu Tyr Leu
 185 190 195

 gaa gcg gtc gat gct gcg cgg act ggt ttc gct ggc acc gca tgc att 739
 Glu Ala Val Asp Ala Ala Arg Thr Gly Phe Ala Gly Thr Ala Cys Ile
 200 205 210

 cac ccc aag cag atc gag att gtt cgg aga gcc tat cgg cca gag gct 787
 His Pro Lys Gln Ile Glu Ile Val Arg Arg Ala Tyr Arg Pro Glu Ala
 215 220 225

 aac cag ttg gag tgg gcg aag aaa gtg gtg gag gaa gca gaa aac cat 835
 Asn Gln Leu Glu Trp Ala Lys Lys Val Val Glu Glu Ala Glu Asn His
 230 235 240 245

 cca ggt gcg ttc aaa ctg gat ggt cag atg att gat gct ccg ttg att 883
 Pro Gly Ala Phe Lys Leu Asp Gly Gln Met Ile Asp Ala Pro Leu Ile
 250 255 260

 tcg cag gcg cgg atg gtt att tcg cgt cag cct gct tgattagttc 929
 Ser Gln Ala Arg Met Val Ile Ser Arg Gln Pro Ala
 265 270

 aagcgttttt tcg 942

<210> 548

<211> 273

<212> PRT

<213> Corynebacterium glutamicum

<400> 548

Met Ser Glu Leu Ile Cys Gly Pro Ala Ile Leu Phe Ala Pro Ala Gly
 1 5 10 15

Arg Ala Glu Ile Ile Pro Lys Ala Ala Ser Lys Ala Asp Met Val Ile
 20 25 30

Ile Asp Leu Glu Asp Gly Ala Gly Glu Val Asp Arg Glu Val Ala Tyr
 35 40 45

Arg Asn Ile Arg Glu Ser Gly Leu Asp Pro Lys Arg Thr Ile Val Arg
 50 55 60

Thr Val Gly Pro Ser Asp Pro His Phe Leu Ala Asp Val Glu Met Val
 65 70 75 80

Lys Ser Thr Asp Phe Thr Leu Val Met Val Pro Lys Leu Leu Gly Ser
 85 90 95

Val Pro Glu Glu Leu Asp Gly Leu Asn Ile Ile Ala Met Ile Glu Thr
 100 105 110

Pro Gln Ala Ala Thr Ser Ile Pro Gln Ile Ala Ala Asp Pro Lys Val
 115 120 125

Val Gly Met Phe Trp Gly Ala Glu Asp Leu Thr His Leu Leu Gly Gly
 130 135 140

Thr His Ser Arg Phe Leu Gly Asp Glu Ser Asn Glu Gly Ser Tyr Arg
 145 150 155 160

Asp Thr Met Arg Leu Thr Arg Ala Leu Met His Leu His Ala Ala Ala
 165 170 175

Asn Gly Lys Phe Thr Ile Asp Ala Ile His Ala Asp Phe His Asp Glu
 180 185 190

Glu Gly Leu Tyr Leu Glu Ala Val Asp Ala Ala Arg Thr Gly Phe Ala
 195 200 205

Gly Thr Ala Cys Ile His Pro Lys Gln Ile Glu Ile Val Arg Arg Ala
 210 215 220

Tyr Arg Pro Glu Ala Asn Gln Leu Glu Trp Ala Lys Lys Val Val Glu
 225 230 235 240

Glu Ala Glu Asn His Pro Gly Ala Phe Lys Leu Asp Gly Gln Met Ile
 245 250 255

Asp Ala Pro Leu Ile Ser Gln Ala Arg Met Val Ile Ser Arg Gln Pro
 260 265 270

Ala

<210> 549

<211> 2337

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2314)

<223> RXN00519

<400> 549

```

tttccatgcg gggctgaaac tgccaccata ggcgccagca attagtagaa cactgtattc 60

taggtagctg aacaaaagag cccatcaacc aaggagactc atg gct aag atc atc 115
                                         Met Ala Lys Ile Ile
                                         1                               5

tgg acc cgc acc gac gaa gca ccg ctg ctc gcg acc tac tcg ctg aag 163
Trp Thr Arg Thr Asp Glu Ala Pro Leu Leu Ala Thr Tyr Ser Leu Lys
                        10                               15                               20

ccg gtc gtc gag gca ttt gct gct acc gcg ggc att gag gtc gag acc 211
Pro Val Val Glu Ala Phe Ala Ala Thr Ala Gly Ile Glu Val Glu Thr
                        25                               30                               35

cgg gac att tca ctc gct gga cgc atc ctc gcc cag ttc cca gag cgc 259
Arg Asp Ile Ser Leu Ala Gly Arg Ile Leu Ala Gln Phe Pro Glu Arg
                        40                               45                               50

ctc acc gaa gat cag aag gta ggc aac gca ctc gca gaa ctc ggc gag 307
Leu Thr Glu Asp Gln Lys Val Gly Asn Ala Leu Ala Glu Leu Gly Glu
                        55                               60                               65

ctt gct aag act cct gaa gca aac atc att aag ctt cca aac atc tcc 355
Leu Ala Lys Thr Pro Glu Ala Asn Ile Ile Lys Leu Pro Asn Ile Ser
                        70                               75                               80                               85

gct tct gtt cca cag ctc aag gct gct att aag gaa ctg cag gac cag 403
Ala Ser Val Pro Gln Leu Lys Ala Ala Ile Lys Glu Leu Gln Asp Gln
                        90                               95                               100

ggc tac gac atc cca gaa ctg cct gat aac gcc acc acc gac gag gaa 451
Gly Tyr Asp Ile Pro Glu Leu Pro Asp Asn Ala Thr Thr Asp Glu Glu
                        105                               110                               115

aaa gac atc ctc gca cgc tac aac gct gtt aag ggt tcc gct gtg aac 499
Lys Asp Ile Leu Ala Arg Tyr Asn Ala Val Lys Gly Ser Ala Val Asn
                        120                               125                               130

cca gtg ctg cgt gaa ggc aac tct gac cgc cgc gca cca atc gct gtc 547
Pro Val Leu Arg Glu Gly Asn Ser Asp Arg Arg Ala Pro Ile Ala Val
                        135                               140                               145

aag aac ttt gtt aag aag ttc cca cac cgc atg ggc gag tgg tct gca 595
Lys Asn Phe Val Lys Lys Phe Pro His Arg Met Gly Glu Trp Ser Ala
                        150                               155                               160                               165

gat tcc aag acc aac gtt gca acc atg gat gca aac gac ttc cgc cac 643
Asp Ser Lys Thr Asn Val Ala Thr Met Asp Ala Asn Asp Phe Arg His
                        170                               175                               180

aac gag aag tcc atc atc ctc gac gct gct gat gaa gtt cag atc aag 691
Asn Glu Lys Ser Ile Ile Leu Asp Ala Ala Asp Glu Val Gln Ile Lys
                        185                               190                               195

cac atc gca gct gac ggc acc gag acc atc ctc aag gac agc ctc aag 739

```

His	Ile	Ala	Ala	Asp	Gly	Thr	Glu	Thr	Ile	Leu	Lys	Asp	Ser	Leu	Lys	
		200					205					210				
ctt	ctt	gaa	ggc	gaa	gtt	cta	gac	gga	acc	gtt	ctg	tcc	gca	aag	gca	787
Leu	Leu	Glu	Gly	Glu	Val	Leu	Asp	Gly	Thr	Val	Leu	Ser	Ala	Lys	Ala	
		215				220				225						
ctg	gac	gca	ttc	ctt	ctc	gag	cag	gtc	gct	cgc	gca	aag	gca	gaa	ggc	835
Leu	Asp	Ala	Phe	Leu	Leu	Glu	Gln	Val	Ala	Arg	Ala	Lys	Ala	Glu	Gly	
230					235				240						245	
atc	ctc	ttc	tcc	gca	cac	ctg	aag	gcc	acc	atg	atg	aag	gtc	tcc	gac	883
Ile	Leu	Phe	Ser	Ala	His	Leu	Lys	Ala	Thr	Met	Met	Lys	Val	Ser	Asp	
				250				255						260		
cca	atc	atc	ttc	ggc	cac	gtt	gtg	cgc	gct	tac	ttc	gca	gac	gtt	ttc	931
Pro	Ile	Ile	Phe	Gly	His	Val	Val	Arg	Ala	Tyr	Phe	Ala	Asp	Val	Phe	
			265					270					275			
gca	cag	tac	ggc	gag	cag	ctg	ctc	gca	gct	ggc	ctc	aac	ggc	gaa	aac	979
Ala	Gln	Tyr	Gly	Glu	Gln	Leu	Leu	Ala	Ala	Gly	Leu	Asn	Gly	Glu	Asn	
		280				285						290				
ggc	ctc	gct	gca	atc	ctc	tcc	ggc	ttg	gag	tcc	ctg	gac	aac	ggc	gaa	1027
Gly	Leu	Ala	Ala	Ile	Leu	Ser	Gly	Leu	Glu	Ser	Leu	Asp	Asn	Gly	Glu	
	295				300						305					
gaa	atc	aag	gct	gca	ttc	gag	aag	ggc	ttg	gaa	gac	ggc	cca	gac	ctg	1075
Glu	Ile	Lys	Ala	Ala	Phe	Glu	Lys	Gly	Leu	Glu	Asp	Gly	Pro	Asp	Leu	
310					315				320						325	
gcc	atg	gtt	aac	tcc	gct	cgc	ggc	atc	acc	aac	ctg	cat	gtc	cct	tcc	1123
Ala	Met	Val	Asn	Ser	Ala	Arg	Gly	Ile	Thr	Asn	Leu	His	Val	Pro	Ser	
				330				335						340		
gat	gtc	atc	gtg	gac	gct	tcc	atg	cca	gca	atg	att	cgt	acc	tcc	ggc	1171
Asp	Val	Ile	Val	Asp	Ala	Ser	Met	Pro	Ala	Met	Ile	Arg	Thr	Ser	Gly	
			345					350					355			
cac	atg	tgg	aac	aaa	gac	gac	cag	gag	cag	gac	acc	ctg	gca	atc	atc	1219
His	Met	Trp	Asn	Lys	Asp	Asp	Gln	Glu	Gln	Asp	Thr	Leu	Ala	Ile	Ile	
		360					365					370				
cca	gac	tcc	tcc	tac	gct	ggc	gtc	tac	cag	acc	gtt	atc	gaa	gac	tgc	1267
Pro	Asp	Ser	Ser	Tyr	Ala	Gly	Val	Tyr	Gln	Thr	Val	Ile	Glu	Asp	Cys	
		375				380					385					
cgc	aag	aac	ggc	gca	ttc	gat	cca	acc	acc	atg	ggc	acc	gtc	cct	aac	1315
Arg	Lys	Asn	Gly	Ala	Phe	Asp	Pro	Thr	Thr	Met	Gly	Thr	Val	Pro	Asn	
390					395				400						405	
gtt	ggc	ctg	atg	gct	cag	aag	gct	gaa	gag	tac	ggc	tcc	cat	gac	aag	1363
Val	Gly	Leu	Met	Ala	Gln	Lys	Ala	Glu	Glu	Tyr	Gly	Ser	His	Asp	Lys	
				410				415					420			
acc	ttc	cgc	atc	gaa	gca	gac	ggc	gtg	gtt	cag	gtt	gtt	tcc	tcc	aac	1411
Thr	Phe	Arg	Ile	Glu	Ala	Asp	Gly	Val	Val	Gln	Val	Val	Ser	Ser	Asn	
			425					430					435			
ggc	gac	gtt	ctc	atc	gag	cac	gac	gtt	gag	gca	aat	gac	atc	tgg	cgt	1459
Gly	Asp	Val	Leu	Ile	Glu	His	Asp	Val	Glu	Ala	Asn	Asp	Ile	Trp	Arg	

440	445	450	
gca tgc cag gtc aag gat gcc cca atc cag gat tgg gta aag ctt gct Ala Cys Gln Val Lys Asp Ala Pro Ile Gln Asp Trp Val Lys Leu Ala 455 460 465			1507
gtc acc cgc tcc cgt ctc tcc gga atg cct gca gtg ttc tgg ttg gat Val Thr Arg Ser Arg Leu Ser Gly Met Pro Ala Val Phe Trp Leu Asp 470 475 480 485			1555
cca gag cgc gca cac gac cgc aac ctg gct tcc ctc gtt gag aag tac Pro Glu Arg Ala His Asp Arg Asn Leu Ala Ser Leu Val Glu Lys Tyr 490 495 500			1603
ctg gct gac cac gac acc gag ggc ctg gac atc cag atc ctc tcc cct Leu Ala Asp His Asp Thr Glu Gly Leu Asp Ile Gln Ile Leu Ser Pro 505 510 515			1651
gtt gag gca acc cag ctc tcc atc gac cgc atc cgc cgt ggc gag gac Val Glu Ala Thr Gln Leu Ser Ile Asp Arg Ile Arg Arg Gly Glu Asp 520 525 530			1699
acc atc tct gtc acc ggt aac gtt ctg cgt gac tac aac acc gac ctc Thr Ile Ser Val Thr Gly Asn Val Leu Arg Asp Tyr Asn Thr Asp Leu 535 540 545			1747
ttc cca atc ctg gag ctg ggc acc tct gca aag atg ctg tct gtc gtt Phe Pro Ile Leu Glu Leu Gly Thr Ser Ala Lys Met Leu Ser Val Val 550 555 560 565			1795
cct ttg atg gct ggc ggc gga ctg ttc gag acc ggt gct ggt gga tct Pro Leu Met Ala Gly Gly Gly Leu Phe Glu Thr Gly Ala Gly Gly Ser 570 575 580			1843
gct cct aag cac gtc cag cag gtt cag gaa gaa aac cac ctg cgt tgg Ala Pro Lys His Val Gln Gln Val Gln Glu Glu Asn His Leu Arg Trp 585 590 595			1891
gat tcc ctc ggt gag ttc ctc gca ctg gct gag tcc ttc cgc cac gag Asp Ser Leu Gly Glu Phe Leu Ala Leu Ala Glu Ser Phe Arg His Glu 600 605 610			1939
ctc aac aac aac ggc aac acc aag gcc ggc gtt ctg gct gac gct ctg Leu Asn Asn Asn Gly Asn Thr Lys Ala Gly Val Leu Ala Asp Ala Leu 615 620 625			1987
gac aag gca act gag aag ctg ctg aac gaa gag aag tcc cca tcc cgc Asp Lys Ala Thr Glu Lys Leu Leu Asn Glu Glu Lys Ser Pro Ser Arg 630 635 640 645			2035
aag gtt ggc gag atc gac aac cgt ggc tcc cac ttc tgg ctg acc aag Lys Val Gly Glu Ile Asp Asn Arg Gly Ser His Phe Trp Leu Thr Lys 650 655 660			2083
ttc tgg gct gac gag ctc gct gct cag acc gag gac gca gat ctg gct Phe Trp Ala Asp Glu Leu Ala Ala Gln Thr Glu Asp Ala Asp Leu Ala 665 670 675			2131
gct acc ttc gca cca gtc gca gaa gca ctg aac aca ggc gct gca gac Ala Thr Phe Ala Pro Val Ala Glu Ala Leu Asn Thr Gly Ala Ala Asp 680 685 690			2179

atc gat gct gca ctg ctc gca gtt cag ggt gga gca act gac ctt ggt 2227
 Ile Asp Ala Ala Leu Leu Ala Val Gln Gly Gly Ala Thr Asp Leu Gly
 695 700 705

ggc tac tac tcc cct aac gag gag aag ctc acc aac atc atg cgc cca 2275
 Gly Tyr Tyr Ser Pro Asn Glu Glu Lys Leu Thr Asn Ile Met Arg Pro
 710 715 720 725

gtc gca cag ttc aac gag atc gtt gac gca ctg aag aag taaagtctct 2324
 Val Ala Gln Phe Asn Glu Ile Val Asp Ala Leu Lys Lys
 730 735

tcacaaaaag cgc 2337

<210> 550

<211> 738

<212> PRT

<213> Corynebacterium glutamicum

<400> 550

Met Ala Lys Ile Ile Trp Thr Arg Thr Asp Glu Ala Pro Leu Leu Ala
 1 5 10 15

Thr Tyr Ser Leu Lys Pro Val Val Glu Ala Phe Ala Ala Thr Ala Gly
 20 25 30

Ile Glu Val Glu Thr Arg Asp Ile Ser Leu Ala Gly Arg Ile Leu Ala
 35 40 45

Gln Phe Pro Glu Arg Leu Thr Glu Asp Gln Lys Val Gly Asn Ala Leu
 50 55 60

Ala Glu Leu Gly Glu Leu Ala Lys Thr Pro Glu Ala Asn Ile Ile Lys
 65 70 75 80

Leu Pro Asn Ile Ser Ala Ser Val Pro Gln Leu Lys Ala Ala Ile Lys
 85 90 95

Glu Leu Gln Asp Gln Gly Tyr Asp Ile Pro Glu Leu Pro Asp Asn Ala
 100 105 110

Thr Thr Asp Glu Glu Lys Asp Ile Leu Ala Arg Tyr Asn Ala Val Lys
 115 120 125

Gly Ser Ala Val Asn Pro Val Leu Arg Glu Gly Asn Ser Asp Arg Arg
 130 135 140

Ala Pro Ile Ala Val Lys Asn Phe Val Lys Lys Phe Pro His Arg Met
 145 150 155 160

Gly Glu Trp Ser Ala Asp Ser Lys Thr Asn Val Ala Thr Met Asp Ala
 165 170 175

Asn Asp Phe Arg His Asn Glu Lys Ser Ile Ile Leu Asp Ala Ala Asp
 180 185 190

Glu Val Gln Ile Lys His Ile Ala Ala Asp Gly Thr Glu Thr Ile Leu
 195 200 205

Lys Asp Ser Leu Lys Leu Leu Glu Gly Glu Val Leu Asp Gly Thr Val
 210 215 220
 Leu Ser Ala Lys Ala Leu Asp Ala Phe Leu Leu Glu Gln Val Ala Arg
 225 230 235 240
 Ala Lys Ala Glu Gly Ile Leu Phe Ser Ala His Leu Lys Ala Thr Met
 245 250 255
 Met Lys Val Ser Asp Pro Ile Ile Phe Gly His Val Val Arg Ala Tyr
 260 265 270
 Phe Ala Asp Val Phe Ala Gln Tyr Gly Glu Gln Leu Leu Ala Ala Gly
 275 280 285
 Leu Asn Gly Glu Asn Gly Leu Ala Ala Ile Leu Ser Gly Leu Glu Ser
 290 295 300
 Leu Asp Asn Gly Glu Glu Ile Lys Ala Ala Phe Glu Lys Gly Leu Glu
 305 310 315 320
 Asp Gly Pro Asp Leu Ala Met Val Asn Ser Ala Arg Gly Ile Thr Asn
 325 330 335
 Leu His Val Pro Ser Asp Val Ile Val Asp Ala Ser Met Pro Ala Met
 340 345 350
 Ile Arg Thr Ser Gly His Met Trp Asn Lys Asp Asp Gln Glu Gln Asp
 355 360 365
 Thr Leu Ala Ile Ile Pro Asp Ser Ser Tyr Ala Gly Val Tyr Gln Thr
 370 375 380
 Val Ile Glu Asp Cys Arg Lys Asn Gly Ala Phe Asp Pro Thr Thr Met
 385 390 395 400
 Gly Thr Val Pro Asn Val Gly Leu Met Ala Gln Lys Ala Glu Glu Tyr
 405 410 415
 Gly Ser His Asp Lys Thr Phe Arg Ile Glu Ala Asp Gly Val Val Gln
 420 425 430
 Val Val Ser Ser Asn Gly Asp Val Leu Ile Glu His Asp Val Glu Ala
 435 440 445
 Asn Asp Ile Trp Arg Ala Cys Gln Val Lys Asp Ala Pro Ile Gln Asp
 450 455 460
 Trp Val Lys Leu Ala Val Thr Arg Ser Arg Leu Ser Gly Met Pro Ala
 465 470 475 480
 Val Phe Trp Leu Asp Pro Glu Arg Ala His Asp Arg Asn Leu Ala Ser
 485 490 495
 Leu Val Glu Lys Tyr Leu Ala Asp His Asp Thr Glu Gly Leu Asp Ile
 500 505 510
 Gln Ile Leu Ser Pro Val Glu Ala Thr Gln Leu Ser Ile Asp Arg Ile
 515 520 525
 Arg Arg Gly Glu Asp Thr Ile Ser Val Thr Gly Asn Val Leu Arg Asp

530 535 540
 Tyr Asn Thr Asp Leu Phe Pro Ile Leu Glu Leu Gly Thr Ser Ala Lys
 545 550 555 560
 Met Leu Ser Val Val Pro Leu Met Ala Gly Gly Gly Leu Phe Glu Thr
 565 570 575
 Gly Ala Gly Gly Ser Ala Pro Lys His Val Gln Gln Val Gln Glu Glu
 580 585 590
 Asn His Leu Arg Trp Asp Ser Leu Gly Glu Phe Leu Ala Leu Ala Glu
 595 600 605
 Ser Phe Arg His Glu Leu Asn Asn Asn Gly Asn Thr Lys Ala Gly Val
 610 615 620
 Leu Ala Asp Ala Leu Asp Lys Ala Thr Glu Lys Leu Leu Asn Glu Glu
 625 630 635 640
 Lys Ser Pro Ser Arg Lys Val Gly Glu Ile Asp Asn Arg Gly Ser His
 645 650 655
 Phe Trp Leu Thr Lys Phe Trp Ala Asp Glu Leu Ala Ala Gln Thr Glu
 660 665 670
 Asp Ala Asp Leu Ala Ala Thr Phe Ala Pro Val Ala Glu Ala Leu Asn
 675 680 685
 Thr Gly Ala Ala Asp Ile Asp Ala Ala Leu Leu Ala Val Gln Gly Gly
 690 695 700
 Ala Thr Asp Leu Gly Gly Tyr Tyr Ser Pro Asn Glu Glu Lys Leu Thr
 705 710 715 720
 Asn Ile Met Arg Pro Val Ala Gln Phe Asn Glu Ile Val Asp Ala Leu
 725 730 735
 Lys Lys

<210> 551
 <211> 1059
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1059)
 <223> FRXA00521

<400> 551
 ctc gac gct gct gat gaa gtt cag atc aag cac atc gca gct gac ggc 48
 Leu Asp Ala Ala Asp Glu Val Gln Ile Lys His Ile Ala Ala Asp Gly
 1 5 10 15
 acc gag acc atc ctc aag gac agc ctc aag ctt ctt gaa ggc gaa gtt 96
 Thr Glu Thr Ile Leu Lys Asp Ser Leu Lys Leu Leu Glu Gly Glu Val
 20 25 30

cta gac gga acc gtt ctg tcc gca aag gca ctg gac gca ttc ctt ctc	144
Leu Asp Gly Thr Val Leu Ser Ala Lys Ala Leu Asp Ala Phe Leu Leu	
35 40 45	
gag cag gtc gct cgc gca aag gca gaa ggt atc ctc ttc tcc gca cac	192
Glu Gln Val Ala Arg Ala Lys Ala Glu Gly Ile Leu Phe Ser Ala His	
50 55 60	
ctg aag gcc acc atg atg aag gtc tcc gac cca atc atc ttc ggc cac	240
Leu Lys Ala Thr Met Met Lys Val Ser Asp Pro Ile Ile Phe Gly His	
65 70 75 80	
gtt gtg cgc gct tac ttc gca gac gtt ttc gca cag tac ggt gag cag	288
Val Val Arg Ala Tyr Phe Ala Asp Val Phe Ala Gln Tyr Gly Glu Gln	
85 90 95	
ctg ctc gca gct ggc ctc aac ggc gaa aac ggc ctc gct gca atc ctc	336
Leu Leu Ala Ala Gly Leu Asn Gly Glu Asn Gly Leu Ala Ala Ile Leu	
100 105 110	
tcc ggc ttg gag tcc ctg gac aac ggc gaa gaa atc aag gct gca ttc	384
Ser Gly Leu Glu Ser Leu Asp Asn Gly Glu Glu Ile Lys Ala Ala Phe	
115 120 125	
gag aag ggc ttg gaa gac ggc cca gac ctg gcc atg gtt aac tcc gct	432
Glu Lys Gly Leu Glu Asp Gly Pro Asp Leu Ala Met Val Asn Ser Ala	
130 135 140	
cgc ggc atc acc aac ctg cat gtc cct tcc gat gtc atc gtg gac gct	480
Arg Gly Ile Thr Asn Leu His Val Pro Ser Asp Val Ile Val Asp Ala	
145 150 155 160	
tcc atg cca gca atg att cgt acc tcc ggc cac atg tgg aac aaa gac	528
Ser Met Pro Ala Met Ile Arg Thr Ser Gly His Met Trp Asn Lys Asp	
165 170 175	
gac cag gag cag gac acc ctg gca atc atc cca gac tcc tcc tac gct	576
Asp Gln Glu Gln Asp Thr Leu Ala Ile Ile Pro Asp Ser Ser Tyr Ala	
180 185 190	
ggc gtc tac cag acc gtt atc gaa gac tgc cgc aag aac ggc gca ttc	624
Gly Val Tyr Gln Thr Val Ile Glu Asp Cys Arg Lys Asn Gly Ala Phe	
195 200 205	
gat cca acc acc atg ggt acc gtc cct aac gtt ggt ctg atg gct cag	672
Asp Pro Thr Thr Met Gly Thr Val Pro Asn Val Gly Leu Met Ala Gln	
210 215 220	
aag gct gaa gag tac ggc tcc cat gac aag acc ttc cgc atc gaa gca	720
Lys Ala Glu Glu Tyr Gly Ser His Asp Lys Thr Phe Arg Ile Glu Ala	
225 230 235 240	
gac ggt gtg gtt cag gtt gtt tcc tcc aac ggc gac gtt ctc atc gag	768
Asp Gly Val Val Gln Val Val Ser Ser Asn Gly Asp Val Leu Ile Glu	
245 250 255	
cac gac gtt gag gca aat gac atc tgg cgt gca tgc cag gtc aag gat	816
His Asp Val Glu Ala Asn Asp Ile Trp Arg Ala Cys Gln Val Lys Asp	
260 265 270	
gcc cca atc cag gat tgg gta aag ctt gct gtc acc cgc tcc cgt ctc	864

Ala Pro Ile Gln Asp Trp Val Lys Leu Ala Val Thr Arg Ser Arg Leu
 275 280 285

tcc gga atg cct gca gtg ttc tgg ttg gat cca gag cgc gca cac gac 912
 Ser Gly Met Pro Ala Val Phe Trp Leu Asp Pro Glu Arg Ala His Asp
 290 295 300

cgc aac ctg gct tcc ctc gtt gag aag tac ctg gct gac cac gac acc 960
 Arg Asn Leu Ala Ser Leu Val Glu Lys Tyr Leu Ala Asp His Asp Thr
 305 310 315 320

gag ggc ctg gac atc cag atc ctc tac cct gtt gag gca acc cag ctc 1008
 Glu Gly Leu Asp Ile Gln Ile Leu Tyr Pro Val Glu Ala Thr Gln Leu
 325 330 335

tcc atc gac cgc atc cgc cgt ggc gag gac acc atc tct gtc acc ggt 1056
 Ser Ile Asp Arg Ile Arg Arg Gly Glu Asp Thr Ile Ser Val Thr Gly
 340 345 350

aac 1059
 Asn

<210> 552
 <211> 353
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 552
 Leu Asp Ala Ala Asp Glu Val Gln Ile Lys His Ile Ala Ala Asp Gly
 1 5 10 15

Thr Glu Thr Ile Leu Lys Asp Ser Leu Lys Leu Leu Glu Gly Glu Val
 20 25 30

Leu Asp Gly Thr Val Leu Ser Ala Lys Ala Leu Asp Ala Phe Leu Leu
 35 40 45

Glu Gln Val Ala Arg Ala Lys Ala Glu Gly Ile Leu Phe Ser Ala His
 50 55 60

Leu Lys Ala Thr Met Met Lys Val Ser Asp Pro Ile Ile Phe Gly His
 65 70 75 80

Val Val Arg Ala Tyr Phe Ala Asp Val Phe Ala Gln Tyr Gly Glu Gln
 85 90 95

Leu Leu Ala Ala Gly Leu Asn Gly Glu Asn Gly Leu Ala Ala Ile Leu
 100 105 110

Ser Gly Leu Glu Ser Leu Asp Asn Gly Glu Glu Ile Lys Ala Ala Phe
 115 120 125

Glu Lys Gly Leu Glu Asp Gly Pro Asp Leu Ala Met Val Asn Ser Ala
 130 135 140

Arg Gly Ile Thr Asn Leu His Val Pro Ser Asp Val Ile Val Asp Ala
 145 150 155 160

Ser Met Pro Ala Met Ile Arg Thr Ser Gly His Met Trp Asn Lys Asp

165										170					175				
Asp	Gln	Glu	Gln	Asp	Thr	Leu	Ala	Ile	Ile	Pro	Asp	Ser	Ser	Tyr	Ala				
			180						185					190					
Gly	Val	Tyr	Gln	Thr	Val	Ile	Glu	Asp	Cys	Arg	Lys	Asn	Gly	Ala	Phe				
		195					200					205							
Asp	Pro	Thr	Thr	Met	Gly	Thr	Val	Pro	Asn	Val	Gly	Leu	Met	Ala	Gln				
	210					215					220								
Lys	Ala	Glu	Glu	Tyr	Gly	Ser	His	Asp	Lys	Thr	Phe	Arg	Ile	Glu	Ala				
225					230					235					240				
Asp	Gly	Val	Val	Gln	Val	Val	Ser	Ser	Asn	Gly	Asp	Val	Leu	Ile	Glu				
				245					250					255					
His	Asp	Val	Glu	Ala	Asn	Asp	Ile	Trp	Arg	Ala	Cys	Gln	Val	Lys	Asp				
		260					265						270						
Ala	Pro	Ile	Gln	Asp	Trp	Val	Lys	Leu	Ala	Val	Thr	Arg	Ser	Arg	Leu				
	275					280						285							
Ser	Gly	Met	Pro	Ala	Val	Phe	Trp	Leu	Asp	Pro	Glu	Arg	Ala	His	Asp				
	290					295					300								
Arg	Asn	Leu	Ala	Ser	Leu	Val	Glu	Lys	Tyr	Leu	Ala	Asp	His	Asp	Thr				
305					310					315					320				
Glu	Gly	Leu	Asp	Ile	Gln	Ile	Leu	Tyr	Pro	Val	Glu	Ala	Thr	Gln	Leu				
			325					330						335					
Ser	Ile	Asp	Arg	Ile	Arg	Arg	Gly	Glu	Asp	Thr	Ile	Ser	Val	Thr	Gly				
		340					345						350						

Asn

<210> 553

<211> 1694

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1671)

<223> RXN02209

<400> 553

acc	gag	tcc	acc	gtt	gtt	cct	tcc	atc	gct	ggc	cct	aag	cgc	cca	cag	48
Thr	Glu	Ser	Thr	Val	Val	Pro	Ser	Ile	Ala	Gly	Pro	Lys	Arg	Pro	Gln	
1				5					10					15		

gac	cgc	atc	ctt	ctc	tcc	gag	gca	aag	gag	cag	ttc	cgt	aag	gat	ctg	96
Asp	Arg	Ile	Leu	Ser	Glu	Ala	Lys	Glu	Gln	Phe	Arg	Lys	Asp	Leu		
		20					25					30				

cca	acc	tac	acc	gac	gac	gct	gtt	tcc	gta	gac	acc	tcc	atc	cct	gca	144
Pro	Thr	Tyr	Thr	Asp	Asp	Ala	Val	Ser	Val	Asp	Thr	Ser	Ile	Pro	Ala	
		35					40					45				

acc cgc atg gtt aac gaa ggt ggc gga cag cct gaa ggc ggc gtc gaa	192
Thr Arg Met Val Asn Glu Gly Gly Gly Gln Pro Glu Gly Gly Val Glu	
50 55 60	
gct gac aac tac aac gct tcc tgg gct ggc tcc ggc gag tcc ttg gct	240
Ala Asp Asn Tyr Asn Ala Ser Trp Ala Gly Ser Gly Glu Ser Leu Ala	
65 70 75 80	
act ggc gca gaa gga cgt cct tcc aag cca gtc acc gtt gca tcc cca	288
Thr Gly Ala Glu Gly Arg Pro Ser Lys Pro Val Thr Val Ala Ser Pro	
85 90 95	
cag ggt ggc gag tac acc atc gac cac ggc atg gtt gca att gca tcc	336
Gln Gly Gly Glu Tyr Thr Ile Asp His Gly Met Val Ala Ile Ala Ser	
100 105 110	
atc acc tct tgc acc aac acc tct aac cca tcc gtg atg atc ggc gct	384
Ile Thr Ser Cys Thr Asn Thr Ser Asn Pro Ser Val Met Ile Gly Ala	
115 120 125	
ggc ctg atc gca cgt aag gca gca gaa aag ggc ctc aag tcc aag cct	432
Gly Leu Ile Ala Arg Lys Ala Ala Glu Lys Gly Leu Lys Ser Lys Pro	
130 135 140	
tgg gtt aag acc atc tgt gca cca ggt tcc cag gtt gtc gac ggc tac	480
Trp Val Lys Thr Ile Cys Ala Pro Gly Ser Gln Val Val Asp Gly Tyr	
145 150 155 160	
tac cag cgc gca gac ctc tgg aag gac ctt gag gcc atg ggc ttc tac	528
Tyr Gln Arg Ala Asp Leu Trp Lys Asp Leu Glu Ala Met Gly Phe Tyr	
165 170 175	
ctc tcc ggc ttc ggc tgc acc acc tgt att ggt aac tcc ggc cca ctg	576
Leu Ser Gly Phe Gly Cys Thr Thr Cys Ile Gly Asn Ser Gly Pro Leu	
180 185 190	
cca gag gaa atc tcc gct gcg atc aac gag cac gac ctg acc gca acc	624
Pro Glu Glu Ile Ser Ala Ala Ile Asn Glu His Asp Leu Thr Ala Thr	
195 200 205	
gca gtt ttg tcc ggt aac cgt aac ttc gag gga cgt atc tcc cct gac	672
Ala Val Leu Ser Gly Asn Arg Asn Phe Glu Gly Arg Ile Ser Pro Asp	
210 215 220	
gtt aag atg aac tac ctg gca tcc cca atc atg gtc att gct tac gca	720
Val Lys Met Asn Tyr Leu Ala Ser Pro Ile Met Val Ile Ala Tyr Ala	
225 230 235 240	
atc gct ggc acc atg gac ttc gac ttc gag aac gaa gct ctt gga cag	768
Ile Ala Gly Thr Met Asp Phe Asp Phe Glu Asn Glu Ala Leu Gly Gln	
245 250 255	
gac cag gac ggc aac gac gtc ttc ctg aag gac atc tgg cct tcc acc	816
Asp Gln Asp Gly Asn Asp Val Phe Leu Lys Asp Ile Trp Pro Ser Thr	
260 265 270	
gag gaa atc gaa gac acc atc cag cag gca atc tcc cgt gag ctt tac	864
Glu Glu Ile Glu Asp Thr Ile Gln Gln Ala Ile Ser Arg Glu Leu Tyr	
275 280 285	

gaa gct gac tac gca gat gtc ttc aag ggt gac aag cag tgg cag gaa	912
Glu Ala Asp Tyr Ala Asp Val Phe Lys Gly Asp Lys Gln Trp Gln Glu	
290 295 300	
ctc gat gtt cct acc ggt gac acc ttc gag tgg gac gag aac tcc acc	960
Leu Asp Val Pro Thr Gly Asp Thr Phe Glu Trp Asp Glu Asn Ser Thr	
305 310 315 320	
tac atc cgc aag gca cct tac ttc gac ggc atg cct gtc gag cca gtg	1008
Tyr Ile Arg Lys Ala Pro Tyr Phe Asp Gly Met Pro Val Glu Pro Val	
325 330 335	
gca gtc acc gac atc cag ggc gca cgc gtt ctg gct aag ctc ggc gac	1056
Ala Val Thr Asp Ile Gln Gly Ala Arg Val Leu Ala Lys Leu Gly Asp	
340 345 350	
tct gtc acc acc gac cac atc tcc cct gct tcc tcc att aag cca ggt	1104
Ser Val Thr Thr Asp His Ile Ser Pro Ala Ser Ser Ile Lys Pro Gly	
355 360 365	
acc cct gca gct cag tac ttg gat gag cac ggt gtg gaa cgc cac gac	1152
Thr Pro Ala Ala Gln Tyr Leu Asp Glu His Gly Val Glu Arg His Asp	
370 375 380	
tac aac tcc ctg ggt tcc agg cgt ggt aac cac gag gtc atg atg cgc	1200
Tyr Asn Ser Leu Gly Ser Arg Arg Gly Asn His Glu Val Met Met Arg	
385 390 395 400	
ggc acc ttc gcc aac atc cgc ctc cag aac cag ctg gtt gac atc gca	1248
Gly Thr Phe Ala Asn Ile Arg Leu Gln Asn Gln Leu Val Asp Ile Ala	
405 410 415	
ggt ggc tac acc cgc gac ttc acc cag gag ggt gct cca cag gcg ttc	1296
Gly Gly Tyr Thr Arg Asp Phe Thr Gln Glu Gly Ala Pro Gln Ala Phe	
420 425 430	
atc tac gac gct tcc gtc aac tac aag gct gct ggc att ccg ctg gtc	1344
Ile Tyr Asp Ala Ser Val Asn Tyr Lys Ala Ala Gly Ile Pro Leu Val	
435 440 445	
gtc ttg ggc ggc aag gag tac ggc acc ggt tct tcc cgt gac tgg gca	1392
Val Leu Gly Gly Lys Glu Tyr Gly Thr Gly Ser Ser Arg Asp Trp Ala	
450 455 460	
gct aag ggc act aac ctg ctc gga att cgc gca gtt atc acc gag tcc	1440
Ala Lys Gly Thr Asn Leu Leu Gly Ile Arg Ala Val Ile Thr Glu Ser	
465 470 475 480	
ttc gag cgt att cac cgc tcc aac ctc atc ggt atg ggc gtt gtc cca	1488
Phe Glu Arg Ile His Arg Ser Asn Leu Ile Gly Met Gly Val Val Pro	
485 490 495	
ctg cag ttc cct gca ggc gaa tcc cac gag tcc ctg ggc ctt gac ggc	1536
Leu Gln Phe Pro Ala Gly Glu Ser His Glu Ser Leu Gly Leu Asp Gly	
500 505 510	
acc gag acc ttc gac atc acc gga ctg acc gca ctt aac gag ggc gag	1584
Thr Glu Thr Phe Asp Ile Thr Gly Leu Thr Ala Leu Asn Glu Gly Glu	
515 520 525	
act cct aag act gtc aag gtc acc gca acc aag gag aac ggc gac gtc	1632

Thr Pro Lys Thr Val Lys Val Thr Ala Thr Lys Glu Asn Gly Asp Val
 530 535 540
 gtc gag ttc gac gca att tgt ccg cat cga cac ccc agg tgaggctgac 1681
 Val Glu Phe Asp Ala Ile Cys Pro His Arg His Pro Arg
 545 550 555
 tactaccgcc acg 1694
 <210> 554
 <211> 557
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 554
 Thr Glu Ser Thr Val Val Pro Ser Ile Ala Gly Pro Lys Arg Pro Gln
 1 5 10 15
 Asp Arg Ile Leu Leu Ser Glu Ala Lys Glu Gln Phe Arg Lys Asp Leu
 20 25 30
 Pro Thr Tyr Thr Asp Asp Ala Val Ser Val Asp Thr Ser Ile Pro Ala
 35 40 45
 Thr Arg Met Val Asn Glu Gly Gly Gly Gln Pro Glu Gly Gly Val Glu
 50 55 60
 Ala Asp Asn Tyr Asn Ala Ser Trp Ala Gly Ser Gly Glu Ser Leu Ala
 65 70 75 80
 Thr Gly Ala Glu Gly Arg Pro Ser Lys Pro Val Thr Val Ala Ser Pro
 85 90 95
 Gln Gly Gly Glu Tyr Thr Ile Asp His Gly Met Val Ala Ile Ala Ser
 100 105 110
 Ile Thr Ser Cys Thr Asn Thr Ser Asn Pro Ser Val Met Ile Gly Ala
 115 120 125
 Gly Leu Ile Ala Arg Lys Ala Ala Glu Lys Gly Leu Lys Ser Lys Pro
 130 135 140
 Trp Val Lys Thr Ile Cys Ala Pro Gly Ser Gln Val Val Asp Gly Tyr
 145 150 155 160
 Tyr Gln Arg Ala Asp Leu Trp Lys Asp Leu Glu Ala Met Gly Phe Tyr
 165 170 175
 Leu Ser Gly Phe Gly Cys Thr Thr Cys Ile Gly Asn Ser Gly Pro Leu
 180 185 190
 Pro Glu Glu Ile Ser Ala Ala Ile Asn Glu His Asp Leu Thr Ala Thr
 195 200 205
 Ala Val Leu Ser Gly Asn Arg Asn Phe Glu Gly Arg Ile Ser Pro Asp
 210 215 220
 Val Lys Met Asn Tyr Leu Ala Ser Pro Ile Met Val Ile Ala Tyr Ala
 225 230 235 240

Ile Ala Gly Thr Met Asp Phe Asp Phe Glu Asn Glu Ala Leu Gly Gln
 245 250 255
 Asp Gln Asp Gly Asn Asp Val Phe Leu Lys Asp Ile Trp Pro Ser Thr
 260 265 270
 Glu Glu Ile Glu Asp Thr Ile Gln Gln Ala Ile Ser Arg Glu Leu Tyr
 275 280 285
 Glu Ala Asp Tyr Ala Asp Val Phe Lys Gly Asp Lys Gln Trp Gln Glu
 290 295 300
 Leu Asp Val Pro Thr Gly Asp Thr Phe Glu Trp Asp Glu Asn Ser Thr
 305 310 315 320
 Tyr Ile Arg Lys Ala Pro Tyr Phe Asp Gly Met Pro Val Glu Pro Val
 325 330 335
 Ala Val Thr Asp Ile Gln Gly Ala Arg Val Leu Ala Lys Leu Gly Asp
 340 345 350
 Ser Val Thr Thr Asp His Ile Ser Pro Ala Ser Ser Ile Lys Pro Gly
 355 360 365
 Thr Pro Ala Ala Gln Tyr Leu Asp Glu His Gly Val Glu Arg His Asp
 370 375 380
 Tyr Asn Ser Leu Gly Ser Arg Arg Gly Asn His Glu Val Met Met Arg
 385 390 395 400
 Gly Thr Phe Ala Asn Ile Arg Leu Gln Asn Gln Leu Val Asp Ile Ala
 405 410 415
 Gly Gly Tyr Thr Arg Asp Phe Thr Gln Glu Gly Ala Pro Gln Ala Phe
 420 425 430
 Ile Tyr Asp Ala Ser Val Asn Tyr Lys Ala Ala Gly Ile Pro Leu Val
 435 440 445
 Val Leu Gly Gly Lys Glu Tyr Gly Thr Gly Ser Ser Arg Asp Trp Ala
 450 455 460
 Ala Lys Gly Thr Asn Leu Leu Gly Ile Arg Ala Val Ile Thr Glu Ser
 465 470 475 480
 Phe Glu Arg Ile His Arg Ser Asn Leu Ile Gly Met Gly Val Val Pro
 485 490 495
 Leu Gln Phe Pro Ala Gly Glu Ser His Glu Ser Leu Gly Leu Asp Gly
 500 505 510
 Thr Glu Thr Phe Asp Ile Thr Gly Leu Thr Ala Leu Asn Glu Gly Glu
 515 520 525
 Thr Pro Lys Thr Val Lys Val Thr Ala Thr Lys Glu Asn Gly Asp Val
 530 535 540
 Val Glu Phe Asp Ala Ile Cys Pro His Arg His Pro Arg
 545 550 555

<210> 555
 <211> 1682
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1659)
 <223> FRXA02209

<400> 555
 gtt gtt cct tcc atc gct ggc cct aag cgc cca cag gac cgc atc ctt 48
 Val Val Pro Ser Ile Ala Gly Pro Lys Arg Pro Gln Asp Arg Ile Leu
 1 5 10 15
 ctc tcc gag gca aag gag cag ttc cgt aag gat ctg cca acc tac acc 96
 Leu Ser Glu Ala Lys Glu Gln Phe Arg Lys Asp Leu Pro Thr Tyr Thr
 20 25 30
 gac gac gct gtt tcc gta gac acc tcc atc cct gca acc cgc atg gtt 144
 Asp Asp Ala Val Ser Val Asp Thr Ser Ile Pro Ala Thr Arg Met Val
 35 40 45
 aac gaa ggt ggc gga cag cct gaa ggc ggc gtc gaa gct gac aac tac 192
 Asn Glu Gly Gly Gly Gln Pro Glu Gly Gly Val Glu Ala Asp Asn Tyr
 50 55 60
 aac gct tcc tgg gct ggc tcc ggc gag tcc ttg gct act ggc gca gaa 240
 Asn Ala Ser Trp Ala Gly Ser Gly Glu Ser Leu Ala Thr Gly Ala Glu
 65 70 75 80
 gga cgt cct tcc aag cca gtc acc gtt gca tcc cca cag ggt ggc gag 288
 Gly Arg Pro Ser Lys Pro Val Thr Val Ala Ser Pro Gln Gly Gly Glu
 85 90 95
 tac acc atc gac cac ggc atg gtt gca att gca tcc atc acc tct tgc 336
 Tyr Thr Ile Asp His Gly Met Val Ala Ile Ala Ser Ile Thr Ser Cys
 100 105 110
 acc aac acc tct aac cca tcc gtg atg atc ggc gct ggc ctg atc gca 384
 Thr Asn Thr Ser Asn Pro Ser Val Met Ile Gly Ala Gly Leu Ile Ala
 115 120 125
 cgt aag gca gca gaa aag ggc ctc aag tcc aag cct tgg gtt aag acc 432
 Arg Lys Ala Ala Glu Lys Gly Leu Lys Ser Lys Pro Trp Val Lys Thr
 130 135 140
 atc tgt gca cca ggt tcc cag gtt gtc gac ggc tac tac cag cgc gca 480
 Ile Cys Ala Pro Gly Ser Gln Val Val Asp Gly Tyr Tyr Gln Arg Ala
 145 150 155 160
 gac ctc tgg aag gac ctt gag gcc atg ggc ttc tac ctc tcc ggc ttc 528
 Asp Leu Trp Lys Asp Leu Glu Ala Met Gly Phe Tyr Leu Ser Gly Phe
 165 170 175
 ggc tgc acc acc tgt att ggt aac tcc ggc cca ctg cca gag gaa atc 576
 Gly Cys Thr Thr Cys Ile Gly Asn Ser Gly Pro Leu Pro Glu Glu Ile
 180 185 190
 tcc gct gcg atc aac gag cac gac ctg acc gca acc gca gtt ttg tcc 624
 Ser Ala Ala Ile Asn Glu His Asp Leu Thr Ala Thr Ala Val Leu Ser

195					200					205					
ggt aac cgt aac ttc gag gga cgt atc tcc cct gac gtt aag atg aac	672														
Gly Asn Arg Asn Phe Glu Gly Arg Ile Ser Pro Asp Val Lys Met Asn															
210	215					220									
tac ctg gca tcc cca atc atg gtc att gct tac gca atc gct ggc acc	720														
Tyr Leu Ala Ser Pro Ile Met Val Ile Ala Tyr Ala Ile Ala Gly Thr															
225	230					235					240				
atg gac ttc gac ttc gag aac gaa gct ctt gga cag gac cag gac ggc	768														
Met Asp Phe Asp Phe Glu Asn Glu Ala Leu Gly Gln Asp Gln Asp Gly															
	245					250					255				
aac gac gtc ttc ctg aag gac atc tgg cct tcc acc gag gaa atc gaa	816														
Asn Asp Val Phe Leu Lys Asp Ile Trp Pro Ser Thr Glu Glu Ile Glu															
	260					265					270				
gac acc atc cag cag gca atc tcc cgt gag ctt tac gaa gct gac tac	864														
Asp Thr Ile Gln Gln Ala Ile Ser Arg Glu Leu Tyr Glu Ala Asp Tyr															
	275					280					285				
gca gat gtc ttc aag ggt gac aag cag tgg cag gaa ctc gat gtt cct	912														
Ala Asp Val Phe Lys Gly Asp Lys Gln Trp Gln Glu Leu Asp Val Pro															
	290					295					300				
acc ggt gac acc ttc gag tgg gac gag aac tcc acc tac atc cgc aag	960														
Thr Gly Asp Thr Phe Glu Trp Asp Glu Asn Ser Thr Tyr Ile Arg Lys															
	305					310					315				
gca cct tac ttc gac ggc atg cct gtc gag cca gtg gca gtc acc gac	1008														
Ala Pro Tyr Phe Asp Gly Met Pro Val Glu Pro Val Ala Val Thr Asp															
	325					330					335				
atc cag ggc gca cgc gtt ctg gct aag ctc ggc gac tct gtc acc acc	1056														
Ile Gln Gly Ala Arg Val Leu Ala Lys Leu Gly Asp Ser Val Thr Thr															
	340					345					350				
gac cac atc tcc cct gct tcc tcc att aag cca ggt acc cct gca gct	1104														
Asp His Ile Ser Pro Ala Ser Ser Ile Lys Pro Gly Thr Pro Ala Ala															
	355					360					365				
cag tac ttg gat gag cac ggt gtg gaa cgc cac gac tac aac tcc ctg	1152														
Gln Tyr Leu Asp Glu His Gly Val Glu Arg His Asp Tyr Asn Ser Leu															
	370					375					380				
ggt tcc agg cgt ggt aac cac gag gtc atg atg cgc ggc acc ttc gcc	1200														
Gly Ser Arg Arg Gly Asn His Glu Val Met Met Arg Gly Thr Phe Ala															
	385					390					395				
aac atc cgc ctc cag aac cag ctg gtt gac atc gca ggt ggc tac acc	1248														
Asn Ile Arg Leu Gln Asn Gln Leu Val Asp Ile Ala Gly Gly Tyr Thr															
	405					410					415				
cgc gac ttc acc cag gag ggt gct cca cag gcg ttc atc tac gac gct	1296														
Arg Asp Phe Thr Gln Glu Gly Ala Pro Gln Ala Phe Ile Tyr Asp Ala															
	420					425					430				
tcc gtc aac tac aag gct gct ggc att ccg ctg gtc gtc ttg ggc ggc	1344														
Ser Val Asn Tyr Lys Ala Ala Gly Ile Pro Leu Val Val Leu Gly Gly															
	435					440					445				

aag gag tac ggc acc ggt tct tcc cgt gac tgg gca gct aag ggc act 1392
Lys Glu Tyr Gly Thr Gly Ser Ser Arg Asp Trp Ala Ala Lys Gly Thr
450 455 460

aac ctg ctc gga att cgc gca gtt atc acc gag tcc ttc gag cgt att 1440
Asn Leu Leu Gly Ile Arg Ala Val Ile Thr Glu Ser Phe Glu Arg Ile
465 470 475 480

cac cgc tcc aac ctc atc ggt atg ggc gtt gtc cca ctg cag ttc cct 1488
His Arg Ser Asn Leu Ile Gly Met Gly Val Val Pro Leu Gln Phe Pro
485 490 495

gca ggc gaa tcc cac gag tcc ctg ggc ctt gac ggc acc gag acc ttc 1536
Ala Gly Glu Ser His Glu Ser Leu Gly Leu Asp Gly Thr Glu Thr Phe
500 505 510

gac atc acc gga ctg acc gca ctt aac gag ggc gag act cct aag act 1584
Asp Ile Thr Gly Leu Thr Ala Leu Asn Glu Gly Glu Thr Pro Lys Thr
515 520 525

gtc aag gtc acc gca acc aag gag aac ggc gac gtc gtc gag ttc gac 1632
Val Lys Val Thr Ala Thr Lys Glu Asn Gly Asp Val Val Glu Phe Asp
530 535 540

gca att tgt ccg cat cga cac ccc agg tgaggctgac tactaccgcc 1679
Ala Ile Cys Pro His Arg His Pro Arg
545 550

acg 1682

<210> 556
<211> 553
<212> PRT
<213> Corynebacterium glutamicum

<400> 556
Val Val Pro Ser Ile Ala Gly Pro Lys Arg Pro Gln Asp Arg Ile Leu
1 5 10 15

Leu Ser Glu Ala Lys Glu Gln Phe Arg Lys Asp Leu Pro Thr Tyr Thr
20 25 30

Asp Asp Ala Val Ser Val Asp Thr Ser Ile Pro Ala Thr Arg Met Val
35 40 45

Asn Glu Gly Gly Gly Gln Pro Glu Gly Gly Val Glu Ala Asp Asn Tyr
50 55 60

Asn Ala Ser Trp Ala Gly Ser Gly Glu Ser Leu Ala Thr Gly Ala Glu
65 70 75 80

Gly Arg Pro Ser Lys Pro Val Thr Val Ala Ser Pro Gln Gly Gly Glu
85 90 95

Tyr Thr Ile Asp His Gly Met Val Ala Ile Ala Ser Ile Thr Ser Cys
100 105 110

Thr Asn Thr Ser Asn Pro Ser Val Met Ile Gly Ala Gly Leu Ile Ala
115 120 125

Arg Lys Ala Ala Glu Lys Gly Leu Lys Ser Lys Pro Trp Val Lys Thr
 130 135 140
 Ile Cys Ala Pro Gly Ser Gln Val Val Asp Gly Tyr Tyr Gln Arg Ala
 145 150 155 160
 Asp Leu Trp Lys Asp Leu Glu Ala Met Gly Phe Tyr Leu Ser Gly Phe
 165 170 175
 Gly Cys Thr Thr Cys Ile Gly Asn Ser Gly Pro Leu Pro Glu Glu Ile
 180 185 190
 Ser Ala Ala Ile Asn Glu His Asp Leu Thr Ala Thr Ala Val Leu Ser
 195 200 205
 Gly Asn Arg Asn Phe Glu Gly Arg Ile Ser Pro Asp Val Lys Met Asn
 210 215 220
 Tyr Leu Ala Ser Pro Ile Met Val Ile Ala Tyr Ala Ile Ala Gly Thr
 225 230 235 240
 Met Asp Phe Asp Phe Glu Asn Glu Ala Leu Gly Gln Asp Gln Asp Gly
 245 250 255
 Asn Asp Val Phe Leu Lys Asp Ile Trp Pro Ser Thr Glu Glu Ile Glu
 260 265 270
 Asp Thr Ile Gln Gln Ala Ile Ser Arg Glu Leu Tyr Glu Ala Asp Tyr
 275 280 285
 Ala Asp Val Phe Lys Gly Asp Lys Gln Trp Gln Glu Leu Asp Val Pro
 290 295 300
 Thr Gly Asp Thr Phe Glu Trp Asp Glu Asn Ser Thr Tyr Ile Arg Lys
 305 310 315 320
 Ala Pro Tyr Phe Asp Gly Met Pro Val Glu Pro Val Ala Val Thr Asp
 325 330 335
 Ile Gln Gly Ala Arg Val Leu Ala Lys Leu Gly Asp Ser Val Thr Thr
 340 345 350
 Asp His Ile Ser Pro Ala Ser Ser Ile Lys Pro Gly Thr Pro Ala Ala
 355 360 365
 Gln Tyr Leu Asp Glu His Gly Val Glu Arg His Asp Tyr Asn Ser Leu
 370 375 380
 Gly Ser Arg Arg Gly Asn His Glu Val Met Met Arg Gly Thr Phe Ala
 385 390 395 400
 Asn Ile Arg Leu Gln Asn Gln Leu Val Asp Ile Ala Gly Gly Tyr Thr
 405 410 415
 Arg Asp Phe Thr Gln Glu Gly Ala Pro Gln Ala Phe Ile Tyr Asp Ala
 420 425 430
 Ser Val Asn Tyr Lys Ala Ala Gly Ile Pro Leu Val Val Leu Gly Gly
 435 440 445

Lys Glu Tyr Gly Thr Gly Ser Ser Arg Asp Trp Ala Ala Lys Gly Thr
 450 455 460
 Asn Leu Leu Gly Ile Arg Ala Val Ile Thr Glu Ser Phe Glu Arg Ile
 465 470 475 480
 His Arg Ser Asn Leu Ile Gly Met Gly Val Val Pro Leu Gln Phe Pro
 485 490 495
 Ala Gly Glu Ser His Glu Ser Leu Gly Leu Asp Gly Thr Glu Thr Phe
 500 505 510
 Asp Ile Thr Gly Leu Thr Ala Leu Asn Glu Gly Glu Thr Pro Lys Thr
 515 520 525
 Val Lys Val Thr Ala Thr Lys Glu Asn Gly Asp Val Val Glu Phe Asp
 530 535 540
 Ala Ile Cys Pro His Arg His Pro Arg
 545 550

<210> 557
 <211> 874
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(874)
 <223> RXN02213

<400> 557
 ttctgtggaa tgagaatccg atgtttttct caccgccggct cagccgaagc agacgccgctc 60
 gcgaaatctc accctaataaaa agttagaatt ggagctcact gtg act gaa agc aag 115
 Val Thr Glu Ser Lys
 1 5
 aac tcc ttc aat gct aag agc acc ctt gaa gtt ggc gac aag tcc tat 163
 Asn Ser Phe Asn Ala Lys Ser Thr Leu Glu Val Gly Asp Lys Ser Tyr
 10 15 20
 gac tac ttc gcc ctc tct gca gtg cct ggc atg gag aag ctg ccg tac 211
 Asp Tyr Phe Ala Leu Ser Ala Val Pro Gly Met Glu Lys Leu Pro Tyr
 25 30 35
 tcc ctc aag gtt ctc gga gag aac ctt ctt cgt acc gaa gac ggc gca 259
 Ser Leu Lys Val Leu Gly Glu Asn Leu Leu Arg Thr Glu Asp Gly Ala
 40 45 50
 aac atc acc aac gag cac att gag gct atc gcc aac tgg gat gca tct 307
 Asn Ile Thr Asn Glu His Ile Glu Ala Ile Ala Asn Trp Asp Ala Ser
 55 60 65
 tcc gat cca agc atc gaa atc cag ttc acc cca gcc cgt gtt ctc atg 355
 Ser Asp Pro Ser Ile Glu Ile Gln Phe Thr Pro Ala Arg Val Leu Met
 70 75 80 85
 cag gac ttc acc ggt gtc cct tgt gta gtt gac ctc gca acc atg cgt 403
 Gln Asp Phe Thr Gly Val Pro Cys Val Val Asp Leu Ala Thr Met Arg

90										95										100																			
gag gca gtt gct gca ctc ggt ggc gac cct aac gac gtc aac cca ctg	Glu Ala Val Ala Ala Leu Gly Gly Asp Pro Asn Asp Val Asn Pro Leu	451																																					
105										110										115																			
aac cca gcc gag atg gtc att gac cac tcc gtc atc gtg gag gct ttc	Asn Pro Ala Glu Met Val Ile Asp His Ser Val Ile Val Glu Ala Phe	499																																					
120										125										130																			
ggc cgc cca gat gca ctg gct aag aac gtt gag atc gag tac gag cgc	Gly Arg Pro Asp Ala Leu Ala Lys Asn Val Glu Ile Glu Tyr Glu Arg	547																																					
135										140										145																			
aac gag gag cgt tac cag ttc ctg cgt tgg ggt tcc gag tcc ttc tcc	Asn Glu Glu Arg Tyr Gln Phe Leu Arg Trp Gly Ser Glu Ser Phe Ser	595																																					
150										155										160										165									
aac ttc cgc gtt gtt cct cca gga acc ggt atc gtc cac cag gtc aac	Asn Phe Arg Val Val Pro Pro Gly Thr Gly Ile Val His Gln Val Asn	643																																					
170										175										180																			
att gag tac ttg gct cgc gtc gtc ttc gac aac gag ggc ctt gca tac	Ile Glu Tyr Leu Ala Arg Val Val Phe Asp Asn Glu Gly Leu Ala Tyr	691																																					
185										190										195																			
cca gat acc tgc atc ggt acc gac tcc cac acc acc atg gaa aac ggc	Pro Asp Thr Cys Ile Gly Thr Asp Ser His Thr Thr Met Glu Asn Gly	739																																					
200										205										210																			
ctg ggc atc ctg ggc tgg ggc gtt ggt ggc att gag gct gaa gca gca	Leu Gly Ile Leu Gly Trp Gly Val Gly Gly Ile Glu Ala Glu Ala Ala	787																																					
215										220										225																			
atg ctc ggc cag cca gtg tcc atg ctg atc cct cgc gtt gtt ggc ttc	Met Leu Gly Gln Pro Val Ser Met Leu Ile Pro Arg Val Val Gly Phe	835																																					
230										235										240										245									
aag ttg acc ggc gag atc cca gta ggc gtt acc gca act	Lys Leu Thr Gly Glu Ile Pro Val Gly Val Thr Ala Thr	874																																					
250										255																													

<210> 558

<211> 258

<212> PRT

<213> Corynebacterium glutamicum

<400> 558

Val Thr Glu Ser Lys Asn Ser Phe Asn Ala Lys Ser Thr Leu Glu Val	
1	5 10 15

Gly Asp Lys Ser Tyr Asp Tyr Phe Ala Leu Ser Ala Val Pro Gly Met	
20	25 30

Glu Lys Leu Pro Tyr Ser Leu Lys Val Leu Gly Glu Asn Leu Leu Arg	
35	40 45

Thr Glu Asp Gly Ala Asn Ile Thr Asn Glu His Ile Glu Ala Ile Ala	
50	55 60

Asn Trp Asp Ala Ser Ser Asp Pro Ser Ile Glu Ile Gln Phe Thr Pro
 65 70 75 80
 Ala Arg Val Leu Met Gln Asp Phe Thr Gly Val Pro Cys Val Val Asp
 85 90 95
 Leu Ala Thr Met Arg Glu Ala Val Ala Ala Leu Gly Gly Asp Pro Asn
 100 105 110
 Asp Val Asn Pro Leu Asn Pro Ala Glu Met Val Ile Asp His Ser Val
 115 120 125
 Ile Val Glu Ala Phe Gly Arg Pro Asp Ala Leu Ala Lys Asn Val Glu
 130 135 140
 Ile Glu Tyr Glu Arg Asn Glu Glu Arg Tyr Gln Phe Leu Arg Trp Gly
 145 150 155 160
 Ser Glu Ser Phe Ser Asn Phe Arg Val Val Pro Pro Gly Thr Gly Ile
 165 170 175
 Val His Gln Val Asn Ile Glu Tyr Leu Ala Arg Val Val Phe Asp Asn
 180 185 190
 Glu Gly Leu Ala Tyr Pro Asp Thr Cys Ile Gly Thr Asp Ser His Thr
 195 200 205
 Thr Met Glu Asn Gly Leu Gly Ile Leu Gly Trp Gly Val Gly Gly Ile
 210 215 220
 Glu Ala Glu Ala Ala Met Leu Gly Gln Pro Val Ser Met Leu Ile Pro
 225 230 235 240
 Arg Val Val Gly Phe Lys Leu Thr Gly Glu Ile Pro Val Gly Val Thr
 245 250 255

Ala Thr

<210> 559

<211> 817

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(817)

<223> FRXA02213

<400> 559

ttctgtggaa tgagaatccg atgtttttct cacgccggct cagccgaagc agacgccgtc 60

gcgaaatctc accctaaaaa agttagaatt ggagctcact gtg act gaa agc aag 115
 Val Thr Glu Ser Lys
 1 5

aac tcc ttc aat gct aag agc acc ctt gaa gtt ggc gac aag tcc tat 163
 Asn Ser Phe Asn Ala Lys Ser Thr Leu Glu Val Gly Asp Lys Ser Tyr
 10 15 20

gac tac ttc gcc ctc tct gca gtg cct ggc atg gag aag ctg ccg tac 211
 Asp Tyr Phe Ala Leu Ser Ala Val Pro Gly Met Glu Lys Leu Pro Tyr
 25 30 35

tcc ctc aag gtt ctc gga gag aac ctt ctt cgt acc gaa gac ggc gca 259
 Ser Leu Lys Val Leu Gly Glu Asn Leu Leu Arg Thr Glu Asp Gly Ala
 40 45 50

aac atc acc aac gag cac att gag gct atc gcc aac tgg gat gca tct 307
 Asn Ile Thr Asn Glu His Ile Glu Ala Ile Ala Asn Trp Asp Ala Ser
 55 60 65

tcc gat cca agc atc gaa atc cag ttc acc cca gcc cgt gtt ctc atg 355
 Ser Asp Pro Ser Ile Glu Ile Gln Phe Thr Pro Ala Arg Val Leu Met
 70 75 80 85

cag gac ttc acc ggt gtc cct tgt gta gtt gac ctc gca acc atg cgt 403
 Gln Asp Phe Thr Gly Val Pro Cys Val Val Asp Leu Ala Thr Met Arg
 90 95 100

gag gca gtt gct gca ctc ggt ggc gac cct aac gac gtc aac cca ctg 451
 Glu Ala Val Ala Ala Leu Gly Gly Asp Pro Asn Asp Val Asn Pro Leu
 105 110 115

aac ccag gcc gag atg gtc att gac cac tcc gtc atc gtg gag gct ttc 499
 Asn Pro Ala Glu Met Val Ile Asp His Ser Val Ile Val Glu Ala Phe
 120 125 130

ggc cgc cca gat gca ctg gct aag aac gtt gag atc gag tac gag cgc 547
 Gly Arg Pro Asp Ala Leu Ala Lys Asn Val Glu Ile Glu Tyr Glu Arg
 135 140 145

aac gag gag cgt tac cag ttc ctg cgt tgg ggt tcc gag tcc ttc tcc 595
 Asn Glu Glu Arg Tyr Gln Phe Leu Arg Trp Gly Ser Glu Ser Phe Ser
 150 155 160 165

aac ttc cgc gtt gtt cct cca gga acc ggt atc gtc cac cag gtc aac 643
 Asn Phe Arg Val Val Pro Pro Gly Thr Gly Ile Val His Gln Val Asn
 170 175 180

att gag tac ttg gct cgc gtc gtc ttc gac aac gag ggc ctt gca tac 691
 Ile Glu Tyr Leu Ala Arg Val Val Phe Asp Asn Glu Gly Leu Ala Tyr
 185 190 195

cca gat acc tgc atc ggt acc gac tcc cac acc acc atg gaa aac ggc 739
 Pro Asp Thr Cys Ile Gly Thr Asp Ser His Thr Thr Met Glu Asn Gly
 200 205 210

ctg ggc atc ctg ggc tgg ggc gtt ggt ggc att gag gct gaa gca gca 787
 Leu Gly Ile Leu Gly Trp Gly Val Gly Gly Ile Glu Ala Glu Ala Ala
 215 220 225

atg ctc ggc cag cca gtg tcc atg ctg atc 817
 Met Leu Gly Gln Pro Val Ser Met Leu Ile
 230 235

<210> 560

<211> 239

<212> PRT

<213> Corynebacterium glutamicum

<400> 560

Val Thr Glu Ser Lys Asn Ser Phe Asn Ala Lys Ser Thr Leu Glu Val
 1 5 10 15

Gly Asp Lys Ser Tyr Asp Tyr Phe Ala Leu Ser Ala Val Pro Gly Met
 20 25 30

Glu Lys Leu Pro Tyr Ser Leu Lys Val Leu Gly Glu Asn Leu Leu Arg
 35 40 45

Thr Glu Asp Gly Ala Asn Ile Thr Asn Glu His Ile Glu Ala Ile Ala
 50 55 60

Asn Trp Asp Ala Ser Ser Asp Pro Ser Ile Glu Ile Gln Phe Thr Pro
 65 70 75 80

Ala Arg Val Leu Met Gln Asp Phe Thr Gly Val Pro Cys Val Val Asp
 85 90 95

Leu Ala Thr Met Arg Glu Ala Val Ala Ala Leu Gly Gly Asp Pro Asn
 100 105 110

Asp Val Asn Pro Leu Asn Pro Ala Glu Met Val Ile Asp His Ser Val
 115 120 125

Ile Val Glu Ala Phe Gly Arg Pro Asp Ala Leu Ala Lys Asn Val Glu
 130 135 140

Ile Glu Tyr Glu Arg Asn Glu Glu Arg Tyr Gln Phe Leu Arg Trp Gly
 145 150 155 160

Ser Glu Ser Phe Ser Asn Phe Arg Val Val Pro Pro Gly Thr Gly Ile
 165 170 175

Val His Gln Val Asn Ile Glu Tyr Leu Ala Arg Val Val Phe Asp Asn
 180 185 190

Glu Gly Leu Ala Tyr Pro Asp Thr Cys Ile Gly Thr Asp Ser His Thr
 195 200 205

Thr Met Glu Asn Gly Leu Gly Ile Leu Gly Trp Gly Val Gly Gly Ile
 210 215 220

Glu Ala Glu Ala Ala Met Leu Gly Gln Pro Val Ser Met Leu Ile
 225 230 235

<210> 561

<211> 2891

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(2868)

<223> RXA02056

<400> 561

cgc cac tct gtt cca cgt cta acc aag ggc cag ggc acc atc atc ggt 48
 Arg His Ser Val Pro Arg Leu Thr Lys Gly Gln Gly Thr Ile Ile Gly

1	5	10	15	
gtc ggt tcc atg gat tac cca gca gag ttc cag ggc gct tca gaa gac				96
Val Gly Ser Met Asp Tyr Pro Ala Glu Phe Gln Gly Ala Ser Glu Asp				
20		25	30	
cgc ctt gca gag ctc ggc gtt ggc aaa ctt gtc acc atc acc tcc acc				144
Arg Leu Ala Glu Leu Gly Val Gly Lys Leu Val Thr Ile Thr Ser Thr				
35		40	45	
tac gat cac cgc gtg atc cag ggt gct gtg tcc ggt gaa ttc ctg cgc				192
Tyr Asp His Arg Val Ile Gln Gly Ala Val Ser Gly Glu Phe Leu Arg				
50		55	60	
acc atg tct cgc ctg ctc acc gat gat tcc ttc tgg gat gag atc ttc				240
Thr Met Ser Arg Leu Leu Thr Asp Asp Ser Phe Trp Asp Glu Ile Phe				
65		70	75	80
gac gca atg aac gtt cct tac acc cca atg cgt tgg gca cag gac gtt				288
Asp Ala Met Asn Val Pro Tyr Thr Pro Met Arg Trp Ala Gln Asp Val				
85		90	95	
cca aac acc ggt gtt gat aag aac acc cgc gtc atg cag ctc att gag				336
Pro Asn Thr Gly Val Asp Lys Asn Thr Arg Val Met Gln Leu Ile Glu				
100		105	110	
gca tac cgc tcc cgt gga cac ctc atc gct gac acc aac cca ctt tca				384
Ala Tyr Arg Ser Arg Gly His Leu Ile Ala Asp Thr Asn Pro Leu Ser				
115		120	125	
tgg gtt cag cct ggc atg cca gtt cca gac cac cgc gac ctc gac atc				432
Trp Val Gln Pro Gly Met Pro Val Pro Asp His Arg Asp Leu Asp Ile				
130		135	140	
gag acc cac aac ctg acc atc tgg gat ctg gac cgt acc ttc aac gtc				480
Glu Thr His Asn Leu Thr Ile Trp Asp Leu Asp Arg Thr Phe Asn Val				
145		150	155	160
ggt ggc ttc ggc ggc aag gag acc atg acc ctg cgc gag gta ctg tcc				528
Gly Gly Phe Gly Gly Lys Glu Thr Met Thr Leu Arg Glu Val Leu Ser				
165		170	175	
cgc ctc cgc gct gcg tac acc ctc aag gtc ggc tcc gaa tac acc cac				576
Arg Leu Arg Ala Ala Tyr Thr Leu Lys Val Gly Ser Glu Tyr Thr His				
180		185	190	
atc ctg gac cgc gac gag cgc acc tgg ctg cag gac cgc ctc gag gcc				624
Ile Leu Asp Arg Asp Glu Arg Thr Trp Leu Gln Asp Arg Leu Glu Ala				
195		200	205	
gga atg cca aag cca acc cag gca gag cag aag tac atc ctg cag aag				672
Gly Met Pro Lys Pro Thr Gln Ala Glu Gln Lys Tyr Ile Leu Gln Lys				
210		215	220	
ctg aac gcc gcg gag gct ttc gag aac ttc ctg cag acc aag tac gtc				720
Leu Asn Ala Ala Glu Ala Phe Glu Asn Phe Leu Gln Thr Lys Tyr Val				
225		230	235	240
ggc cag aag cgc ttc tcc ctc gaa ggt gca gaa gca ctt atc cca ctg				768
Gly Gln Lys Arg Phe Ser Leu Glu Gly Ala Glu Ala Leu Ile Pro Leu				
245		250	255	

atg gac tcc gcc atc gac acc gcc gca ggc caa ggc ctc gac gaa gtt	816
Met Asp Ser Ala Ile Asp Thr Ala Ala Gly Gln Gly Leu Asp Glu Val	
260 265 270	
gtc atc ggt atg cca cac cgt ggt cgc ctc aac gtg ctg ttc aac atc	864
Val Ile Gly Met Pro His Arg Gly Arg Leu Asn Val Leu Phe Asn Ile	
275 280 285	
gtg ggc aag cca ctg gca tcc atc ttc aac gag ttt gaa ggc caa atg	912
Val Gly Lys Pro Leu Ala Ser Ile Phe Asn Glu Phe Glu Gly Gln Met	
290 295 300	
gag cag ggc cag atc ggt ggc tcc ggt gac gtg aag tac cac ctc ggt	960
Glu Gln Gly Gln Ile Gly Gly Ser Gly Asp Val Lys Tyr His Leu Gly	
305 310 315 320	
tcc gaa ggc cag cac ctg cag atg ttc ggc gac ggc gag atc aag gtc	1008
Ser Glu Gly Gln His Leu Gln Met Phe Gly Asp Gly Glu Ile Lys Val	
325 330 335	
tcc ctg act gct aac ccg tcc cac ctg gaa gct gtt aac cca gcg atg	1056
Ser Leu Thr Ala Asn Pro Ser His Leu Glu Ala Val Asn Pro Ala Met	
340 345 350	
gaa ggt att gtc cgc gca aag cag gac tac ctg gac aag ggc gta gac	1104
Glu Gly Ile Val Arg Ala Lys Gln Asp Tyr Leu Asp Lys Gly Val Asp	
355 360 365	
ggc aag act gtt gtg cca ctg ctg ctc cac ggt gac gct gca ttc gca	1152
Gly Lys Thr Val Val Pro Leu Leu Leu His Gly Asp Ala Ala Phe Ala	
370 375 380	
ggc ctg ggc atc gtg cca gaa acc atc aac ctg gct aag ctg cgt ggc	1200
Gly Leu Gly Ile Val Pro Glu Thr Ile Asn Leu Ala Lys Leu Arg Gly	
385 390 395 400	
tac gac gtc ggc ggc acc atc cac atc gtg gtg aac aac cag atc ggc	1248
Tyr Asp Val Gly Gly Thr Ile His Ile Val Val Asn Asn Gln Ile Gly	
405 410 415	
ttc acc acc acc cca gac tcc agc cgc tcc atg cac tac gca acc gac	1296
Phe Thr Thr Thr Pro Asp Ser Ser Arg Ser Met His Tyr Ala Thr Asp	
420 425 430	
tac gcc aag gca ttc ggc tgc cca gtc ttc cac gtc aac ggc gac gac	1344
Tyr Ala Lys Ala Phe Gly Cys Pro Val Phe His Val Asn Gly Asp Asp	
435 440 445	
cca gag gca gtt gtc tgg gtt ggc cag ctg gcc acc gag tac cgt cgt	1392
Pro Glu Ala Val Val Trp Val Gly Gln Leu Ala Thr Glu Tyr Arg Arg	
450 455 460	
cgc ttc ggc aag gac gtc ttc atc gac ctc gtc tgc tac cgc ctc cgc	1440
Arg Phe Gly Lys Asp Val Phe Ile Asp Leu Val Cys Tyr Arg Leu Arg	
465 470 475 480	
ggc cac aac gaa gct gat gat cct tcc atg acc cag cca aag atg tat	1488
Gly His Asn Glu Ala Asp Asp Pro Ser Met Thr Gln Pro Lys Met Tyr	
485 490 495	

gag ctc atc acc ggc cgc gag acc gtt cgt gct cag tac acc gaa gac	1536
Glu Leu Ile Thr Gly Arg Glu Thr Val Arg Ala Gln Tyr Thr Glu Asp	
500 505 510	
ctg ctc gga cgt gga gac ctc tcc aac gaa gat gca gaa gca gtc gtc	1584
Leu Leu Gly Arg Gly Asp Leu Ser Asn Glu Asp Ala Glu Ala Val Val	
515 520 525	
cgc gac ttc cac gac cag atg gaa tct gtg ttc aac gaa gtc aag gaa	1632
Arg Asp Phe His Asp Gln Met Glu Ser Val Phe Asn Glu Val Lys Glu	
530 535 540	
ggc ggc aag aag cag gct gag gca cag acc ggc atc acc ggc tcc cag	1680
Gly Gly Lys Lys Gln Ala Glu Ala Gln Thr Gly Ile Thr Gly Ser Gln	
545 550 555 560	
aag ctt cca cac ggc ctt gag acc aac atc tcc cgt gaa gag ctc ctg	1728
Lys Leu Pro His Gly Leu Glu Thr Asn Ile Ser Arg Glu Glu Leu Leu	
565 570 575	
gaa ctg gga cag gct ttc gcc aac acc cca gaa ggc ttc aac tac cac	1776
Glu Leu Gly Gln Ala Phe Ala Asn Thr Pro Glu Gly Phe Asn Tyr His	
580 585 590	
cca cgt gtg gct ccc gtt gct aag aag cgc gtc tcc tct gtc acc gaa	1824
Pro Arg Val Ala Pro Val Ala Lys Lys Arg Val Ser Ser Val Thr Glu	
595 600 605	
ggt ggc atc gac tgg gca tgg ggc gag ctc ctc gcc ttc ggt tcc ctg	1872
Gly Gly Ile Asp Trp Ala Trp Gly Glu Leu Leu Ala Phe Gly Ser Leu	
610 615 620	
gct aac tcc ggc cgc ttg gtt cgc ctt gca ggt gaa gat tcc cgc cgc	1920
Ala Asn Ser Gly Arg Leu Val Arg Leu Ala Gly Glu Asp Ser Arg Arg	
625 630 635 640	
ggt acc ttc acc cag cgc cac gca gtt gcc atc gac cca gcg acc gct	1968
Gly Thr Phe Thr Gln Arg His Ala Val Ala Ile Asp Pro Ala Thr Ala	
645 650 655	
gaa gag ttc aac cca ctc cac gag ctt gca cag tcc aag ggc aac aac	2016
Glu Glu Phe Asn Pro Leu His Glu Leu Ala Gln Ser Lys Gly Asn Asn	
660 665 670	
ggt aag ttc ctg gtc tac aac tcc gca ctg acc gag tac gca ggc atg	2064
Gly Lys Phe Leu Val Tyr Asn Ser Ala Leu Thr Glu Tyr Ala Gly Met	
675 680 685	
ggc ttc gag tac ggc tac tcc gta gga aac gaa gac tcc atc gtt gca	2112
Gly Phe Glu Tyr Gly Tyr Ser Val Gly Asn Glu Asp Ser Ile Val Ala	
690 695 700	
tgg gaa gca cag ttc ggc gac ttc gcc aac ggc gct cag acc atc atc	2160
Trp Glu Ala Gln Phe Gly Asp Phe Ala Asn Gly Ala Gln Thr Ile Ile	
705 710 715 720	
gat gag tac gtc tcc tca ggc gaa gct aag tgg ggc cag acc tcc aag	2208
Asp Glu Tyr Val Ser Ser Gly Glu Ala Lys Trp Gly Gln Thr Ser Lys	
725 730 735	
ctg atc ctt ctg ctg cct cac ggc tac gaa ggc cag ggc cca gac cac	2256

Leu	Ile	Leu	Leu	Leu	Pro	His	Gly	Tyr	Glu	Gly	Gln	Gly	Pro	Asp	His		
			740					745					750				
tct	tcc	gca	cgt	atc	gag	cgc	ttc	ctg	cag	ctg	tgc	gct	gag	ggt	tcc	2304	
Ser	Ser	Ala	Arg	Ile	Glu	Arg	Phe	Leu	Gln	Leu	Cys	Ala	Glu	Gly	Ser		
		755					760				765						
atg	act	gtt	gct	cag	cca	tcc	acc	cca	gca	aac	cac	ttc	cac	cta	ctg	2352	
Met	Thr	Val	Ala	Gln	Pro	Ser	Thr	Pro	Ala	Asn	His	Phe	His	Leu	Leu		
	770					775					780						
cgt	cgt	cac	gct	ctg	tcc	gac	ctg	aag	cgt	cca	ctg	gtt	atc	ttc	acc	2400	
Arg	Arg	His	Ala	Leu	Ser	Asp	Leu	Lys	Arg	Pro	Leu	Val	Ile	Phe	Thr		
785					790				795						800		
ccg	aag	tcc	atg	ctg	cgt	aac	aag	gct	gct	gcc	tcc	gca	cca	gaa	gac	2448	
Pro	Lys	Ser	Met	Leu	Arg	Asn	Lys	Ala	Ala	Ala	Ser	Ala	Pro	Glu	Asp		
				805				810						815			
ttc	act	gag	gtc	acc	aag	ttc	cag	tcc	gtg	atc	aac	gat	cca	aac	gtt	2496	
Phe	Thr	Glu	Val	Thr	Lys	Phe	Gln	Ser	Val	Ile	Asn	Asp	Pro	Asn	Val		
		820					825					830					
gca	gat	gca	gcc	aag	gtg	aag	aag	gtc	atg	ctg	gtc	tcc	ggc	aag	ctg	2544	
Ala	Asp	Ala	Ala	Lys	Val	Lys	Lys	Val	Met	Leu	Val	Ser	Gly	Lys	Leu		
	835					840						845					
tac	tac	gaa	ttg	gca	aag	cgc	aag	gag	aag	gac	gga	cgc	gac	gac	atc	2592	
Tyr	Tyr	Glu	Leu	Ala	Lys	Arg	Lys	Glu	Lys	Asp	Gly	Arg	Asp	Asp	Ile		
	850					855					860						
gcg	atc	gtt	cgt	atc	gaa	atg	ctc	cac	cca	att	ccg	ttc	aac	cgc	atc	2640	
Ala	Ile	Val	Arg	Ile	Glu	Met	Leu	His	Pro	Ile	Pro	Phe	Asn	Arg	Ile		
865					870				875						880		
tcc	gag	gct	ctt	gcc	ggc	tac	cct	aac	gct	gag	gaa	gtc	ctc	ttc	gtt	2688	
Ser	Glu	Ala	Leu	Ala	Gly	Tyr	Pro	Asn	Ala	Glu	Glu	Val	Leu	Phe	Val		
				885				890						895			
cag	gat	gag	cca	gca	aac	cag	ggc	cca	tgg	ccg	ttc	tac	cag	gag	cac	2736	
Gln	Asp	Glu	Pro	Ala	Asn	Gln	Gly	Pro	Trp	Pro	Phe	Tyr	Gln	Glu	His		
			900				905						910				
ctc	cca	gag	ctg	atc	ccg	aac	atg	cca	aag	atg	cgc	cgc	gtt	tcc	cgc	2784	
Leu	Pro	Glu	Leu	Ile	Pro	Asn	Met	Pro	Lys	Met	Arg	Arg	Val	Ser	Arg		
	915					920					925						
cgc	gct	cag	tcc	tcc	acc	gca	act	ggt	gtt	gcc	aag	gtg	cac	cag	ctg	2832	
Arg	Ala	Gln	Ser	Ser	Thr	Ala	Thr	Gly	Val	Ala	Lys	Val	His	Gln	Leu		
	930					935					940						
gag	gag	aag	cag	ctt	atc	gac	gag	gct	ttc	gag	gct	taagtcttta				2878	
Glu	Glu	Lys	Gln	Leu	Ile	Asp	Glu	Ala	Phe	Glu	Ala						
945					950					955							
tagtcctgca	cta																2891

<210> 562
 <211> 956
 <212> PRT

<213> Corynebacterium glutamicum

<400> 562

Arg His Ser Val Pro Arg Leu Thr Lys Gly Gln Gly Thr Ile Ile Gly
 1 5 10 15
 Val Gly Ser Met Asp Tyr Pro Ala Glu Phe Gln Gly Ala Ser Glu Asp
 20 25 30
 Arg Leu Ala Glu Leu Gly Val Gly Lys Leu Val Thr Ile Thr Ser Thr
 35 40 45
 Tyr Asp His Arg Val Ile Gln Gly Ala Val Ser Gly Glu Phe Leu Arg
 50 55 60
 Thr Met Ser Arg Leu Leu Thr Asp Asp Ser Phe Trp Asp Glu Ile Phe
 65 70 75 80
 Asp Ala Met Asn Val Pro Tyr Thr Pro Met Arg Trp Ala Gln Asp Val
 85 90 95
 Pro Asn Thr Gly Val Asp Lys Asn Thr Arg Val Met Gln Leu Ile Glu
 100 105 110
 Ala Tyr Arg Ser Arg Gly His Leu Ile Ala Asp Thr Asn Pro Leu Ser
 115 120 125
 Trp Val Gln Pro Gly Met Pro Val Pro Asp His Arg Asp Leu Asp Ile
 130 135 140
 Glu Thr His Asn Leu Thr Ile Trp Asp Leu Asp Arg Thr Phe Asn Val
 145 150 155 160
 Gly Gly Phe Gly Gly Lys Glu Thr Met Thr Leu Arg Glu Val Leu Ser
 165 170 175
 Arg Leu Arg Ala Ala Tyr Thr Leu Lys Val Gly Ser Glu Tyr Thr His
 180 185 190
 Ile Leu Asp Arg Asp Glu Arg Thr Trp Leu Gln Asp Arg Leu Glu Ala
 195 200 205
 Gly Met Pro Lys Pro Thr Gln Ala Glu Gln Lys Tyr Ile Leu Gln Lys
 210 215 220
 Leu Asn Ala Ala Glu Ala Phe Glu Asn Phe Leu Gln Thr Lys Tyr Val
 225 230 235 240
 Gly Gln Lys Arg Phe Ser Leu Glu Gly Ala Glu Ala Leu Ile Pro Leu
 245 250 255
 Met Asp Ser Ala Ile Asp Thr Ala Ala Gly Gln Gly Leu Asp Glu Val
 260 265 270
 Val Ile Gly Met Pro His Arg Gly Arg Leu Asn Val Leu Phe Asn Ile
 275 280 285
 Val Gly Lys Pro Leu Ala Ser Ile Phe Asn Glu Phe Glu Gly Gln Met
 290 295 300
 Glu Gln Gly Gln Ile Gly Gly Ser Gly Asp Val Lys Tyr His Leu Gly

305	310	315	320
Ser Glu Gly Gln His Leu Gln Met Phe Gly Asp Gly Glu Ile Lys Val	325	330	335
Ser Leu Thr Ala Asn Pro Ser His Leu Glu Ala Val Asn Pro Ala Met	340	345	350
Glu Gly Ile Val Arg Ala Lys Gln Asp Tyr Leu Asp Lys Gly Val Asp	355	360	365
Gly Lys Thr Val Val Pro Leu Leu Leu His Gly Asp Ala Ala Phe Ala	370	375	380
Gly Leu Gly Ile Val Pro Glu Thr Ile Asn Leu Ala Lys Leu Arg Gly	385	390	395
Tyr Asp Val Gly Gly Thr Ile His Ile Val Val Asn Asn Gln Ile Gly	405	410	415
Phe Thr Thr Thr Pro Asp Ser Ser Arg Ser Met His Tyr Ala Thr Asp	420	425	430
Tyr Ala Lys Ala Phe Gly Cys Pro Val Phe His Val Asn Gly Asp Asp	435	440	445
Pro Glu Ala Val Val Trp Val Gly Gln Leu Ala Thr Glu Tyr Arg Arg	450	455	460
Arg Phe Gly Lys Asp Val Phe Ile Asp Leu Val Cys Tyr Arg Leu Arg	465	470	475
Gly His Asn Glu Ala Asp Asp Pro Ser Met Thr Gln Pro Lys Met Tyr	485	490	495
Glu Leu Ile Thr Gly Arg Glu Thr Val Arg Ala Gln Tyr Thr Glu Asp	500	505	510
Leu Leu Gly Arg Gly Asp Leu Ser Asn Glu Asp Ala Glu Ala Val Val	515	520	525
Arg Asp Phe His Asp Gln Met Glu Ser Val Phe Asn Glu Val Lys Glu	530	535	540
Gly Gly Lys Lys Gln Ala Glu Ala Gln Thr Gly Ile Thr Gly Ser Gln	545	550	555
Lys Leu Pro His Gly Leu Glu Thr Asn Ile Ser Arg Glu Glu Leu Leu	565	570	575
Glu Leu Gly Gln Ala Phe Ala Asn Thr Pro Glu Gly Phe Asn Tyr His	580	585	590
Pro Arg Val Ala Pro Val Ala Lys Lys Arg Val Ser Ser Val Thr Glu	595	600	605
Gly Gly Ile Asp Trp Ala Trp Gly Glu Leu Leu Ala Phe Gly Ser Leu	610	615	620
Ala Asn Ser Gly Arg Leu Val Arg Leu Ala Gly Glu Asp Ser Arg Arg	625	630	635
			640

Gly Thr Phe Thr Gln Arg His Ala Val Ala Ile Asp Pro Ala Thr Ala
 645 650 655
 Glu Glu Phe Asn Pro Leu His Glu Leu Ala Gln Ser Lys Gly Asn Asn
 660 665 670
 Gly Lys Phe Leu Val Tyr Asn Ser Ala Leu Thr Glu Tyr Ala Gly Met
 675 680 685
 Gly Phe Glu Tyr Gly Tyr Ser Val Gly Asn Glu Asp Ser Ile Val Ala
 690 695 700
 Trp Glu Ala Gln Phe Gly Asp Phe Ala Asn Gly Ala Gln Thr Ile Ile
 705 710 715 720
 Asp Glu Tyr Val Ser Ser Gly Glu Ala Lys Trp Gly Gln Thr Ser Lys
 725 730 735
 Leu Ile Leu Leu Leu Pro His Gly Tyr Glu Gly Gln Gly Pro Asp His
 740 745 750
 Ser Ser Ala Arg Ile Glu Arg Phe Leu Gln Leu Cys Ala Glu Gly Ser
 755 760 765
 Met Thr Val Ala Gln Pro Ser Thr Pro Ala Asn His Phe His Leu Leu
 770 775 780
 Arg Arg His Ala Leu Ser Asp Leu Lys Arg Pro Leu Val Ile Phe Thr
 785 790 795 800
 Pro Lys Ser Met Leu Arg Asn Lys Ala Ala Ala Ser Ala Pro Glu Asp
 805 810 815
 Phe Thr Glu Val Thr Lys Phe Gln Ser Val Ile Asn Asp Pro Asn Val
 820 825 830
 Ala Asp Ala Ala Lys Val Lys Lys Val Met Leu Val Ser Gly Lys Leu
 835 840 845
 Tyr Tyr Glu Leu Ala Lys Arg Lys Glu Lys Asp Gly Arg Asp Asp Ile
 850 855 860
 Ala Ile Val Arg Ile Glu Met Leu His Pro Ile Pro Phe Asn Arg Ile
 865 870 875 880
 Ser Glu Ala Leu Ala Gly Tyr Pro Asn Ala Glu Glu Val Leu Phe Val
 885 890 895
 Gln Asp Glu Pro Ala Asn Gln Gly Pro Trp Pro Phe Tyr Gln Glu His
 900 905 910
 Leu Pro Glu Leu Ile Pro Asn Met Pro Lys Met Arg Arg Val Ser Arg
 915 920 925
 Arg Ala Gln Ser Ser Thr Ala Thr Gly Val Ala Lys Val His Gln Leu
 930 935 940
 Glu Glu Lys Gln Leu Ile Asp Glu Ala Phe Glu Ala
 945 950 955

<210> 563
 <211> 1517
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1494)
 <223> RXA01745

<400> 563
 atc ctt gca gac gaa gac gac acc gtc gac gtc ggc gca gtc atc gcc 48
 Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly Ala Val Ile Ala
 1 5 10 15
 cgc atc ggt gac gca aac gca gct gca gca cct gcc gaa gag gaa gca 96
 Arg Ile Gly Asp Ala Asn Ala Ala Ala Ala Pro Ala Glu Glu Glu Ala
 20 25 30
 gct cct gcc gaa gag gaa gaa cca gtt aag gaa gag cca aag aag gag 144
 Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu Pro Lys Lys Glu
 35 40 45
 gca gct cct gaa gct cca gca gca act ggc gcc gca acc gat gtg gaa 192
 Ala Ala Pro Glu Ala Pro Ala Ala Thr Gly Ala Ala Thr Asp Val Glu
 50 55 60
 atg cca gaa ctc ggc gaa tcc gtc acc gaa ggc acc att acc cag tgg 240
 Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly Thr Ile Thr Gln Trp
 65 70 75 80
 ctc aag gct gtc ggc gac acc gtc gaa gta gac gaa cca ctt ctt gag 288
 Leu Lys Ala Val Gly Asp Thr Val Glu Val Asp Glu Pro Leu Leu Glu
 85 90 95
 gtc tcc acc gac aag gtc gac acc gaa atc cca tcc cca gta gca ggc 336
 Val Ser Thr Asp Lys Val Asp Thr Glu Ile Pro Ser Pro Val Ala Gly
 100 105 110
 acc atc gtg gag atc ctt gca gac gaa gac gac acc gtc gac gtc ggc 384
 Thr Ile Val Glu Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly
 115 120 125
 gca gtc atc gcc cgc atc ggt gac gca aac gca gct gca gca cct gcc 432
 Ala Val Ile Ala Arg Ile Gly Asp Ala Asn Ala Ala Ala Ala Pro Ala
 130 135 140
 gaa gag gaa gca gct cct gcc gaa gag gag gaa cca gtt aag gaa gag 480
 Glu Glu Glu Ala Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu
 145 150 155 160
 cca aag aag gaa gag ccc aag aag gaa gag ccc aag aag gaa gca gct 528
 Pro Lys Lys Glu Glu Pro Lys Lys Glu Glu Pro Lys Lys Glu Ala Ala
 165 170 175
 act aca cct gct gcg gca tcc gca act gtg tcc gct tct ggc gac aac 576
 Thr Thr Pro Ala Ala Ala Ser Ala Thr Val Ser Ala Ser Gly Asp Asn
 180 185 190
 gtt cca tac gtc acc cca ctg gtg cgc aag ctt gct gaa aag cac ggc 624

Val	Pro	Tyr	Val	Thr	Pro	Leu	Val	Arg	Lys	Leu	Ala	Glu	Lys	His	Gly	
195							200					205				
gtt	gac	ttg	aac	acc	gtg	acc	ggg	acc	ggg	atc	ggg	ggc	cgt	atc	cgc	672
Val	Asp	Leu	Asn	Thr	Val	Thr	Gly	Thr	Gly	Ile	Gly	Gly	Arg	Ile	Arg	
210							215				220					
aag	cag	gat	gtt	ttg	gct	gct	gcg	aac	ggc	gag	gct	gca	cct	gct	gag	720
Lys	Gln	Asp	Val	Leu	Ala	Ala	Ala	Asn	Gly	Glu	Ala	Ala	Pro	Ala	Glu	
225					230					235					240	
gct	gct	gct	cct	gtt	tcc	gct	tgg	tcc	act	aag	tct	gtt	gac	cct	gag	768
Ala	Ala	Ala	Pro	Val	Ser	Ala	Trp	Ser	Thr	Lys	Ser	Val	Asp	Pro	Glu	
				245					250					255		
aag	gct	aag	ctc	cgt	ggg	acc	act	cag	aag	gtc	aac	cgc	atc	cgt	gag	816
Lys	Ala	Lys	Leu	Arg	Gly	Thr	Thr	Gln	Lys	Val	Asn	Arg	Ile	Arg	Glu	
			260					265					270			
atc	acc	gcg	atg	aag	acc	gtc	gag	gct	ctg	cag	att	tct	gct	cag	ctc	864
Ile	Thr	Ala	Met	Lys	Thr	Val	Glu	Ala	Leu	Gln	Ile	Ser	Ala	Gln	Leu	
			275				280					285				
acc	cag	ctg	cac	gag	gtc	gat	atg	act	cgc	gtt	gct	gag	ctg	cgt	aag	912
Thr	Gln	Leu	His	Glu	Val	Asp	Met	Thr	Arg	Val	Ala	Glu	Leu	Arg	Lys	
	290					295					300					
aag	aac	aag	ccc	gcg	ttc	atc	gag	aag	cac	ggg	gtg	aac	ctc	act	tac	960
Lys	Asn	Lys	Pro	Ala	Phe	Ile	Glu	Lys	His	Gly	Val	Asn	Leu	Thr	Tyr	
305					310					315					320	
ctg	cca	ttc	ttc	gtg	aag	gca	gtt	gtc	gag	gct	ttg	gtt	tcc	cat	cca	1008
Leu	Pro	Phe	Phe	Val	Lys	Ala	Val	Val	Glu	Ala	Leu	Val	Ser	His	Pro	
				325					330					335		
aac	gtc	aac	gcg	tct	ttc	aac	gcg	aag	acc	aag	gag	atg	acc	tac	cac	1056
Asn	Val	Asn	Ala	Ser	Phe	Asn	Ala	Lys	Thr	Lys	Glu	Met	Thr	Tyr	His	
			340					345					350			
tcc	tcc	gtt	aac	ctc	tcc	atc	gct	gtt	gat	acc	cca	gct	ggg	ctg	ttg	1104
Ser	Ser	Val	Asn	Leu	Ser	Ile	Ala	Val	Asp	Thr	Pro	Ala	Gly	Leu	Leu	
			355				360					365				
acc	cca	gtc	att	cac	gat	gct	cag	gat	ctc	tcc	atc	cca	gag	atc	gca	1152
Thr	Pro	Val	Ile	His	Asp	Ala	Gln	Asp	Leu	Ser	Ile	Pro	Glu	Ile	Ala	
			370			375					380					
aag	gca	att	gtt	gac	ctg	gct	gat	cgt	tca	cgc	aac	aac	aag	ctg	aag	1200
Lys	Ala	Ile	Val	Asp	Leu	Ala	Asp	Arg	Ser	Arg	Asn	Asn	Lys	Leu	Lys	
385					390					395					400	
cca	aac	gat	ctg	tcc	ggg	ggc	acc	ttc	acc	atc	acc	aac	att	ggg	tct	1248
Pro	Asn	Asp	Leu	Ser	Gly	Gly	Thr	Phe	Thr	Ile	Thr	Asn	Ile	Gly	Ser	
				405					410					415		
gaa	ggc	gca	ctg	tct	gat	acc	cca	atc	ctg	gtt	cca	cca	cag	gct	ggc	1296
Glu	Gly	Ala	Leu	Ser	Asp	Thr	Pro	Ile	Leu	Val	Pro	Pro	Gln	Ala	Gly	
			420					425					430			
atc	ttg	ggc	acc	ggc	gcg	atc	gtg	aag	cgt	cca	gtt	gtc	atc	acc	gag	1344
Ile	Leu	Gly	Thr	Gly	Ala	Ile	Val	Lys	Arg	Pro	Val	Val	Ile	Thr	Glu	

435	440	445	
gat gga att gat tcc atc gcg atc cgt cag atg gtc ttc cta cca ctg			1392
Asp Gly Ile Asp Ser Ile Ala Ile Arg Gln Met Val Phe Leu Pro Leu			
450	455	460	
acc tac gac cac cag gtt gta gat ggc gca gat gct ggt cgc ttc ctg			1440
Thr Tyr Asp His Gln Val Val Asp Gly Ala Asp Ala Gly Arg Phe Leu			
465	470	475	480
acc acc atc aag gac cgc ctt gag acc gct aac ttc gaa ggc gat ctg			1488
Thr Thr Ile Lys Asp Arg Leu Glu Thr Ala Asn Phe Glu Gly Asp Leu			
	485	490	495
cag ctc taagatctct gcaagttaaa acc			1517
Gln Leu			

<210> 564

<211> 498

<212> PRT

<213> Corynebacterium glutamicum

<400> 564

Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly Ala Val Ile Ala			
1	5	10	15
Arg Ile Gly Asp Ala Asn Ala Ala Ala Ala Pro Ala Glu Glu Glu Ala			
20	25	30	
Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu Pro Lys Lys Glu			
35	40	45	
Ala Ala Pro Glu Ala Pro Ala Ala Thr Gly Ala Ala Thr Asp Val Glu			
50	55	60	
Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly Thr Ile Thr Gln Trp			
65	70	75	80
Leu Lys Ala Val Gly Asp Thr Val Glu Val Asp Glu Pro Leu Leu Glu			
85	90	95	
Val Ser Thr Asp Lys Val Asp Thr Glu Ile Pro Ser Pro Val Ala Gly			
100	105	110	
Thr Ile Val Glu Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly			
115	120	125	
Ala Val Ile Ala Arg Ile Gly Asp Ala Asn Ala Ala Ala Ala Pro Ala			
130	135	140	
Glu Glu Glu Ala Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu			
145	150	155	160
Pro Lys Lys Glu Glu Pro Lys Lys Glu Glu Pro Lys Lys Glu Ala Ala			
165	170	175	
Thr Thr Pro Ala Ala Ala Ser Ala Thr Val Ser Ala Ser Gly Asp Asn			
180	185	190	

Val Pro Tyr Val Thr Pro Leu Val Arg Lys Leu Ala Glu Lys His Gly
 195 200 205
 Val Asp Leu Asn Thr Val Thr Gly Thr Gly Ile Gly Gly Arg Ile Arg
 210 215 220
 Lys Gln Asp Val Leu Ala Ala Asn Gly Glu Ala Ala Pro Ala Glu
 225 230 235 240
 Ala Ala Ala Pro Val Ser Ala Trp Ser Thr Lys Ser Val Asp Pro Glu
 245 250 255
 Lys Ala Lys Leu Arg Gly Thr Thr Gln Lys Val Asn Arg Ile Arg Glu
 260 265 270
 Ile Thr Ala Met Lys Thr Val Glu Ala Leu Gln Ile Ser Ala Gln Leu
 275 280 285
 Thr Gln Leu His Glu Val Asp Met Thr Arg Val Ala Glu Leu Arg Lys
 290 295 300
 Lys Asn Lys Pro Ala Phe Ile Glu Lys His Gly Val Asn Leu Thr Tyr
 305 310 315 320
 Leu Pro Phe Phe Val Lys Ala Val Val Glu Ala Leu Val Ser His Pro
 325 330 335
 Asn Val Asn Ala Ser Phe Asn Ala Lys Thr Lys Glu Met Thr Tyr His
 340 345 350
 Ser Ser Val Asn Leu Ser Ile Ala Val Asp Thr Pro Ala Gly Leu Leu
 355 360 365
 Thr Pro Val Ile His Asp Ala Gln Asp Leu Ser Ile Pro Glu Ile Ala
 370 375 380
 Lys Ala Ile Val Asp Leu Ala Asp Arg Ser Arg Asn Asn Lys Leu Lys
 385 390 395 400
 Pro Asn Asp Leu Ser Gly Gly Thr Phe Thr Ile Thr Asn Ile Gly Ser
 405 410 415
 Glu Gly Ala Leu Ser Asp Thr Pro Ile Leu Val Pro Pro Gln Ala Gly
 420 425 430
 Ile Leu Gly Thr Gly Ala Ile Val Lys Arg Pro Val Val Ile Thr Glu
 435 440 445
 Asp Gly Ile Asp Ser Ile Ala Ile Arg Gln Met Val Phe Leu Pro Leu
 450 455 460
 Thr Tyr Asp His Gln Val Val Asp Gly Ala Asp Ala Gly Arg Phe Leu
 465 470 475 480
 Thr Thr Ile Lys Asp Arg Leu Glu Thr Ala Asn Phe Glu Gly Asp Leu
 485 490 495
 Gln Leu

```
<220>  
<221> CDS  
<222> (101)..(982)  
<223> RXA00782
```

811

ggc ggt gac cca atc atc ggt aca acc cat atc gac gct ctg gag gcc 691
 Gly Gly Asp Pro Ile Ile Gly Thr Thr His Ile Asp Ala Leu Glu Ala
 185 190 195

ttt gaa gct gat cct gag acc aag gca atc gtc atg atc ggt gag atc 739
 Phe Glu Ala Asp Pro Glu Thr Lys Ala Ile Val Met Ile Gly Glu Ile
 200 205 210

ggt gga gat gca gag gaa cgc gct gct gac ttc att tct aag cac gtg 787
 Gly Gly Asp Ala Glu Glu Arg Ala Ala Asp Phe Ile Ser Lys His Val
 215 220 225

aca aaa cca gtt gtg ggt tac gtg gca ggc ttt acc gcc cct gaa gga 835
 Thr Lys Pro Val Val Gly Tyr Val Ala Gly Phe Thr Ala Pro Glu Gly
 230 235 240 245

aag acc atg ggg cat gct ggc gcc atc gtg aca ggt tca gaa ggc act 883
 Lys Thr Met Gly His Ala Gly Ala Ile Val Thr Gly Ser Glu Gly Thr
 250 255 260

gcg cga gca aag aag cat gca ttg gag gcc gtg ggt gtt cgc gtg gga 931
 Ala Arg Ala Lys Lys His Ala Leu Glu Ala Val Gly Val Arg Val Gly
 265 270 275

aca act ccg agt gaa acc gcg aag ctt atg cgt gag gta gtt gca gct 979
 Thr Thr Pro Ser Glu Thr Ala Lys Leu Met Arg Glu Val Val Ala Ala
 280 285 290

ttg taactaacag gccacagatc tta 1005
 Leu

<210> 566

<211> 294

<212> PRT

<213> Corynebacterium glutamicum

<400> 566

Met Ser Ile Phe Leu Asn Ser Asp Ser Arg Ile Ile Ile Gln Gly Ile
 1 5 10 15

Thr Gly Ser Glu Gly Ser Glu His Ala Arg Arg Ile Leu Ala Ser Gly
 20 25 30

Ala Lys Leu Val Gly Gly Thr Asn Pro Arg Lys Ala Gly Gln Thr Ile
 35 40 45

Leu Ile Asn Asp Thr Glu Leu Pro Val Phe Gly Thr Val Lys Glu Ala
 50 55 60

Met Glu Glu Thr Gly Ala Asp Val Thr Val Ile Phe Val Pro Pro Ala
 65 70 75 80

Phe Ala Lys Ala Ala Ile Ile Glu Ala Ile Asp Ala His Ile Pro Leu
 85 90 95

Cys Val Ile Ile Thr Glu Gly Ile Pro Val Arg Asp Ala Ser Glu Ala
 100 105 110

Trp Ala Tyr Ala Lys Lys Val Gly His Thr Arg Ile Ile Gly Pro Asn

115					120					125					
Cys	Pro	Gly	Ile	Ile	Thr	Pro	Gly	Glu	Ser	Leu	Ala	Gly	Ile	Thr	Pro
130						135					140				
Ala	Asn	Ile	Ala	Gly	Ser	Gly	Pro	Ile	Gly	Leu	Ile	Ser	Lys	Ser	Gly
145				150						155					160
Thr	Leu	Thr	Tyr	Gln	Met	Met	Tyr	Glu	Leu	Ser	Asp	Ile	Gly	Ile	Ser
				165					170					175	
Thr	Ala	Ile	Gly	Ile	Gly	Gly	Asp	Pro	Ile	Ile	Gly	Thr	Thr	His	Ile
		180						185					190		
Asp	Ala	Leu	Glu	Ala	Phe	Glu	Ala	Asp	Pro	Glu	Thr	Lys	Ala	Ile	Val
	195						200					205			
Met	Ile	Gly	Glu	Ile	Gly	Gly	Asp	Ala	Glu	Glu	Arg	Ala	Ala	Asp	Phe
210					215						220				
Ile	Ser	Lys	His	Val	Thr	Lys	Pro	Val	Val	Gly	Tyr	Val	Ala	Gly	Phe
225					230					235					240
Thr	Ala	Pro	Glu	Gly	Lys	Thr	Met	Gly	His	Ala	Gly	Ala	Ile	Val	Thr
				245					250					255	
Gly	Ser	Glu	Gly	Thr	Ala	Arg	Ala	Lys	Lys	His	Ala	Leu	Glu	Ala	Val
			260					265					270		
Gly	Val	Arg	Val	Gly	Thr	Thr	Pro	Ser	Glu	Thr	Ala	Lys	Leu	Met	Arg
	275						280					285			
Glu	Val	Val	Ala	Ala	Leu										
290															

<210> 567
 <211> 1395
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1372)
 <223> RXA00783

<400> 567
 aaagtccca aggggtgggg gctgagcacc acggatccaa tttgttgca atttgcaaag 60

tttacagtgt tagacttcac aatacgatca tattggtgag ttg aaa cac tta ctt 115
 Leu Lys His Leu Leu
 1 5

tta cgg gaa gac ttt gtt aaa gac gca gaa ggc tct aag cat ggg ccg 163
 Leu Arg Glu Asp Phe Val Lys Asp Ala Glu Gly Ser Lys His Gly Pro
 10 15 20

gaa atg gaa ttg gca gtg gat ctt ttt gaa tac caa gca cgg gac ctc 211
 Glu Met Glu Leu Ala Val Asp Leu Phe Glu Tyr Gln Ala Arg Asp Leu
 25 30 35

ttt gaa acc cat ggt gtg cca gtg ttg aag gga att gtg gca tca aca	259
Phe Glu Thr His Gly Val Pro Val Leu Lys Gly Ile Val Ala Ser Thr	
40 45 50	
cca gag gcg gcg agg aaa gcg gct gag gaa atc ggc gga ctg acc gtc	307
Pro Glu Ala Ala Arg Lys Ala Ala Glu Glu Ile Gly Gly Leu Thr Val	
55 60 65	
gtc aag gct cag gtc aag gtg ggc gga cgt ggc aag gcg ggt ggc gtc	355
Val Lys Ala Gln Val Lys Val Gly Gly Arg Gly Lys Ala Gly Gly Val	
70 75 80 85	
cgt gtg gca ccg acg tcg gct cag gct ttt gat gct gcg gat gcg att	403
Arg Val Ala Pro Thr Ser Ala Gln Ala Phe Asp Ala Ala Asp Ala Ile	
90 95 100	
ctc ggc atg gat atc aaa gga cac act gtt aat cag gtg atg gtg gcg	451
Leu Gly Met Asp Ile Lys Gly His Thr Val Asn Gln Val Met Val Ala	
105 110 115	
cag ggc gct gac att gct gag gaa tac tat ttc tcc att ttg ttg gat	499
Gln Gly Ala Asp Ile Ala Glu Glu Tyr Tyr Phe Ser Ile Leu Leu Asp	
120 125 130	
cgc gcg aat cgt tcg tat ctg gct atg tgc tct gtt gaa ggt ggc atg	547
Arg Ala Asn Arg Ser Tyr Leu Ala Met Cys Ser Val Glu Gly Gly Met	
135 140 145	
gag atc gag atc ctg gcg aag gaa aag cct gaa gct ttg gca aag gtg	595
Glu Ile Glu Ile Leu Ala Lys Glu Lys Pro Glu Ala Leu Ala Lys Val	
150 155 160 165	
gaa gtg gat ccc ctc act ggt att gat gag gac aaa gcg cgg gag att	643
Glu Val Asp Pro Leu Thr Gly Ile Asp Glu Asp Lys Ala Arg Glu Ile	
170 175 180	
gtc act gct gct ggc ttt gaa act gag gtg gca gag aaa gtc att ccg	691
Val Thr Ala Ala Gly Phe Glu Thr Glu Val Ala Glu Lys Val Ile Pro	
185 190 195	
gtg ctg atc aag atc tgg cag gtg tat tac gaa gag gaa gca aca ctc	739
Val Leu Ile Lys Ile Trp Gln Val Tyr Tyr Glu Glu Ala Thr Leu	
200 205 210	
gtt gag gtg aac ccg ttg gtg ctc acg gat gac ggc gat gtg att gcg	787
Val Glu Val Asn Pro Leu Val Leu Thr Asp Asp Gly Asp Val Ile Ala	
215 220 225	
ctt gat ggc aag atc acg ctg gat gat aac gct gat ttc cgc cat gat	835
Leu Asp Gly Lys Ile Thr Leu Asp Asp Asn Ala Asp Phe Arg His Asp	
230 235 240 245	
aac cgt ggt gcg ttg gct gaa tct gcc ggt ggc ttg gac att ttg gaa	883
Asn Arg Gly Ala Leu Ala Glu Ser Ala Gly Gly Leu Asp Ile Leu Glu	
250 255 260	
ctg aag gcc aag aag aat gat ctg aac tac gtg aaa ctt gat ggc tct	931
Leu Lys Ala Lys Lys Asn Asp Leu Asn Tyr Val Lys Leu Asp Gly Ser	
265 270 275	
gtg ggc atc att ggc aat ggt gca ggt ttg gtg atg tcc acg ttg gat	979

Val Gly Ile Ile Gly Asn Gly Ala Gly Leu Val Met Ser Thr Leu Asp
 280 285 290

atc gtg gct gca gct ggt gaa cgc cat ggt ggg cag cgc ccc gcg aac 1027
 Ile Val Ala Ala Ala Gly Glu Arg His Gly Gly Gln Arg Pro Ala Asn
 295 300 305

ttc cta gac att ggt ggc gga gca tca gct gaa tcg atg gct gct ggt 1075
 Phe Leu Asp Ile Gly Gly Gly Ala Ser Ala Glu Ser Met Ala Ala Gly
 310 315 320 325

ctc gat gtg atc ctt ggg gat agc cag gta cgc agt gtg ttt gtg aat 1123
 Leu Asp Val Ile Leu Gly Asp Ser Gln Val Arg Ser Val Phe Val Asn
 330 335 340

gtg ttt ggt ggc atc acc gcg tgt gat gtg gtg gca aag gga atc gtt 1171
 Val Phe Gly Gly Ile Thr Ala Cys Asp Val Val Ala Lys Gly Ile Val
 345 350 355

gga gct ttg gat gtg ctc ggc gat caa gca acg aag cct ctt gtg gtg 1219
 Gly Ala Leu Asp Val Leu Gly Asp Gln Ala Thr Lys Pro Leu Val Val
 360 365 370

cgc ctt gat ggc aac aac gtg gtg gaa ggc aga cga atc ctc gcg gaa 1267
 Arg Leu Asp Gly Asn Asn Val Val Glu Gly Arg Arg Ile Leu Ala Glu
 375 380 385

tat aac cac cct ttg gtc acc gtt gtg gag ggt atg gat gca gcg gct 1315
 Tyr Asn His Pro Leu Val Thr Val Val Glu Gly Met Asp Ala Ala Ala
 390 395 400 405

gat cac gct gcc cat ttg gcc aat ctt gcc cag cac ggc cag ttc gca 1363
 Asp His Ala Ala His Leu Ala Asn Leu Ala Gln His Gly Gln Phe Ala
 410 415 420

acc gct aat tagttaagga gcacctgttt aat 1395
 Thr Ala Asn

<210> 568

<211> 424

<212> PRT

<213> Corynebacterium glutamicum

<400> 568

Leu Lys His Leu Leu Leu Arg Glu Asp Phe Val Lys Asp Ala Glu Gly
 1 5 10 15

Ser Lys His Gly Pro Glu Met Glu Leu Ala Val Asp Leu Phe Glu Tyr
 20 25 30

Gln Ala Arg Asp Leu Phe Glu Thr His Gly Val Pro Val Leu Lys Gly
 35 40 45

Ile Val Ala Ser Thr Pro Glu Ala Ala Arg Lys Ala Ala Glu Glu Ile
 50 55 60

Gly Gly Leu Thr Val Val Lys Ala Gln Val Lys Val Gly Gly Arg Gly
 65 70 75 80

Lys	Ala	Gly	Gly	Val	Arg	Val	Ala	Pro	Thr	Ser	Ala	Gln	Ala	Phe	Asp	
				85					90					95		
Ala	Ala	Asp	Ala	Ile	Leu	Gly	Met	Asp	Ile	Lys	Gly	His	Thr	Val	Asn	
			100					105					110			
Gln	Val	Met	Val	Ala	Gln	Gly	Ala	Asp	Ile	Ala	Glu	Glu	Tyr	Tyr	Phe	
		115					120					125				
Ser	Ile	Leu	Leu	Asp	Arg	Ala	Asn	Arg	Ser	Tyr	Leu	Ala	Met	Cys	Ser	
	130					135					140					
Val	Glu	Gly	Gly	Met	Glu	Ile	Glu	Ile	Leu	Ala	Lys	Glu	Lys	Pro	Glu	
145					150					155					160	
Ala	Leu	Ala	Lys	Val	Glu	Val	Asp	Pro	Leu	Thr	Gly	Ile	Asp	Glu	Asp	
				165					170					175		
Lys	Ala	Arg	Glu	Ile	Val	Thr	Ala	Ala	Gly	Phe	Glu	Thr	Glu	Val	Ala	
			180					185					190			
Glu	Lys	Val	Ile	Pro	Val	Leu	Ile	Lys	Ile	Trp	Gln	Val	Tyr	Tyr	Glu	
		195					200					205				
Glu	Glu	Ala	Thr	Leu	Val	Glu	Val	Asn	Pro	Leu	Val	Leu	Thr	Asp	Asp	
	210					215					220					
Gly	Asp	Val	Ile	Ala	Leu	Asp	Gly	Lys	Ile	Thr	Leu	Asp	Asp	Asn	Ala	
225					230					235					240	
Asp	Phe	Arg	His	Asp	Asn	Arg	Gly	Ala	Leu	Ala	Glu	Ser	Ala	Gly	Gly	
				245					250					255		
Leu	Asp	Ile	Leu	Glu	Leu	Lys	Ala	Lys	Lys	Asn	Asp	Leu	Asn	Tyr	Val	
			260					265					270			
Lys	Leu	Asp	Gly	Ser	Val	Gly	Ile	Ile	Gly	Asn	Gly	Ala	Gly	Leu	Val	
		275					280					285				
Met	Ser	Thr	Leu	Asp	Ile	Val	Ala	Ala	Ala	Gly	Glu	Arg	His	Gly	Gly	
	290					295					300					
Gln	Arg	Pro	Ala	Asn	Phe	Leu	Asp	Ile	Gly	Gly	Gly	Ala	Ser	Ala	Glu	
305					310					315					320	
Ser	Met	Ala	Ala	Gly	Leu	Asp	Val	Ile	Leu	Gly	Asp	Ser	Gln	Val	Arg	
				325					330					335		
Ser	Val	Phe	Val	Asn	Val	Phe	Gly	Gly	Ile	Thr	Ala	Cys	Asp	Val	Val	
			340					345					350			
Ala	Lys	Gly	Ile	Val	Gly	Ala	Leu	Asp	Val	Leu	Gly	Asp	Gln	Ala	Thr	
		355					360					365				
Lys	Pro	Leu	Val	Val	Arg	Leu	Asp	Gly	Asn	Asn	Val	Val	Glu	Gly	Arg	
	370					375					380					
Arg	Ile	Leu	Ala	Glu	Tyr	Asn	His	Pro	Leu	Val	Thr	Val	Val	Glu	Gly	
385					390					395					400	
Met	Asp	Ala	Ala	Ala	Asp	His	Ala	Ala	His	Leu	Ala	Asn	Leu	Ala	Gln	

817

150	155	160	165	
ttg atg gca aag ggc cgt gac ttc tct gat cca gta gca atc tct tgg				643
Leu Met Ala Lys Gly Arg Asp Phe Ser Asp Pro Val Ala Ile Ser Trp				
170		175	180	
atc gat gaa ggc acc gac atc aac tac ggt gct cag acc aag cag tac				691
Ile Asp Glu Gly Thr Asp Ile Asn Tyr Gly Ala Gln Thr Lys Gln Tyr				
185		190	195	
ctg gat gca gct gaa gtt gaa ggc act gaa atc cgc tat ggc cac gaa				739
Leu Asp Ala Ala Glu Val Glu Gly Thr Glu Ile Arg Tyr Gly His Glu				
200		205	210	
gtc aag agc atc aag gct gat ggc gca aag tgg atc gtg acc gtc aag				787
Val Lys Ser Ile Lys Ala Asp Gly Ala Lys Trp Ile Val Thr Val Lys				
215		220	225	
aac gta cac act ggc gac acc aag acc atc aag gca aac ttc gtg ttc				835
Asn Val His Thr Gly Asp Thr Lys Thr Ile Lys Ala Asn Phe Val Phe				
230		235	240	245
gtc ggc gca ggc gga tac gca ctg gat ctg ctt cgc agc gca ggc atc				883
Val Gly Ala Gly Gly Tyr Ala Leu Asp Leu Leu Arg Ser Ala Gly Ile				
250		255	260	
cca cag gtc aag ggc ttc gct gga ttc cca gta tcc ggc ctg tgg ctt				931
Pro Gln Val Lys Gly Phe Ala Gly Phe Pro Val Ser Gly Leu Trp Leu				
265		270	275	
cgt tgc acc aac gag gaa ctg atc gag cag cac gca gcc aag gta tat				979
Arg Cys Thr Asn Glu Glu Leu Ile Glu Gln His Ala Ala Lys Val Tyr				
280		285	290	
ggc aag gca tct gtt ggc gct cct cca atg tct gtt cct cac ctt gac				1027
Gly Lys Ala Ser Val Gly Ala Pro Pro Met Ser Val Pro His Leu Asp				
295		300	305	
acc cgc gtt atc gag ggt gaa aag ggt ctg ctc ttt gga cct tac ggt				1075
Thr Arg Val Ile Glu Gly Glu Lys Gly Leu Leu Phe Gly Pro Tyr Gly				
310		315	320	325
ggc tgg acc cct aag ttc ttg aag gaa ggc tcc tac ctg gac ctg ttc				1123
Gly Trp Thr Pro Lys Phe Leu Lys Glu Gly Ser Tyr Leu Asp Leu Phe				
330		335	340	
aag tcc atc cgc cca gac aac att cct tcc tac ctt ggc gtt gct gct				1171
Lys Ser Ile Arg Pro Asp Asn Ile Pro Ser Tyr Leu Gly Val Ala Ala				
345		350	355	
cag gaa ttt gat ctg acc aag tac ctt gtc act gaa gtt ctc aag gac				1219
Gln Glu Phe Asp Leu Thr Lys Tyr Leu Val Thr Glu Val Leu Lys Asp				
360		365	370	
cag gac aag cgt atg gat gct ctt cgc gag tac atg cca gag gca caa				1267
Gln Asp Lys Arg Met Asp Ala Leu Arg Glu Tyr Met Pro Glu Ala Gln				
375		380	385	
aac ggc gat tgg gag acc atc gtt gcc gga cag cgt gtt cag gtt att				1315
Asn Gly Asp Trp Glu Thr Ile Val Ala Gly Gln Arg Val Gln Val Ile				
390		395	400	405

aag cct gca gga ttc cct aag ttc ggt tcc ctg gaa ttc ggc acc acc 1363
Lys Pro Ala Gly Phe Pro Lys Phe Gly Ser Leu Glu Phe Gly Thr Thr
410 415 420

ttg atc aac aac tcc gaa ggc acc atc gcc gga ttg ctc ggt gct tcc 1411
Leu Ile Asn Asn Ser Glu Gly Thr Ile Ala Gly Leu Leu Gly Ala Ser
425 430 435

cct gga gca tcc atc gca cct tcc gca atg atc gag ctg ctt gag cgt 1459
Pro Gly Ala Ser Ile Ala Pro Ser Ala Met Ile Glu Leu Leu Glu Arg
440 445 450

tgc ttc ggt gac cgc atg atc gag tgg ggc gac aag ctg aag gac atg 1507
Cys Phe Gly Asp Arg Met Ile Glu Trp Gly Asp Lys Leu Lys Asp Met
455 460 465

atc cct tcc tac ggc aag aag ctt gct tcc gag cca gca ctg ttt gag 1555
Ile Pro Ser Tyr Gly Lys Lys Leu Ala Ser Glu Pro Ala Leu Phe Glu
470 475 480 485

cag cag tgg gca cgc acc cag aag acc ctg aag ctt gag gaa gcc 1600
Gln Gln Trp Ala Arg Thr Gln Lys Thr Leu Lys Leu Glu Glu Ala
490 495 500

taaattcttct aactgctttc ttt 1623

<210> 570
<211> 500
<212> PRT
<213> Corynebacterium glutamicum

<400> 570
Met Ser Asp Ser Pro Lys Asn Ala Pro Arg Ile Thr Asp Glu Ala Asp
1 5 10 15
Val Val Leu Ile Gly Ala Gly Ile Met Ser Ser Thr Leu Gly Ala Met
20 25 30
Leu Arg Gln Leu Glu Pro Ser Trp Thr Gln Ile Val Phe Glu Arg Leu
35 40 45
Asp Gly Pro Ala Gln Glu Ser Ser Ser Pro Trp Asn Asn Ala Gly Thr
50 55 60
Gly His Ser Ala Leu Cys Glu Leu Asn Tyr Thr Pro Glu Val Lys Gly
65 70 75 80
Lys Val Glu Ile Ala Lys Ala Val Gly Ile Asn Glu Lys Phe Gln Val
85 90 95
Ser Arg Gln Phe Trp Ser His Leu Val Glu Glu Gly Val Leu Ser Asp
100 105 110
Pro Lys Glu Phe Ile Asn Pro Val Pro His Val Ser Phe Gly Gln Gly
115 120 125
Ala Asp Gln Val Ala Tyr Ile Lys Ala Arg Tyr Glu Ala Leu Lys Asp
130 135 140

His Pro Leu Phe Gln Gly Met Thr Tyr Ala Asp Asp Glu Ala Thr Phe
 145 150 155 160
 Thr Glu Lys Leu Pro Leu Met Ala Lys Gly Arg Asp Phe Ser Asp Pro
 165 170 175
 Val Ala Ile Ser Trp Ile Asp Glu Gly Thr Asp Ile Asn Tyr Gly Ala
 180 185 190
 Gln Thr Lys Gln Tyr Leu Asp Ala Ala Glu Val Glu Gly Thr Glu Ile
 195 200 205
 Arg Tyr Gly His Glu Val Lys Ser Ile Lys Ala Asp Gly Ala Lys Trp
 210 215 220
 Ile Val Thr Val Lys Asn Val His Thr Gly Asp Thr Lys Thr Ile Lys
 225 230 235 240
 Ala Asn Phe Val Phe Val Gly Ala Gly Gly Tyr Ala Leu Asp Leu Leu
 245 250 255
 Arg Ser Ala Gly Ile Pro Gln Val Lys Gly Phe Ala Gly Phe Pro Val
 260 265 270
 Ser Gly Leu Trp Leu Arg Cys Thr Asn Glu Glu Leu Ile Glu Gln His
 275 280 285
 Ala Ala Lys Val Tyr Gly Lys Ala Ser Val Gly Ala Pro Pro Met Ser
 290 295 300
 Val Pro His Leu Asp Thr Arg Val Ile Glu Gly Glu Lys Gly Leu Leu
 305 310 315 320
 Phe Gly Pro Tyr Gly Gly Trp Thr Pro Lys Phe Leu Lys Glu Gly Ser
 325 330 335
 Tyr Leu Asp Leu Phe Lys Ser Ile Arg Pro Asp Asn Ile Pro Ser Tyr
 340 345 350
 Leu Gly Val Ala Ala Gln Glu Phe Asp Leu Thr Lys Tyr Leu Val Thr
 355 360 365
 Glu Val Leu Lys Asp Gln Asp Lys Arg Met Asp Ala Leu Arg Glu Tyr
 370 375 380
 Met Pro Glu Ala Gln Asn Gly Asp Trp Glu Thr Ile Val Ala Gly Gln
 385 390 395 400
 Arg Val Gln Val Ile Lys Pro Ala Gly Phe Pro Lys Phe Gly Ser Leu
 405 410 415
 Glu Phe Gly Thr Thr Leu Ile Asn Asn Ser Glu Gly Thr Ile Ala Gly
 420 425 430
 Leu Leu Gly Ala Ser Pro Gly Ala Ser Ile Ala Pro Ser Ala Met Ile
 435 440 445
 Glu Leu Leu Glu Arg Cys Phe Gly Asp Arg Met Ile Glu Trp Gly Asp
 450 455 460
 Lys Leu Lys Asp Met Ile Pro Ser Tyr Gly Lys Lys Leu Ala Ser Glu

465 470 475 480

Pro Ala Leu Phe Glu Gln Gln Trp Ala Arg Thr Gln Lys Thr Leu Lys
 485 490 495

Leu Glu Glu Ala
 500

```
<210> 571
<211> 1039
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(1039)  
<223> FRXA01615
```

<400> 571															
tatggccaac	acttgcat	tc	gggtgctggc	gatcatttat	gagatgacgc	cttgtgttgg	60								
tgttcggcag	agaactcgcg	gagataaaag	gaagttgaac	atg	tca	gat	tcc	ccg	115						
				Met	Ser	Asp	Ser	Pro							
				1				5							
aag aac gca ccg agg att acc gat gag gca gat gta gtt ctc att ggt	163														
Lys Asn Ala Pro Arg Ile Thr Asp Glu Ala Asp Val Val Leu Ile Gly															
	10						15						20		
gcc ggt atc atg agc tcc acg ctg ggt gca atg ctg cgt cag ctg gag	211														
Ala Gly Ile Met Ser Ser Thr Leu Gly Ala Met Leu Arg Gln Leu Glu															
	25						30						35		
cca agc tgg act cag atc gtc ttc gag cgt ttg gat gga ccg gca caa	259														
Pro Ser Trp Thr Gln Ile Val Phe Glu Arg Leu Asp Gly Pro Ala Gln															
	40						45					50			
gag tcg tcc tcc ccg tgg aac aat gca gga acc ggc cac tct gct cta	307														
Glu Ser Ser Ser Pro Trp Asn Asn Ala Gly Thr Gly His Ser Ala Leu															
	55					60					65				
tgc gag ctg aac tac acc cca gag gtt aag ggc aag gtt gaa att gcc	355														
Cys Glu Leu Asn Tyr Thr Pro Glu Val Lys Gly Lys Val Glu Ile Ala															
	70					75				80				85	
aag gct gta gga atc aac gag aag ttc cag gtt tcc cgt cag ttc tgg	403														
Lys Ala Val Gly Ile Asn Glu Lys Phe Gln Val Ser Arg Gln Phe Trp															
	90							95						100	
tct cac ctc gtt gaa gag gga gtg ctg tct gat cct aag gaa ttc atc	451														
Ser His Leu Val Glu Glu Gly Val Leu Ser Asp Pro Lys Glu Phe Ile															
	105							110					115		
aac cct gtt cct cac gta tct ttc ggc cag ggc gca gat cag gtt gca	499														
Asn Pro Val Pro His Val Ser Phe Gly Gln Gly Ala Asp Gln Val Ala															
	120						125					130			
tac atc aag gct cgc tac gaa gct ttg aag gat cac cca ctc ttc cag	547														
Tyr Ile Lys Ala Arg Tyr Glu Ala Leu Lys Asp His Pro Leu Phe Gln															
	135					140					145				

ggc atg acc tac gct gac gat gaa gct acc ttc acc gag aag ctg cct 595
 Gly Met Thr Tyr Ala Asp Asp Glu Ala Thr Phe Thr Glu Lys Leu Pro
 150 155 160 165

ttg atg gca aag ggc cgt gac ttc tct gat cca gta gca atc tct tgg 643
 Leu Met Ala Lys Gly Arg Asp Phe Ser Asp Pro Val Ala Ile Ser Trp
 170 175 180

atc gat gaa ggc acc gac atc aac tac ggt gct cag acc aag cag tac 691
 Ile Asp Glu Gly Thr Asp Ile Asn Tyr Gly Ala Gln Thr Lys Gln Tyr
 185 190 195

ctg gat gca gct gaa gtt gaa ggc act gaa atc cgc tat ggc cac gaa 739
 Leu Asp Ala Ala Glu Val Glu Gly Thr Glu Ile Arg Tyr Gly His Glu
 200 205 210

gtc aag agc atc aag gct gat ggc gca aag tgg atc gtg acc gtc aag 787
 Val Lys Ser Ile Lys Ala Asp Gly Ala Lys Trp Ile Val Thr Val Lys
 215 220 225

aac gta cac act ggc gac acc aag acc atc aag gca aac ttc gtg ttc 835
 Asn Val His Thr Gly Asp Thr Lys Thr Ile Lys Ala Asn Phe Val Phe
 230 235 240 245

gtc ggc gca ggc gga tac gca ctg gat ctg ctt cgc agc gca ggc atc 883
 Val Gly Ala Gly Gly Tyr Ala Leu Asp Leu Leu Arg Ser Ala Gly Ile
 250 255 260

cca cag gtc aag ggc ttc gct gga ttc cca gta tcc ggc ctg tgg ctt 931
 Pro Gln Val Lys Gly Phe Ala Gly Phe Pro Val Ser Gly Leu Trp Leu
 265 270 275

cgt tgc acc aac gag gaa ctg atc gag cag cac gca gcc aag gta tat 979
 Arg Cys Thr Asn Glu Glu Leu Ile Glu Gln His Ala Ala Lys Val Tyr
 280 285 290

ggc aag gca tct gtt ggc gct cct cca atg tct gtt cct cac ctt gac 1027
 Gly Lys Ala Ser Val Gly Ala Pro Pro Met Ser Val Pro His Leu Asp
 295 300 305

acc cgc gtt atc 1039
 Thr Arg Val Ile
 310

<210> 572
 <211> 313
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 572
 Met Ser Asp Ser Pro Lys Asn Ala Pro Arg Ile Thr Asp Glu Ala Asp
 1 5 10 15
 Val Val Leu Ile Gly Ala Gly Ile Met Ser Ser Thr Leu Gly Ala Met
 20 25 30
 Leu Arg Gln Leu Glu Pro Ser Trp Thr Gln Ile Val Phe Glu Arg Leu
 35 40 45

Asp Gly Pro Ala Gln Glu Ser Ser Ser Pro Trp Asn Asn Ala Gly Thr
 50 55 60
 Gly His Ser Ala Leu Cys Glu Leu Asn Tyr Thr Pro Glu Val Lys Gly
 65 70 75 80
 Lys Val Glu Ile Ala Lys Ala Val Gly Ile Asn Glu Lys Phe Gln Val
 85 90 95
 Ser Arg Gln Phe Trp Ser His Leu Val Glu Glu Gly Val Leu Ser Asp
 100 105 110
 Pro Lys Glu Phe Ile Asn Pro Val Pro His Val Ser Phe Gly Gln Gly
 115 120 125
 Ala Asp Gln Val Ala Tyr Ile Lys Ala Arg Tyr Glu Ala Leu Lys Asp
 130 135 140
 His Pro Leu Phe Gln Gly Met Thr Tyr Ala Asp Asp Glu Ala Thr Phe
 145 150 155 160
 Thr Glu Lys Leu Pro Leu Met Ala Lys Gly Arg Asp Phe Ser Asp Pro
 165 170 175
 Val Ala Ile Ser Trp Ile Asp Glu Gly Thr Asp Ile Asn Tyr Gly Ala
 180 185 190
 Gln Thr Lys Gln Tyr Leu Asp Ala Ala Glu Val Glu Gly Thr Glu Ile
 195 200 205
 Arg Tyr Gly His Glu Val Lys Ser Ile Lys Ala Asp Gly Ala Lys Trp
 210 215 220
 Ile Val Thr Val Lys Asn Val His Thr Gly Asp Thr Lys Thr Ile Lys
 225 230 235 240
 Ala Asn Phe Val Phe Val Gly Ala Gly Gly Tyr Ala Leu Asp Leu Leu
 245 250 255
 Arg Ser Ala Gly Ile Pro Gln Val Lys Gly Phe Ala Gly Phe Pro Val
 260 265 270
 Ser Gly Leu Trp Leu Arg Cys Thr Asn Glu Glu Leu Ile Glu Gln His
 275 280 285
 Ala Ala Lys Val Tyr Gly Lys Ala Ser Val Gly Ala Pro Pro Met Ser
 290 295 300
 Val Pro His Leu Asp Thr Arg Val Ile
 305 310

<210> 573

<211> 233

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(210)

<223> FRXA01695

<400> 573

gcc gga ttg ctc ggt gct tcc cct gga gca tcc atc gca cct tcc gca 48
 Ala Gly Leu Leu Gly Ala Ser Pro Gly Ala Ser Ile Ala Pro Ser Ala
 1 5 10 15

atg atc gag ctg ctt gag cgt tgc ttc ggt gac cgc atg atc gag tgg 96
 Met Ile Glu Leu Leu Glu Arg Cys Phe Gly Asp Arg Met Ile Glu Trp
 20 25 30

ggc gac aag ctg aag gac atg atc cct tcc tac ggc aag aag ctt gct 144
 Gly Asp Lys Leu Lys Asp Met Ile Pro Ser Tyr Gly Lys Lys Leu Ala
 35 40 45

tcc gag cca gca ctg ttt gag cag cag tgg gca cgc acc cag aag acc 192
 Ser Glu Pro Ala Leu Phe Glu Gln Gln Trp Ala Arg Thr Gln Lys Thr
 50 55 60

ctg aag ctt gag gaa gcc taaatcttct aactgctttc ttt 233
 Leu Lys Leu Glu Glu Ala
 65 70

<210> 574

<211> 70

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 574

Ala Gly Leu Leu Gly Ala Ser Pro Gly Ala Ser Ile Ala Pro Ser Ala
 1 5 10 15

Met Ile Glu Leu Leu Glu Arg Cys Phe Gly Asp Arg Met Ile Glu Trp
 20 25 30

Gly Asp Lys Leu Lys Asp Met Ile Pro Ser Tyr Gly Lys Lys Leu Ala
 35 40 45

Ser Glu Pro Ala Leu Phe Glu Gln Gln Trp Ala Arg Thr Gln Lys Thr
 50 55 60

Leu Lys Leu Glu Glu Ala
 65 70

<210> 575

<211> 1063

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1063)

<223> RXA00290

<400> 575

agctacagat ttagctagt tttttgttcc agaaccctaa atgaggttct acccttaaca 60

gagcttcccg caaaaacacc gattaacaag gctaaatgat atg acc atc gac ctg 115
 Met Thr Ile Asp Leu
 1 5

cag cgt tcc acc caa aac ctc acc cat gag gaa atc ttc gag gca cac	163
Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu Ile Phe Glu Ala His	
10 15 20	
gag ggc gga aag ctc tcc att agt tcc act cgt ccg ctc cgc gac atg	211
Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg Pro Leu Arg Asp Met	
25 30 35	
cgc gat ctt tcc ctt gct tac acc cct ggt gtt gct cag gtt tgt gaa	259
Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val Ala Gln Val Cys Glu	
40 45 50	
gca atc aag gaa gat cca gag gtt gcg cgc acc cac acg ggc att gga	307
Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr His Thr Gly Ile Gly	
55 60 65	
aac acc gtc gcg gtt att tcc gac ggc acc gct gtt ctt ggc ctt ggc	355
Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala Val Leu Gly Leu Gly	
70 75 80 85	
gat atc gga cct cag gcc tcc ctt ccc gtc atg gag ggc aag gct cag	403
Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met Glu Gly Lys Ala Gln	
90 95 100	
ctg ttt agc tct ttc gct ggc ctg aag gct atc cct atc gtt ttg gac	451
Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile Pro Ile Val Leu Asp	
105 110 115	
gtt cac gat gtt gac gct ttg gtt gag acc atc gca gcc atc gcg cct	499
Val His Asp Val Asp Ala Leu Val Glu Thr Ile Ala Ala Ile Ala Pro	
120 125 130	
tct ttc ggt gct atc aac ttg gag gac atc tcc gct cct cgt tgc ttc	547
Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser Ala Pro Arg Cys Phe	
135 140 145	
gag gtg gag cgc cgc ctc atc gag cgt ctc gat att cca gtt atg cac	595
Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp Ile Pro Val Met His	
150 155 160 165	
gat gac cag cac ggc acc gct gtg gtt atc ctc gct gcg ctg cgc aac	643
Asp Asp Gln His Gly Thr Ala Val Val Ile Leu Ala Ala Leu Arg Asn	
170 175 180	
tcc ctg aag ctg ctg gat cgc aag atc gaa gac ctc aag att gtt att	691
Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp Leu Lys Ile Val Ile	
185 190 195	
tcc ggc gca ggc gca gcg ggc gtt gca gct gta gat atg ctg acc aac	739
Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val Asp Met Leu Thr Asn	
200 205 210	
gct gga gca acc gac atc gtg gtt ctt gat tcc cga ggc atc atc cac	787
Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser Arg Gly Ile Ile His	
215 220 225	
gac agc cgt gag gat ctt tcc cca gtt aag gct gct ctt gca gag aag	835
Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala Leu Ala Glu Lys	
230 235 240 245	

acc aac cct cgt ggc atc agc ggt ggc atc aat gag gct ttc acc ggc 883
 Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn Glu Ala Phe Thr Gly
 250 255 260

gcg gac ctg ttc att ggc gtg tcc ggc ggc aac atc ggc gag gac gct 931
 Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn Ile Gly Glu Asp Ala
 265 270 275

ctc aaa ctc atg gcc ccg gag cca atc ctg ttc acc ctg gcg aac cca 979
 Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe Thr Leu Ala Asn Pro
 280 285 290

acc cca gag atc gat cct gag ctg tct cag aag tac ggc gcc atc gtc 1027
 Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys Tyr Gly Ala Ile Val
 295 300 305

gcg acc ggg ccg gtc ttg acc tgc cta acc aga tca 1063
 Ala Thr Gly Pro Val Leu Thr Cys Leu Thr Arg Ser
 310 315 320

<210> 576

<211> 321

<212> PRT

<213> Corynebacterium glutamicum

<400> 576

Met Thr Ile Asp Leu Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu
 1 5 10 15

Ile Phe Glu Ala His Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg
 20 25 30

Pro Leu Arg Asp Met Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val
 35 40 45

Ala Gln Val Cys Glu Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr
 50 55 60

His Thr Gly Ile Gly Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala
 65 70 75 80

Val Leu Gly Leu Gly Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met
 85 90 95

Glu Gly Lys Ala Gln Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile
 100 105 110

Pro Ile Val Leu Asp Val His Asp Val Asp Ala Leu Val Glu Thr Ile
 115 120 125

Ala Ala Ile Ala Pro Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser
 130 135 140

Ala Pro Arg Cys Phe Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp
 145 150 155 160

Ile Pro Val Met His Asp Asp Gln His Gly Thr Ala Val Val Ile Leu
 165 170 175

Ala Ala Leu Arg Asn Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp

180 185 190
 Leu Lys Ile Val Ile Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val
 195 200 205
 Asp Met Leu Thr Asn Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser
 210 215 220
 Arg Gly Ile Ile His Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala
 225 230 235 240
 Ala Leu Ala Glu Lys Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn
 245 250 255
 Glu Ala Phe Thr Gly Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn
 260 265 270
 Ile Gly Glu Asp Ala Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe
 275 280 285
 Thr Leu Ala Asn Pro Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys
 290 295 300
 Tyr Gly Ala Ile Val Ala Thr Gly Pro Val Leu Thr Cys Leu Thr Arg
 305 310 315 320
 Ser

<210> 577
 <211> 1347
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1324)
 <223> RXN01048

<400> 577
 agctacagat ttagctagt tttttgttcc agaaccctaa atgaggttct acccttaaca 60
 gagcttcccg caaaaacacc gattaacaag gctaaatgat atg acc atc gac ctg 115
 Met Thr Ile Asp Leu
 1 5
 cag cgt tcc acc caa aac ctc acc cat gag gaa atc ttc gag gca cac 163
 Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu Ile Phe Glu Ala His
 10 15 20
 gag ggc gga aag ctc tcc att agt tcc act cgt ccg ctc cgc gac atg 211
 Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg Pro Leu Arg Asp Met
 25 30 35
 cgc gat ctt tcc ctt gct tac acc cct ggt gtt gct cag gtt tgt gaa 259
 Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val Ala Gln Val Cys Glu
 40 45 50
 gca atc aag gaa gat cca gag gtt gcg cgc acc cac acg ggc att gga 307
 Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr His Thr Gly Ile Gly

55	60	65	
aac acc gtc gcg gtt att tcc gac ggc acc gct gtt ctt ggc ctt ggc Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala Val Leu Gly Leu Gly 70 75 80 85			355
gat atc gga cct cag gcc tcc ctt ccc gtc atg gag ggc aag gct cag Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met Glu Gly Lys Ala Gln 90 95 100			403
ctg ttt agc tct ttc gct ggc ctg aag gct atc cct atc gtt ttg gac Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile Pro Ile Val Leu Asp 105 110 115			451
gtt cac gat gtt gac gct ttg gtt gag acc atc gca gcc atc gcg cct Val His Asp Val Asp Ala Leu Val Glu Thr Ile Ala Ala Ile Ala Pro 120 125 130			499
tct ttc ggt gct atc aac ttg gag gac atc tcc gct cct cgt tgc ttc Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser Ala Pro Arg Cys Phe 135 140 145			547
gag gtg gag cgc cgc ctc atc gag cgt ctc gat att cca gtt atg cac Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp Ile Pro Val Met His 150 155 160 165			595
gat gac cag cac ggc acc gct gtg gtt atc ctc gct gcg ctg cgc aac Asp Asp Gln His Gly Thr Ala Val Val Ile Leu Ala Ala Leu Arg Asn 170 175 180			643
tcc ctg aag ctg ctg gat cgc aag atc gaa gac ctc aag att gtt att Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp Leu Lys Ile Val Ile 185 190 195			691
tcc ggc gca ggc gca gcg ggc gtt gca gct gta gat atg ctg acc aac Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val Asp Met Leu Thr Asn 200 205 210			739
gct gga gca acc gac atc gtg gtt ctt gat tcc cga ggc atc atc cac Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser Arg Gly Ile Ile His 215 220 225			787
gac agc cgt gag gat ctt tcc cca gtt aag gct gct ctt gca gag aag Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala Ala Leu Ala Glu Lys 230 235 240 245			835
acc aac cct cgt ggc atc agc ggt ggc atc aat gag gct ttc acc ggc Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn Glu Ala Phe Thr Gly 250 255 260			883
gcg gac ctg ttc att ggc gtg tcc ggc ggc aac atc ggc gag gac gct Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn Ile Gly Glu Asp Ala 265 270 275			931
ctc aaa ctc atg gcc ccg gag cca atc ctg ttc acc ctg gcg aac cca Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe Thr Leu Ala Asn Pro 280 285 290			979
acc cca gag atc gat cct gag ctg tct cag aag tac ggc gcc atc gtc Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys Tyr Gly Ala Ile Val 295 300 305			1027

gcg acc ggg cgc tct gac ctg cct aac cag atc aac aac gtg ctg gcg 1075
 Ala Thr Gly Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala
 310 315 320 325

ttc cca gga att ttc gcc ggc gct ctc gca gcc aag gct aag aag atc 1123
 Phe Pro Gly Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile
 330 335 340

acc ccc gag atg aag ctc gcc gct cag agg caa tcg cag aca tcg cag 1171
 Thr Pro Glu Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln
 345 350 355

ctg agg acc tcg agg tcg gcc gca tcg tgc cta ccg ccc tgg atc ccc 1219
 Leu Arg Thr Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro
 360 365 370

gcg ttg ccc caa cag tca agg cag ctg tcc agg ccg tcg cca aag cgc 1267
 Ala Leu Pro Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg
 375 380 385

aaa acg ctt aaa aat ttg ctt atc gac gcc tcc ctc ccc gtc gag gcg 1315
 Lys Thr Leu Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala
 390 395 400 405

cca ata ttt taagagcaaa cttgaggccc aca 1347
 Pro Ile Phe

<210> 578

<211> 408

<212> PRT

<213> Corynebacterium glutamicum

<400> 578

Met Thr Ile Asp Leu Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu
 1 5 10 15

Ile Phe Glu Ala His Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg
 20 25 30

Pro Leu Arg Asp Met Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val
 35 40 45

Ala Gln Val Cys Glu Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr
 50 55 60

His Thr Gly Ile Gly Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala
 65 70 75 80

Val Leu Gly Leu Gly Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met
 85 90 95

Glu Gly Lys Ala Gln Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile
 100 105 110

Pro Ile Val Leu Asp Val His Asp Val Asp Ala Leu Val Glu Thr Ile
 115 120 125

Ala Ala Ile Ala Pro Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser

130	135	140
Ala Pro Arg Cys Phe Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp 145 150 155 160		
Ile Pro Val Met His Asp Asp Gln His Gly Thr Ala Val Val Ile Leu 165 170 175		
Ala Ala Leu Arg Asn Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp 180 185 190		
Leu Lys Ile Val Ile Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val 195 200 205		
Asp Met Leu Thr Asn Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser 210 215 220		
Arg Gly Ile Ile His Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala 225 230 235 240		
Ala Leu Ala Glu Lys Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn 245 250 255		
Glu Ala Phe Thr Gly Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn 260 265 270		
Ile Gly Glu Asp Ala Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe 275 280 285		
Thr Leu Ala Asn Pro Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys 290 295 300		
Tyr Gly Ala Ile Val Ala Thr Gly Arg Ser Asp Leu Pro Asn Gln Ile 305 310 315 320		
Asn Asn Val Leu Ala Phe Pro Gly Ile Phe Ala Gly Ala Leu Ala Ala 325 330 335		
Lys Ala Lys Lys Ile Thr Pro Glu Met Lys Leu Ala Ala Gln Arg Gln 340 345 350		
Ser Gln Thr Ser Gln Leu Arg Thr Ser Arg Ser Ala Ala Ser Cys Leu 355 360 365		
Pro Pro Trp Ile Pro Ala Leu Pro Gln Gln Ser Arg Gln Leu Ser Arg 370 375 380		
Pro Ser Pro Lys Arg Lys Thr Leu Lys Asn Leu Leu Ile Asp Ala Ser 385 390 395 400		
Leu Pro Val Glu Ala Pro Ile Phe 405		

```
<210> 579
<211> 311
<212> DNA
<213> Corynebacterium glutamicum
```

<220>
<221> CDS

<222> (1)..(288)

<223> FRXA01048

<400> 579

```

cgc tct gac ttg cct aac cag atc aac aac gtg ctg gcg ttc cca gga      48
Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala Phe Pro Gly
  1              5              10              15

att ttc gcc ggc gct ctc gca gcc aag gct aag aag atc acc ccc gag      96
Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile Thr Pro Glu
          20              25              30

atg aag ctc gcc gct cag agg caa tcg cag aca tcg cag ctg agg acc      144
Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln Leu Arg Thr
          35              40              45

tcg agg tcg gcc gca tcg tgc cta ccg ccc tgg atc ccc gcg ttg ccc      192
Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro Ala Leu Pro
          50              55              60

caa cag tca agg cag ctg tcc agg ccg tcg cca aag cgc aaa acg ctt      240
Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg Lys Thr Leu
          65              70              75              80

aaa aat ttg ctt atc gac gcc tcc ctc ccc gtc gag gcg cca ata ttt      288
Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala Pro Ile Phe
          85              90              95

taagagcaaaa cttgaggccc aca                                          311

```

<210> 580

<211> 96

<212> PRT

<213> Corynebacterium glutamicum

<400> 580

```

Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala Phe Pro Gly
  1              5              10              15

Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile Thr Pro Glu
          20              25              30

Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln Leu Arg Thr
          35              40              45

Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro Ala Leu Pro
          50              55              60

Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg Lys Thr Leu
          65              70              75              80

Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala Pro Ile Phe
          85              90              95

```

<210> 581

<211> 1063

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1063)

<223> FRXA00290

<400> 581

```

agctacagat ttagctagtg tttttgttcc agaaccctaa atgaggttct acccttaaca 60

gagcttcccg caaaaacacc gattaacaag gctaaatgat atg acc atc gac ctg      115
                               Met Thr Ile Asp Leu
                               1          5

cag cgt tcc acc caa aac ctc acc cat gag gaa atc ttc gag gca cac      163
Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu Ile Phe Glu Ala His
                               10          15          20

gag ggc gga aag ctc tcc att agt tcc act cgt ccg ctc cgc gac atg      211
Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg Pro Leu Arg Asp Met
                               25          30          35

cgc gat ctt tcc ctt gct tac acc cct ggt gtt gct cag gtt tgt gaa      259
Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val Ala Gln Val Cys Glu
                               40          45          50

gca atc aag gaa gat cca gag gtt gcg cgc acc cac acg ggc att gga      307
Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr His Thr Gly Ile Gly
                               55          60          65

aac acc gtc gcg gtt att tcc gac ggc acc gct gtt ctt ggc ctt ggc      355
Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala Val Leu Gly Leu Gly
                               70          75          80          85

gat atc gga cct cag gcc tcc ctt ccc gtc atg gag ggc aag gct cag      403
Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met Glu Gly Lys Ala Gln
                               90          95          100

ctg ttt agc tct ttc gct ggc ctg aag gct atc cct atc gtt ttg gac      451
Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile Pro Ile Val Leu Asp
                               105          110          115

gtt cac gat gtt gac gct ttg gtt gag acc atc gca gcc atc gcg cct      499
Val His Asp Val Asp Ala Leu Val Glu Thr Ile Ala Ala Ile Ala Pro
                               120          125          130

tct ttc ggt gct atc aac ttg gag gac atc tcc gct cct cgt tgc ttc      547
Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser Ala Pro Arg Cys Phe
                               135          140          145

gag gtg gag cgc cgc ctc atc gag cgt ctc gat att cca gtt atg cac      595
Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp Ile Pro Val Met His
                               150          155          160          165

gat gac cag cac ggc acc gct gtg gtt atc ctc gct gcg ctg cgc aac      643
Asp Asp Gln His Gly Thr Ala Val Val Ile Leu Ala Ala Leu Arg Asn
                               170          175          180

tcc ctg aag ctg ctg gat cgc aag atc gaa gac ctc aag att gtt att      691
Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp Leu Lys Ile Val Ile

```

185										190					195					
tcc ggc gca ggc gca gcg ggc gtt gca gct gta gat atg ctg acc aac	739																			
Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val Asp Met Leu Thr Asn																				
200 205 210																				
gct gga gca acc gac atc gtg gtt ctt gat tcc cga ggc atc atc cac	787																			
Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser Arg Gly Ile Ile His																				
215 220 225																				
gac agc cgt gag gat ctt tcc cca gtt aag gct gct ctt gca gag aag	835																			
Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala Ala Leu Ala Glu Lys																				
230 235 240 245																				
acc aac cct cgt ggc atc agc ggt ggc atc aat gag gct ttc acc ggc	883																			
Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn Glu Ala Phe Thr Gly																				
250 255 260																				
gcg gac ctg ttc att ggc gtg tcc ggc ggc aac atc ggc gag gac gct	931																			
Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn Ile Gly Glu Asp Ala																				
265 270 275																				
ctc aaa ctc atg gcc ccg gag cca atc ctg ttc acc ctg gcg aac cca	979																			
Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe Thr Leu Ala Asn Pro																				
280 285 290																				
acc cca gag atc gat cct gag ctg tct cag aag tac ggc gcc atc gtc	1027																			
Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys Tyr Gly Ala Ile Val																				
295 300 305																				
gcg acc ggg ccg gtc ttg acc tgc cta acc aga tca	1063																			
Ala Thr Gly Pro Val Leu Thr Cys Leu Thr Arg Ser																				
310 315 320																				

<210> 582

<211> 321

<212> PRT

<213> Corynebacterium glutamicum

<400> 582

Met Thr Ile Asp Leu Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu	
1 5 10 15	
Ile Phe Glu Ala His Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg	
20 25 30	
Pro Leu Arg Asp Met Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val	
35 40 45	
Ala Gln Val Cys Glu Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr	
50 55 60	
His Thr Gly Ile Gly Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala	
65 70 75 80	
Val Leu Gly Leu Gly Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met	
85 90 95	
Glu Gly Lys Ala Gln Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile	
100 105 110	

Pro Ile Val Leu Asp Val His Asp Val Asp Ala Leu Val Glu Thr Ile
 115 120 125

Ala Ala Ile Ala Pro Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser
 130 135 140

Ala Pro Arg Cys Phe Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp
 145 150 155 160

Ile Pro Val Met His Asp Asp Gln His Gly Thr Ala Val Val Ile Leu
 165 170 175

Ala Ala Leu Arg Asn Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp
 180 185 190

Leu Lys Ile Val Ile Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val
 195 200 205

Asp Met Leu Thr Asn Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser
 210 215 220

Arg Gly Ile Ile His Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala
 225 230 235 240

Ala Leu Ala Glu Lys Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn
 245 250 255

Glu Ala Phe Thr Gly Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn
 260 265 270

Ile Gly Glu Asp Ala Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe
 275 280 285

Thr Leu Ala Asn Pro Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys
 290 295 300

Tyr Gly Ala Ile Val Ala Thr Gly Pro Val Leu Thr Cys Leu Thr Arg
 305 310 315 320

Ser

<210> 583

<211> 582

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(582)

<223> RXN03101

<400> 583

atc ctt gca gac gaa gac gac acc gtc gac gtc ggc gca gtc atc gcc 48
 Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly Ala Val Ile Ala
 1 5 10 15

cgc atc ggt gac gca aac gca gct gca gca cct gcc gaa gag gaa gca 96
 Arg Ile Gly Asp Ala Asn Ala Ala Ala Ala Pro Ala Glu Glu Glu Ala

	20	25	30	
gct cct gcc gaa gag gaa gaa cca gtt aag gaa gag cca aag aag gag				144
Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu Pro Lys Lys Glu				
	35	40	45	
gca gct cct gaa gct cca gca gca act ggc gcc gca acc gat gtg gaa				192
Ala Ala Pro Glu Ala Pro Ala Ala Thr Gly Ala Ala Thr Asp Val Glu				
	50	55	60	
atg cca gaa ctc ggc gaa tcc gtc acc gaa ggc acc att acc cag tgg				240
Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly Thr Ile Thr Gln Trp				
	65	70	75	80
ctc aag gct gtc ggc gac acc gtc gaa gta gac gaa cca ctt ctt gag				288
Leu Lys Ala Val Gly Asp Thr Val Glu Val Asp Glu Pro Leu Leu Glu				
	85	90	95	
gtc tcc acc gac aag gtc gac acc gaa atc cca tcc cca gta gca ggc				336
Val Ser Thr Asp Lys Val Asp Thr Glu Ile Pro Ser Pro Val Ala Gly				
	100	105	110	
acc atc gtg gag atc ctt gca gac gaa gac gac acc gtc gac gtc ggc				384
Thr Ile Val Glu Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly				
	115	120	125	
gca gtc atc gcc cgc atc ggt gac gca aac gca gct gca gca cct gcc				432
Ala Val Ile Ala Arg Ile Gly Asp Ala Asn Ala Ala Ala Ala Pro Ala				
	130	135	140	
gaa gag gaa gca gct cct gcc gaa gag gag gaa cca gtt aag gaa gag				480
Glu Glu Glu Ala Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu				
	145	150	155	160
cca aag aag gaa gag ccc aag aag gaa gag ccc aag aag gaa gca gct				528
Pro Lys Lys Glu Glu Pro Lys Lys Glu Glu Pro Lys Lys Glu Ala Ala				
	165	170	175	
act aca cct gct gcg gca tcc gca act gtg tcc gct tct ggc gac aac				576
Thr Thr Pro Ala Ala Ser Ala Thr Val Ser Ala Ser Gly Asp Asn				
	180	185	190	
gtt cca				582
Val Pro				

<210> 584

<211> 194

<212> PRT

<213> Corynebacterium glutamicum

<400> 584

Ile	Leu	Ala	Asp	Glu	Asp	Asp	Thr	Val	Asp	Val	Gly	Ala	Val	Ile	Ala
1				5					10					15	

Arg	Ile	Gly	Asp	Ala	Asn	Ala	Ala	Ala	Ala	Pro	Ala	Glu	Glu	Glu	Ala
			20					25					30		

Ala	Pro	Ala	Glu	Glu	Glu	Glu	Pro	Val	Lys	Glu	Glu	Pro	Lys	Lys	Glu
		35					40					45			

Ala Ala Pro Glu Ala Pro Ala Ala Thr Gly Ala Ala Thr Asp Val Glu
 50 55 60

Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly Thr Ile Thr Gln Trp
 65 70 75 80

Leu Lys Ala Val Gly Asp Thr Val Glu Val Asp Glu Pro Leu Leu Glu
 85 90 95

Val Ser Thr Asp Lys Val Asp Thr Glu Ile Pro Ser Pro Val Ala Gly
 100 105 110

Thr Ile Val Glu Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly
 115 120 125

Ala Val Ile Ala Arg Ile Gly Asp Ala Asn Ala Ala Ala Ala Pro Ala
 130 135 140

Glu Glu Glu Ala Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu
 145 150 155 160

Pro Lys Lys Glu Glu Pro Lys Lys Glu Glu Pro Lys Lys Glu Ala Ala
 165 170 175

Thr Thr Pro Ala Ala Ala Ser Ala Thr Val Ser Ala Ser Gly Asp Asn
 180 185 190

Val Pro

<210> 585
 <211> 540
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(517)
 <223> RXN02046

<400> 585
 tccgtgccat caccaccggc gagatcactg gcacgttgga cgcaaaacaa acagcaacag 60

aaattattaa catccgacgc aacgcttcag gagagtcctc atg aaa gag aca ctg 115
 Met Lys Glu Thr Leu
 1 5

acc acc ggt tta acc cac caa atg acc tac ata gtg cca gca aac cgc 163
 Thr Thr Gly Leu Thr His Gln Met Thr Tyr Ile Val Pro Ala Asn Arg
 10 15 20

aca gtt ccg cat ctg ctt ccc gaa gca gca gaa ttt gaa acc atg cca 211
 Thr Val Pro His Leu Leu Pro Glu Ala Ala Glu Phe Glu Thr Met Pro
 25 30 35

gat gtc ctg gcc act gga tat atg gtc ggc atc atc gag tgg gcc tgc 259
 Asp Val Leu Ala Thr Gly Tyr Met Val Gly Ile Ile Glu Trp Ala Cys
 40 45 50

atg gaa ctt ctg cgt ccc cat ttg gac gac ggt gaa atc tcg ctg ggc 307
 Met Glu Leu Leu Arg Pro His Leu Asp Asp Gly Glu Ile Ser Leu Gly
 55 60 65
 act cat gtg aac ttc tcc cac gca gct cca acg gtt cct gga tcc acg 355
 Thr His Val Asn Phe Ser His Ala Ala Pro Thr Val Pro Gly Ser Thr
 70 75 80 85
 gtc acc atc gat gtt gag gtg aca gag atc aac cgt cgt gca gtt acc 403
 Val Thr Ile Asp Val Glu Val Thr Glu Ile Asn Arg Arg Ala Val Thr
 90 95 100
 ttc aac atc act gca gct gat gag ttc gcc acc atc agc acc ggc acc 451
 Phe Asn Ile Thr Ala Ala Asp Glu Phe Ala Thr Ile Ser Thr Gly Thr
 105 110 115
 cac cag cgc ggt gtg gtt aac cgt gag aag ttt gtc tcc cgt ctg cct 499
 His Gln Arg Gly Val Val Asn Arg Glu Lys Phe Val Ser Arg Leu Pro
 120 125 130
 gaa gca cct aag gaa aac taaatcatgg ccaagttggt tga 540
 Glu Ala Pro Lys Glu Asn
 135

<210> 586

<211> 139

<212> PRT

<213> Corynebacterium glutamicum

<400> 586

Met Lys Glu Thr Leu Thr Thr Gly Leu Thr His Gln Met Thr Tyr Ile
 1 5 10 15
 Val Pro Ala Asn Arg Thr Val Pro His Leu Leu Pro Glu Ala Ala Glu
 20 25 30
 Phe Glu Thr Met Pro Asp Val Leu Ala Thr Gly Tyr Met Val Gly Ile
 35 40 45
 Ile Glu Trp Ala Cys Met Glu Leu Leu Arg Pro His Leu Asp Asp Gly
 50 55 60
 Glu Ile Ser Leu Gly Thr His Val Asn Phe Ser His Ala Ala Pro Thr
 65 70 75 80
 Val Pro Gly Ser Thr Val Thr Ile Asp Val Glu Val Thr Glu Ile Asn
 85 90 95
 Arg Arg Ala Val Thr Phe Asn Ile Thr Ala Ala Asp Glu Phe Ala Thr
 100 105 110
 Ile Ser Thr Gly Thr His Gln Arg Gly Val Val Asn Arg Glu Lys Phe
 115 120 125
 Val Ser Arg Leu Pro Glu Ala Pro Lys Glu Asn
 130 135

<210> 587

<211> 1683

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1660)

<223> RXN00389

<400> 587

```

ccaccactgc gtaacctttc cgagcaagat atcgcggaacc tgcgcgattt gcttgccacc 60

tctggcgcag gttcctaccg ccttcagttg aggtgaaagc atg atc acc gca acc 115
                                         Met Ile Thr Ala Thr
                                         1           5

gca ctg cat ggg tgt tca ctg att gat ggc gag tgg gtc gct gga aaa 163
Ala Leu His Gly Cys Ser Leu Ile Asp Gly Glu Trp Val Ala Gly Lys
                        10                15                20

aat ggt gag att aca gga ttc gat ccg cgc acc aat gcg agt ctg aac 211
Asn Gly Glu Ile Thr Gly Phe Asp Pro Arg Thr Asn Ala Ser Leu Asn
                        25                30                35

cct tcc tac tct tta gca aac agc gca cag ctg cgc gcc gcc aca aca 259
Pro Ser Tyr Ser Leu Ala Asn Ser Ala Gln Leu Arg Ala Ala Thr Thr
                        40                45                50

tcg gcg aag cga gct ttt gaa agc tac cga ctc act act cca gag gtt 307
Ser Ala Lys Arg Ala Phe Glu Ser Tyr Arg Leu Thr Thr Pro Glu Val
                        55                60                65

aga gca gat ttc ctg gat tcc atc gct gac aac atc gat gcg cta tcc 355
Arg Ala Asp Phe Leu Asp Ser Ile Ala Asp Asn Ile Asp Ala Leu Ser
                        70                75                80                85

ggc gag atc gtg caa cgg gcg agc ctg gag aca ggt ttg gga act acc 403
Gly Glu Ile Val Gln Arg Ala Ser Leu Glu Thr Gly Leu Gly Thr Thr
                        90                95                100

cga ctc aca ggc gaa gta gcc cgc acc agc aac cag ctc cgc ctg ttt 451
Arg Leu Thr Gly Glu Val Ala Arg Thr Ser Asn Gln Leu Arg Leu Phe
                        105                110                115

gca gaa acc gtg aga agc gga cag ttc cac cga gta cgc att gaa cga 499
Ala Glu Thr Val Arg Ser Gly Gln Phe His Arg Val Arg Ile Glu Arg
                        120                125                130

gga ccg cgg att gat ctt cgc cag cgt cag gtt ccg ttg gga cca gtc 547
Gly Pro Arg Ile Asp Leu Arg Gln Arg Gln Val Pro Leu Gly Pro Val
                        135                140                145

gcg gta ttc ggg gca agc aac ttc ccc gtc gct ttc tct act gct ggt 595
Ala Val Phe Gly Ala Ser Asn Phe Pro Val Ala Phe Ser Thr Ala Gly
                        150                155                160                165

ggc gat aca gca tca gcg ttg gct gca ggc tgc cct gtg gtt ttt aag 643
Gly Asp Thr Ala Ser Ala Leu Ala Ala Gly Cys Pro Val Val Phe Lys
                        170                175                180

gcg cat aat gcg cac cct gga aca gct gag ctc gtc ggg caa gcg gtg 691
Ala His Asn Ala His Pro Gly Thr Ala Glu Leu Val Gly Gln Ala Val

```

185							190					195					
cg	g	g	g	g	a	a	c	g	t	t	g	g	t	t	a	c	739
Arg	Gly	Ala	Val	Glu	Lys	His	Glu	Phe	Asp	Ala	Gly	Val	Phe	Asn	Leu		
		200					205					210					
g	t	g	c	g	g	g	a	a	g	g	c	g	g	g	g	787	
Val	Tyr	Gly	Arg	Gly	Val	Glu	Ile	Gly	Gln	Glu	Leu	Ala	Ala	Asp	Pro		
	215					220					225						
a	a	a	g	a	a	g	t	a	g	c	c	g	g	g	t	835	
Asn	Ile	Thr	Ala	Ile	Gly	Phe	Thr	Gly	Ser	Arg	Gln	Gly	Gly	Leu	Ala		
230					235					240				245			
c	t	a	c	a	t	a	g	c	c	g	t	c	g	t	g	883	
Leu	Ser	Gln	Thr	Ala	Phe	Ser	Arg	Pro	Val	Pro	Val	Pro	Val	Phe	Ala		
				250					255					260			
g	a	a	g	a	a	c	g	t	t	g	c	g	g	c	g	931	
Glu	Met	Ser	Ala	Thr	Asn	Pro	Val	Phe	Val	Phe	Pro	Gly	Ala	Leu	Ala		
			265				270					275					
g	t	g	g	a	a	c	t	g	g	g	t	a	g	t	g	979	
Asp	Leu	Asp	Ala	Ser	Ser	Ser	Leu	Ala	Glu	Ala	Phe	Thr	Ala	Ser	Val		
		280					285					290					
a	g	g	a	t	g	c	a	t	a	c	g	c	g	t	t	1027	
Thr	Gly	Ser	Ser	Gly	Gln	Leu	Cys	Thr	Lys	Pro	Gly	Leu	Val	Phe	Ile		
	295				300						305						
c	c	g	g	t	g	g	a	g	t	g	c	g	a	g	a	1075	
Pro	Arg	Gly	Val	Val	Gly	Asp	Ala	Phe	Val	Ala	Leu	Val	Ala	Ala	Lys		
310					315					320					325		
t	a	a	g	a	a	c	a	a	t	c	a	g	a	g	c	1123	
Phe	Lys	Glu	Thr	Thr	Gly	Gln	Thr	Met	Leu	Thr	Gln	Gly	Ile	Ala	Gln		
				330					335					340			
g	a	t	c	g	g	g	a	c	c	g	a	c	c	a	g	1171	
Ala	Trp	Gln	Arg	Gly	Val	Asp	Asn	Leu	Ala	Ala	Gln	Pro	Ser	Val	Lys		
			345				350						355				
a	c	c	g	a	a	c	c	g	g	g	a	a	c	c	g	1219	
Ile	Leu	Ala	Gln	Gly	Thr	Pro	Gly	Asp	Gly	Glu	Asn	Ala	Pro	Gly	Pro		
		360					365					370					
g	g	t	g	a	a	g	g	c	t	a	a	a	g	g	t	1267	
Val	Val	Phe	Glu	Ser	Asp	Val	Gln	Ala	Leu	Leu	Asn	Asn	Val	Val	Leu		
		375				380					385						
c	g	a	a	a	t	t	g	g	a	c	g	t	a	g	t	1315	
Gln	Glu	Glu	Ile	Phe	Gly	Ala	Ala	Ser	Leu	Val	Val	Arg	Tyr	Asp	Ser		
390					395				400					405			
c	g	a	c	c	a	g	a	a	t	c	c	g	g	a	t	1363	
Pro	Asp	Gln	Leu	His	Gln	Val	Ala	Asn	Ser	Leu	Glu	Gly	Gln	Leu	Thr		
				410					415					420			
g	a	a	c	g	t	c	g	g	t	t	c	g	a	g	t	1411	
Ala	Thr	Ile	His	Ala	Ser	Gln	Asp	Asp	Phe	Gln	Glu	Val	Ser	Lys	Leu		
			425					430					435				

atc ccc ctc ttg gag gat ctc gcg ggc cgt gtt ctt tac ggc ggc tgg 1459
 Ile Pro Leu Leu Glu Asp Leu Ala Gly Arg Val Leu Tyr Gly Gly Trp
 440 445 450

cca acg ggt gtg gaa gtt ggg cac acg gtt atc cat gga ggc cct tat 1507
 Pro Thr Gly Val Glu Val Gly His Thr Val Ile His Gly Gly Pro Tyr
 455 460 465

ccg gcg acc tca aat gcg cag tcg aca agt gtt gga acc ctg gca atc 1555
 Pro Ala Thr Ser Asn Ala Gln Ser Thr Ser Val Gly Thr Leu Ala Ile
 470 475 480 485

gag aga ttt atg cgc ccg gtt tct tat caa act ttc ccg gct gag ctg 1603
 Glu Arg Phe Met Arg Pro Val Ser Tyr Gln Thr Phe Pro Ala Glu Leu
 490 495 500

ctt cca gat cca gtt tct gag gcg aat aaa tgg gct gta cct cgg gaa 1651
 Leu Pro Asp Pro Val Ser Glu Ala Asn Lys Trp Ala Val Pro Arg Glu
 505 510 515

ata gac cgt taatagctgg tctttacatt tgc 1683
 Ile Asp Arg
 520

<210> 588

<211> 520

<212> PRT

<213> Corynebacterium glutamicum

<400> 588

Met Ile Thr Ala Thr Ala Leu His Gly Cys Ser Leu Ile Asp Gly Glu
 1 5 10 15

Trp Val Ala Gly Lys Asn Gly Glu Ile Thr Gly Phe Asp Pro Arg Thr
 20 25 30

Asn Ala Ser Leu Asn Pro Ser Tyr Ser Leu Ala Asn Ser Ala Gln Leu
 35 40 45

Arg Ala Ala Thr Thr Ser Ala Lys Arg Ala Phe Glu Ser Tyr Arg Leu
 50 55 60

Thr Thr Pro Glu Val Arg Ala Asp Phe Leu Asp Ser Ile Ala Asp Asn
 65 70 75 80

Ile Asp Ala Leu Ser Gly Glu Ile Val Gln Arg Ala Ser Leu Glu Thr
 85 90 95

Gly Leu Gly Thr Thr Arg Leu Thr Gly Glu Val Ala Arg Thr Ser Asn
 100 105 110

Gln Leu Arg Leu Phe Ala Glu Thr Val Arg Ser Gly Gln Phe His Arg
 115 120 125

Val Arg Ile Glu Arg Gly Pro Arg Ile Asp Leu Arg Gln Arg Gln Val
 130 135 140

Pro Leu Gly Pro Val Ala Val Phe Gly Ala Ser Asn Phe Pro Val Ala
 145 150 155 160

Phe Ser Thr Ala Gly Gly Asp Thr Ala Ser Ala Leu Ala Ala Gly Cys
 165 170 175
 Pro Val Val Phe Lys Ala His Asn Ala His Pro Gly Thr Ala Glu Leu
 180 185 190
 Val Gly Gln Ala Val Arg Gly Ala Val Glu Lys His Glu Phe Asp Ala
 195 200 205
 Gly Val Phe Asn Leu Val Tyr Gly Arg Gly Val Glu Ile Gly Gln Glu
 210 215 220
 Leu Ala Ala Asp Pro Asn Ile Thr Ala Ile Gly Phe Thr Gly Ser Arg
 225 230 235 240
 Gln Gly Gly Leu Ala Leu Ser Gln Thr Ala Phe Ser Arg Pro Val Pro
 245 250 255
 Val Pro Val Phe Ala Glu Met Ser Ala Thr Asn Pro Val Phe Val Phe
 260 265 270
 Pro Gly Ala Leu Ala Asp Leu Asp Ala Ser Ser Ser Leu Ala Glu Ala
 275 280 285
 Phe Thr Ala Ser Val Thr Gly Ser Ser Gly Gln Leu Cys Thr Lys Pro
 290 295 300
 Gly Leu Val Phe Ile Pro Arg Gly Val Val Gly Asp Ala Phe Val Ala
 305 310 315 320
 Leu Val Ala Ala Lys Phe Lys Glu Thr Thr Gly Gln Thr Met Leu Thr
 325 330 335
 Gln Gly Ile Ala Gln Ala Trp Gln Arg Gly Val Asp Asn Leu Ala Ala
 340 345 350
 Gln Pro Ser Val Lys Ile Leu Ala Gln Gly Thr Pro Gly Asp Gly Glu
 355 360 365
 Asn Ala Pro Gly Pro Val Val Phe Glu Ser Asp Val Gln Ala Leu Leu
 370 375 380
 Asn Asn Val Val Leu Gln Glu Glu Ile Phe Gly Ala Ala Ser Leu Val
 385 390 395 400
 Val Arg Tyr Asp Ser Pro Asp Gln Leu His Gln Val Ala Asn Ser Leu
 405 410 415
 Glu Gly Gln Leu Thr Ala Thr Ile His Ala Ser Gln Asp Asp Phe Gln
 420 425 430
 Glu Val Ser Lys Leu Ile Pro Leu Leu Glu Asp Leu Ala Gly Arg Val
 435 440 445
 Leu Tyr Gly Gly Trp Pro Thr Gly Val Glu Val Gly His Thr Val Ile
 450 455 460
 His Gly Gly Pro Tyr Pro Ala Thr Ser Asn Ala Gln Ser Thr Ser Val
 465 470 475 480

Gly	Thr	Leu	Ala	Ile	Glu	Arg	Phe	Met	Arg	Pro	Val	Ser	Tyr	Gln	Thr
				485					490					495	
Phe	Pro	Ala	Glu	Leu	Leu	Pro	Asp	Pro	Val	Ser	Glu	Ala	Asn	Lys	Trp
			500					505					510		
Ala	Val	Pro	Arg	Glu	Ile	Asp	Arg								
			515				520								

```
<210> 589
<211> 1467
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(1444)
<223> RXN02399
```

<400> 589																	
ttgacgcacc	aatgcccgat	ggagcaatgt	gtgaaccacg	ccaccacgca	aaccgatgca	60											
catcacgtcg	aaacagtgac	agtgcattag	ctcatacttt	gtg	gtc	ggc	acc	gcc	115								
				Val	Val	Gly	Thr	Ala	5								
				1													
cat	tgc	gaa	tca	gca	ctt	aag	gaa	gtg	act	ttg	atg	tca	aac	gtt	gga	163	
His	Cys	Glu	Ser	Ala	Leu	Lys	Glu	Val	Thr	Leu	Met	Ser	Asn	Val	Gly	20	
				10						15							
aag	cca	cgt	acc	gca	cag	gaa	atc	cag	cag	gat	tgg	gac	acc	aac	cct	211	
Lys	Pro	Arg	Thr	Ala	Gln	Glu	Ile	Gln	Gln	Asp	Trp	Asp	Thr	Asn	Pro	35	
				25						30							
cgt	tgg	aac	ggc	atc	acc	cgc	gac	tac	acc	gca	gac	cag	gta	gct	gat	259	
Arg	Trp	Asn	Gly	Ile	Thr	Arg	Asp	Tyr	Thr	Ala	Asp	Gln	Val	Ala	Asp	50	
				40													
ctg	cag	ggt	tcc	gtc	atc	gag	gag	cac	act	ctt	gct	cgc	cgc	ggc	tca	307	
Leu	Gln	Gly	Ser	Val	Ile	Glu	Glu	His	Thr	Leu	Ala	Arg	Arg	Gly	Ser	65	
				55													
gag	atc	ctc	tgg	gac	gca	gtc	acc	cag	gaa	ggt	gac	gga	tac	atc	aac	355	
Glu	Ile	Leu	Trp	Asp	Ala	Val	Thr	Gln	Glu	Gly	Asp	Gly	Tyr	Ile	Asn	85	
gcg	ctt	ggc	gca	ctc	acc	ggt	aac	cag	gct	gtt	cag	cag	gtt	cgt	gca	403	
Ala	Leu	Gly	Ala	Leu	Thr	Gly	Asn	Gln	Ala	Val	Gln	Gln	Val	Arg	Ala	100	
ggc	ctg	aag	gct	gtc	tac	ctg	tcc	ggt	tgg	cag	gtc	gca	ggt	gac	gcc	451	
Gly	Leu	Lys	Ala	Val	Tyr	Leu	Ser	Gly	Trp	Gln	Val	Ala	Gly	Asp	Ala	115	
aac	ctc	tcc	ggc	cac	acc	tac	cct	gac	cag	tcc	ctc	tac	cca	gcg	aac	499	
Asn	Leu	Ser	Gly	His	Thr	Tyr	Pro	Asp	Gln	Ser	Leu	Tyr	Pro	Ala	Asn	120	
tcc	gtt	cca	agc	gtc	gtt	cgt	cgc	atc	aac	aac	gca	ctg	ctg	cgt	tcc	547	
Ser	Val	Pro	Ser	Val	Val	Arg	Arg	Ile	Asn	Asn	Ala	Leu	Leu	Arg	Ser		

135	140	145	
gat gaa atc gca cgc acc gaa ggc gac acc tcc gtt gac aac tgg gtt Asp Glu Ile Ala Arg Thr Glu Gly Asp Thr Ser Val Asp Asn Trp Val 150 155 160 165			595
gtc cca atc gtc gcg gac ggc gaa gct ggc ttc ggt gga gca ctc aac Val Pro Ile Val Ala Asp Gly Glu Ala Gly Phe Gly Gly Ala Leu Asn 170 175 180			643
gtc tac gaa ctc cag aag gca atg atc gca gct ggc gct gca ggc acc Val Tyr Glu Leu Gln Lys Ala Met Ile Ala Ala Gly Ala Ala Gly Thr 185 190 195			691
cac tgg gaa gac cag ctc gct tct gaa aag aag tgt ggc cac ctc ggc His Trp Glu Asp Gln Leu Ala Ser Glu Lys Lys Cys Gly His Leu Gly 200 205 210			739
ggc aag gtt ctg atc cca acc cag cag cac atc cgc acc ctg aac tct Gly Lys Val Leu Ile Pro Thr Gln Gln His Ile Arg Thr Leu Asn Ser 215 220 225			787
gcc cgc ctt gca gca gac gtt gca aac acc cca act gtt gtt atc gca Ala Arg Leu Ala Ala Asp Val Ala Asn Thr Pro Thr Val Val Ile Ala 230 235 240 245			835
cgt acc gac gct gag gca gca acc ctg atc acc tct gac gtt gat gag Arg Thr Asp Ala Glu Ala Ala Thr Leu Ile Thr Ser Asp Val Asp Glu 250 255 260			883
cgc gac caa cca ttc atc acc ggt gag cgc acc gca gaa ggc tac tac Arg Asp Gln Pro Phe Ile Thr Gly Glu Arg Thr Ala Glu Gly Tyr Tyr 265 270 275			931
cac gtc aag aat ggt ctc gag cca tgt atc gca cgt gca aag tcc tac His Val Lys Asn Gly Leu Glu Pro Cys Ile Ala Arg Ala Lys Ser Tyr 280 285 290			979
gca cca tac gca gat atg atc tgg atg gag acc ggc acc cct gac ctg Ala Pro Tyr Ala Asp Met Ile Trp Met Glu Thr Gly Thr Pro Asp Leu 295 300 305			1027
gag ctc gct aag aag ttc gct gaa ggc gtt cgc tct gag ttc cca gac Glu Leu Ala Lys Lys Phe Ala Glu Gly Val Arg Ser Glu Phe Pro Asp 310 315 320 325			1075
cag ctg ctg tcc tac aac tgc tcc cca tcc ttc aac tgg tct gca cac Gln Leu Leu Ser Tyr Asn Cys Ser Pro Ser Phe Asn Trp Ser Ala His 330 335 340			1123
ctc gag gca gat gag atc gct aag ttc cag aag gaa ctc ggc gca atg Leu Glu Ala Asp Glu Ile Ala Lys Phe Gln Lys Glu Leu Gly Ala Met 345 350 355			1171
ggc ttc aag ttc cag ttc atc acc ctc gca ggc ttc cac tcc ctc aac Gly Phe Lys Phe Gln Phe Ile Thr Leu Ala Gly Phe His Ser Leu Asn 360 365 370			1219
tac ggc atg ttc gac ctg gct tac gga tac gct cgc gaa ggc atg acc Tyr Gly Met Phe Asp Leu Ala Tyr Gly Tyr Ala Arg Glu Gly Met Thr 375 380 385			1267

tcc ttc gtt gac ctg cag aac cgt gag ttc aag gca gct gaa gag cgt 1315
 Ser Phe Val Asp Leu Gln Asn Arg Glu Phe Lys Ala Ala Glu Glu Arg
 390 395 400 405

ggc ttc acc gct gtt aag cac cag cgt gag gtt ggc gca ggc tac ttc 1363
 Gly Phe Thr Ala Val Lys His Gln Arg Glu Val Gly Ala Gly Tyr Phe
 410 415 420

gac cag atc gca acc acc gtt gac ccg aac tct tct acc acc gct ttg 1411
 Asp Gln Ile Ala Thr Thr Val Asp Pro Asn Ser Ser Thr Thr Ala Leu
 425 430 435

aag ggt tcc act gaa gaa ggc cag ttc cac aac taggacctac aggttctgac 1464
 Lys Gly Ser Thr Glu Glu Gly Gln Phe His Asn
 440 445

aat 1467

<210> 590

<211> 448

<212> PRT

<213> Corynebacterium glutamicum

<400> 590

Val Val Gly Thr Ala His Cys Glu Ser Ala Leu Lys Glu Val Thr Leu
 1 5 10 15

Met Ser Asn Val Gly Lys Pro Arg Thr Ala Gln Glu Ile Gln Gln Asp
 20 25 30

Trp Asp Thr Asn Pro Arg Trp Asn Gly Ile Thr Arg Asp Tyr Thr Ala
 35 40 45

Asp Gln Val Ala Asp Leu Gln Gly Ser Val Ile Glu Glu His Thr Leu
 50 55 60

Ala Arg Arg Gly Ser Glu Ile Leu Trp Asp Ala Val Thr Gln Glu Gly
 65 70 75 80

Asp Gly Tyr Ile Asn Ala Leu Gly Ala Leu Thr Gly Asn Gln Ala Val
 85 90 95

Gln Gln Val Arg Ala Gly Leu Lys Ala Val Tyr Leu Ser Gly Trp Gln
 100 105 110

Val Ala Gly Asp Ala Asn Leu Ser Gly His Thr Tyr Pro Asp Gln Ser
 115 120 125

Leu Tyr Pro Ala Asn Ser Val Pro Ser Val Val Arg Arg Ile Asn Asn
 130 135 140

Ala Leu Leu Arg Ser Asp Glu Ile Ala Arg Thr Glu Gly Asp Thr Ser
 145 150 155 160

Val Asp Asn Trp Val Val Pro Ile Val Ala Asp Gly Glu Ala Gly Phe
 165 170 175

Gly Gly Ala Leu Asn Val Tyr Glu Leu Gln Lys Ala Met Ile Ala Ala
 180 185 190

Gly Ala Ala Gly Thr His Trp Glu Asp Gln Leu Ala Ser Glu Lys Lys
 195 200 205
 Cys Gly His Leu Gly Gly Lys Val Leu Ile Pro Thr Gln Gln His Ile
 210 215 220
 Arg Thr Leu Asn Ser Ala Arg Leu Ala Ala Asp Val Ala Asn Thr Pro
 225 230 235 240
 Thr Val Val Ile Ala Arg Thr Asp Ala Glu Ala Ala Thr Leu Ile Thr
 245 250 255
 Ser Asp Val Asp Glu Arg Asp Gln Pro Phe Ile Thr Gly Glu Arg Thr
 260 265 270
 Ala Glu Gly Tyr Tyr His Val Lys Asn Gly Leu Glu Pro Cys Ile Ala
 275 280 285
 Arg Ala Lys Ser Tyr Ala Pro Tyr Ala Asp Met Ile Trp Met Glu Thr
 290 295 300
 Gly Thr Pro Asp Leu Glu Leu Ala Lys Lys Phe Ala Glu Gly Val Arg
 305 310 315 320
 Ser Glu Phe Pro Asp Gln Leu Leu Ser Tyr Asn Cys Ser Pro Ser Phe
 325 330 335
 Asn Trp Ser Ala His Leu Glu Ala Asp Glu Ile Ala Lys Phe Gln Lys
 340 345 350
 Glu Leu Gly Ala Met Gly Phe Lys Phe Gln Phe Ile Thr Leu Ala Gly
 355 360 365
 Phe His Ser Leu Asn Tyr Gly Met Phe Asp Leu Ala Tyr Gly Tyr Ala
 370 375 380
 Arg Glu Gly Met Thr Ser Phe Val Asp Leu Gln Asn Arg Glu Phe Lys
 385 390 395 400
 Ala Ala Glu Glu Arg Gly Phe Thr Ala Val Lys His Gln Arg Glu Val
 405 410 415
 Gly Ala Gly Tyr Phe Asp Gln Ile Ala Thr Thr Val Asp Pro Asn Ser
 420 425 430
 Ser Thr Thr Ala Leu Lys Gly Ser Thr Glu Glu Gly Gln Phe His Asn
 435 440 445

<210> 591

<211> 1419

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1396)

<223> FRXA02399

<400> 591

caaaccgatg cacatcacgt cgaaacagtg acagtgcatt agctcatact ttgtgggtcgg 60

caccgccccat tgcgaatcag cacttaagga agtgactttg atg tca aac gtt gga 115
 Met Ser Asn Val Gly 5
 1

aag cca cgt acc gca cag gaa atc cag cag gat tgg gac acc aac cct 163
 Lys Pro Arg Thr Ala Gln Glu Ile Gln Gln Asp Trp Asp Thr Asn Pro 20
 10 15

cgt tgg aac ggc atc acc cgc gac tac acc gca gac cag gta gct gat 211
 Arg Trp Asn Gly Ile Thr Arg Asp Tyr Thr Ala Asp Gln Val Ala Asp 35
 25 30

ctg cag ggt tcc gtc atc gag gag cac act ctt gct cgc cgc ggc tca 259
 Leu Gln Gly Ser Val Ile Glu Glu His Thr Leu Ala Arg Arg Gly Ser 50
 40 45

gag atc ctc tgg gac gca gtc acc cag gaa ggt gac gga tac atc aac 307
 Glu Ile Leu Trp Asp Ala Val Thr Gln Glu Gly Asp Gly Tyr Ile Asn 65
 55 60

gcg ctt ggc gca ctc acc ggt aac cag gct gtt cag cag gtt cgt gca 355
 Ala Leu Gly Ala Leu Thr Gly Asn Gln Ala Val Gln Gln Val Arg Ala 85
 70 75 80

ggc ctg aag gct gtc tac ctg tcc ggt tgg cag gtc gca ggt gac gcc 403
 Gly Leu Lys Ala Val Tyr Leu Ser Gly Trp Gln Val Ala Gly Asp Ala 100
 90 95

aac ctc tcc ggc cac acc tac cct gac cag tcc ctc tac cca gcg aac 451
 Asn Leu Ser Gly His Thr Tyr Pro Asp Gln Ser Leu Tyr Pro Ala Asn 115
 105 110

tcc gtt cca agc gtc gtt cgt cgc atc aac aac gca ctg ctg cgt tcc 499
 Ser Val Pro Ser Val Val Arg Arg Ile Asn Asn Ala Leu Leu Arg Ser 130
 120 125

gat gaa atc gca cgc acc gaa ggc gac acc tcc gtt gac aac tgg gtt 547
 Asp Glu Ile Ala Arg Thr Glu Gly Asp Thr Ser Val Asp Asn Trp Val 145
 135 140

gtc cca atc gtc gcg gac ggc gaa gct ggc ttc ggt gga gca ctc aac 595
 Val Pro Ile Val Ala Asp Gly Glu Ala Gly Phe Gly Gly Ala Leu Asn 165
 150 155 160

gtc tac gaa ctc cag aag gca atg atc gca gct ggc gct gca ggc acc 643
 Val Tyr Glu Leu Gln Lys Ala Met Ile Ala Ala Gly Ala Ala Gly Thr 180
 170 175

cac tgg gaa gac cag ctc gct tct gaa aag aag tgt ggc cac ctc ggc 691
 His Trp Glu Asp Gln Leu Ala Ser Glu Lys Lys Cys Gly His Leu Gly 195
 185 190

ggc aag gtt ctg atc cca acc cag cag cac atc cgc acc ctg aac tct 739
 Gly Lys Val Leu Ile Pro Thr Gln Gln His Ile Arg Thr Leu Asn Ser 210
 200 205

gcc cgc ctt gca gca gac gtt gca aac acc cca act gtt gtt atc gca 787
 Ala Arg Leu Ala Ala Asp Val Ala Asn Thr Pro Thr Val Val Ile Ala
 215 220 225

cgt acc gac gct gag gca gca acc ctg atc acc tct gac gtt gat gag 835
 Arg Thr Asp Ala Glu Ala Ala Thr Leu Ile Thr Ser Asp Val Asp Glu
 230 235 240 245

cgc gac caa cca ttc atc acc ggt gag cgc acc gca gaa ggc tac tac 883
 Arg Asp Gln Pro Phe Ile Thr Gly Glu Arg Thr Ala Glu Gly Tyr Tyr
 250 255 260

cac gtc aag aat ggt ctc gag cca tgt atc gca cgt gca aag tcc tac 931
 His Val Lys Asn Gly Leu Glu Pro Cys Ile Ala Arg Ala Lys Ser Tyr
 265 270 275

gca cca tac gca gat atg atc tgg atg gag acc ggc acc cct gac ctg 979
 Ala Pro Tyr Ala Asp Met Ile Trp Met Glu Thr Gly Thr Pro Asp Leu
 280 285 290

gag ctc gct aag aag ttc gct gaa ggc gtt cgc tct gag ttc cca gac 1027
 Glu Leu Ala Lys Lys Phe Ala Glu Gly Val Arg Ser Glu Phe Pro Asp
 295 300 305

cag ctg ctg tcc tac aac tgc tcc cca tcc ttc aac tgg tct gca cac 1075
 Gln Leu Leu Ser Tyr Asn Cys Ser Pro Ser Phe Asn Trp Ser Ala His
 310 315 320 325

ctc gag gca gat gag atc gct aag ttc cag aag gaa ctc ggc gca atg 1123
 Leu Glu Ala Asp Glu Ile Ala Lys Phe Gln Lys Glu Leu Gly Ala Met
 330 335 340

ggc ttc aag ttc cag ttc atc acc ctc gca ggc ttc cac tcc ctc aac 1171
 Gly Phe Lys Phe Gln Phe Ile Thr Leu Ala Gly Phe His Ser Leu Asn
 345 350 355

tac ggc atg ttc gac ctg gct tac gga tac gct cgc gaa ggc atg acc 1219
 Tyr Gly Met Phe Asp Leu Ala Tyr Gly Tyr Ala Arg Glu Gly Met Thr
 360 365 370

tcc ttc gtt gac ctg cag aac cgt gag ttc aag gca gct gaa gag cgt 1267
 Ser Phe Val Asp Leu Gln Asn Arg Glu Phe Lys Ala Ala Glu Glu Arg
 375 380 385

ggc ttc acc gct gtt aag cac cag cgt gag gtt ggc gca ggc tac ttc 1315
 Gly Phe Thr Ala Val Lys His Gln Arg Glu Val Gly Ala Gly Tyr Phe
 390 395 400 405

gac cag atc gca acc acc gtt gac ccg aac tct tct acc acc gct ttg 1363
 Asp Gln Ile Ala Thr Thr Val Asp Pro Asn Ser Ser Thr Thr Ala Leu
 410 415 420

aag ggt tcc act gaa gaa ggc cag ttc cac aac taggacctac aggttctgac 1416
 Lys Gly Ser Thr Glu Glu Gly Gln Phe His Asn
 425 430

aat 1419

<210> 592

<211> 432

<212> PRT

<213> Corynebacterium glutamicum

<400> 592

```

Met Ser Asn Val Gly Lys Pro Arg Thr Ala Gln Glu Ile Gln Gln Asp
 1           5           10           15

Trp Asp Thr Asn Pro Arg Trp Asn Gly Ile Thr Arg Asp Tyr Thr Ala
          20           25           30

Asp Gln Val Ala Asp Leu Gln Gly Ser Val Ile Glu Glu His Thr Leu
          35           40           45

Ala Arg Arg Gly Ser Glu Ile Leu Trp Asp Ala Val Thr Gln Glu Gly
          50           55           60

Asp Gly Tyr Ile Asn Ala Leu Gly Ala Leu Thr Gly Asn Gln Ala Val
 65           70           75           80

Gln Gln Val Arg Ala Gly Leu Lys Ala Val Tyr Leu Ser Gly Trp Gln
          85           90           95

Val Ala Gly Asp Ala Asn Leu Ser Gly His Thr Tyr Pro Asp Gln Ser
          100          105          110

Leu Tyr Pro Ala Asn Ser Val Pro Ser Val Val Arg Arg Ile Asn Asn
 115          120          125

Ala Leu Leu Arg Ser Asp Glu Ile Ala Arg Thr Glu Gly Asp Thr Ser
 130          135          140

Val Asp Asn Trp Val Val Pro Ile Val Ala Asp Gly Glu Ala Gly Phe
 145          150          155          160

Gly Gly Ala Leu Asn Val Tyr Glu Leu Gln Lys Ala Met Ile Ala Ala
          165          170          175

Gly Ala Ala Gly Thr His Trp Glu Asp Gln Leu Ala Ser Glu Lys Lys
          180          185          190

Cys Gly His Leu Gly Gly Lys Val Leu Ile Pro Thr Gln Gln His Ile
          195          200          205

Arg Thr Leu Asn Ser Ala Arg Leu Ala Ala Asp Val Ala Asn Thr Pro
 210          215          220

Thr Val Val Ile Ala Arg Thr Asp Ala Glu Ala Ala Thr Leu Ile Thr
 225          230          235          240

Ser Asp Val Asp Glu Arg Asp Gln Pro Phe Ile Thr Gly Glu Arg Thr
          245          250          255

Ala Glu Gly Tyr Tyr His Val Lys Asn Gly Leu Glu Pro Cys Ile Ala
          260          265          270

Arg Ala Lys Ser Tyr Ala Pro Tyr Ala Asp Met Ile Trp Met Glu Thr
          275          280          285

Gly Thr Pro Asp Leu Glu Leu Ala Lys Lys Phe Ala Glu Gly Val Arg
 290          295          300

```

Ser Glu Phe Pro Asp Gln Leu Leu Ser Tyr Asn Cys Ser Pro Ser Phe
 305 310 315 320

Asn Trp Ser Ala His Leu Glu Ala Asp Glu Ile Ala Lys Phe Gln Lys
 325 330 335

Glu Leu Gly Ala Met Gly Phe Lys Phe Gln Phe Ile Thr Leu Ala Gly
 340 345 350

Phe His Ser Leu Asn Tyr Gly Met Phe Asp Leu Ala Tyr Gly Tyr Ala
 355 360 365

Arg Glu Gly Met Thr Ser Phe Val Asp Leu Gln Asn Arg Glu Phe Lys
 370 375 380

Ala Ala Glu Glu Arg Gly Phe Thr Ala Val Lys His Gln Arg Glu Val
 385 390 395 400

Gly Ala Gly Tyr Phe Asp Gln Ile Ala Thr Thr Val Asp Pro Asn Ser
 405 410 415

Ser Thr Thr Ala Leu Lys Gly Ser Thr Glu Glu Gly Gln Phe His Asn
 420 425 430

<210> 593

<211> 2340

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2317)

<223> RXN02404

<400> 593

gttttcacaa ccgttaacgg cgtagccaaa caagaaggat tcgcattcct ctggttttagg 60

cacaggtcat ctaaaaccca tgcttttaaaa ggagccttca atg act gaa cag gaa 115
 Met Thr Glu Gln Glu
 1 5

ctg ttg tct gct cag act gcc gac aac gct gga act gac agc acc gaa 163
 Leu Leu Ser Ala Gln Thr Ala Asp Asn Ala Gly Thr Asp Ser Thr Glu
 10 15 20

cgc gtt gac gcg ggc gga atg cag gtt gca aaa gtt ctc tac gac ttt 211
 Arg Val Asp Ala Gly Gly Met Gln Val Ala Lys Val Leu Tyr Asp Phe
 25 30 35

gta acc gaa gcg gta ctc cct cgc gtg ggt gtg gat gcg gaa aag ttc 259
 Val Thr Glu Ala Val Leu Pro Arg Val Gly Val Asp Ala Glu Lys Phe
 40 45 50

tgg tcc gga ttc gcc gcc atc gcc cgg gac ctc acc cca cgc aac cgc 307
 Trp Ser Gly Phe Ala Ala Ile Ala Arg Asp Leu Thr Pro Arg Asn Arg
 55 60 65

gag	ctg	ctt	gct	cgc	cgc	gat	gaa	ctg	cag	atg	ctt	atc	gac	gac	tac	355
Glu	Leu	Leu	Ala	Arg	Arg	Asp	Glu	Leu	Gln	Met	Leu	Ile	Asp	Asp	Tyr	
70					75					80					85	
cac	cgc	aac	aac	tcc	ggc	acc	atc	gac	caa	gag	gcg	tac	gag	gat	ttc	403
His	Arg	Asn	Asn	Ser	Gly	Thr	Ile	Asp	Gln	Glu	Ala	Tyr	Glu	Asp	Phe	
				90					95					100		
ctc	aaa	gaa	atc	gga	tac	ttg	gtt	gag	gag	cca	gaa	gct	gca	gaa	atc	451
Leu	Lys	Glu	Ile	Gly	Tyr	Leu	Val	Glu	Glu	Pro	Glu	Ala	Ala	Glu	Ile	
			105					110					115			
cgt	acc	caa	aac	gtc	gat	acg	gaa	atc	tcc	agc	acc	gca	gga	cct	cag	499
Arg	Thr	Gln	Asn	Val	Asp	Thr	Glu	Ile	Ser	Ser	Thr	Ala	Gly	Pro	Gln	
		120					125					130				
ctg	gtt	gtt	cca	att	ctg	aac	gca	cgc	ttc	gcg	ctg	aac	gct	gcc	aat	547
Leu	Val	Val	Pro	Ile	Leu	Asn	Ala	Arg	Phe	Ala	Leu	Asn	Ala	Ala	Asn	
	135					140					145					
gct	cgc	tgg	ggt	tcc	ctc	tac	gat	gcg	ttg	tac	ggc	acc	aac	gcc	atc	595
Ala	Arg	Trp	Gly	Ser	Leu	Tyr	Asp	Ala	Leu	Tyr	Gly	Thr	Asn	Ala	Ile	
150					155					160					165	
cca	gaa	act	gat	ggc	gct	gaa	aag	ggc	aag	gag	tac	aac	ccg	gtc	cgc	643
Pro	Glu	Thr	Asp	Gly	Ala	Glu	Lys	Gly	Lys	Glu	Tyr	Asn	Pro	Val	Arg	
				170				175						180		
ggc	cag	aag	gtc	atc	gag	tgg	ggt	cgt	gaa	ttc	ctc	gac	agc	gtt	gtc	691
Gly	Gln	Lys	Val	Ile	Glu	Trp	Gly	Arg	Glu	Phe	Leu	Asp	Ser	Val	Val	
			185					190					195			
cca	ctg	gac	ggt	gct	tcg	cat	gcc	gat	gtt	gag	aag	tac	aac	atc	acc	739
Pro	Leu	Asp	Gly	Ala	Ser	His	Ala	Asp	Val	Glu	Lys	Tyr	Asn	Ile	Thr	
		200					205					210				
gat	gga	aag	ctt	gca	gcc	cac	att	gga	gat	agc	gtc	tac	cga	ctg	aaa	787
Asp	Gly	Lys	Leu	Ala	Ala	His	Ile	Gly	Asp	Ser	Val	Tyr	Arg	Leu	Lys	
	215					220					225					
aac	cgt	gaa	tcc	tac	cgt	ggc	ttc	acc	ggc	aac	ttc	ctt	gat	cca	gaa	835
Asn	Arg	Glu	Ser	Tyr	Arg	Gly	Phe	Thr	Gly	Asn	Phe	Leu	Asp	Pro	Glu	
230					235					240					245	
gca	atc	ctg	ctg	gaa	acc	aac	ggc	ctg	cac	atc	gag	ctg	cag	atc	gat	883
Ala	Ile	Leu	Leu	Glu	Thr	Asn	Gly	Leu	His	Ile	Glu	Leu	Gln	Ile	Asp	
				250				255						260		
cct	gtc	cac	cca	atc	ggc	aag	gca	gac	aag	act	ggt	ctc	aaa	gac	atc	931
Pro	Val	His	Pro	Ile	Gly	Lys	Ala	Asp	Lys	Thr	Gly	Leu	Lys	Asp	Ile	
			265					270					275			
gtt	ttg	gaa	tct	gcg	atc	acc	acg	atc	atg	gac	ttc	gaa	gac	tcc	gtt	979
Val	Leu	Glu	Ser	Ala	Ile	Thr	Thr	Ile	Met	Asp	Phe	Glu	Asp	Ser	Val	
			280				285					290				
gca	gct	gtt	gat	gct	gaa	gac	aag	acc	tta	ggt	tac	tct	aac	tgg	ttc	1027
Ala	Ala	Val	Asp	Ala	Glu	Asp	Lys	Thr	Leu	Gly	Tyr	Ser	Asn	Trp	Phe	
	295					300					305					
gga	ctc	aac	acc	ggc	gaa	ctg	aaa	gaa	gag	atg	tcc	aag	aac	gga	cgc	1075

Gly 310	Leu	Asn	Thr	Gly 315	Glu	Leu	Lys	Glu	Glu	Met 320	Ser	Lys	Asn	Gly	Arg 325	
atc	ttc	acc	cgt	gag	ctc	aac	aag	gac	cgc	gtc	tac	att	ggc	cgc	aat	1123
Ile	Phe	Thr	Arg	Glu 330	Leu	Asn	Lys	Asp	Arg 335	Val	Tyr	Ile	Gly	Arg	Asn 340	
ggt	acc	gag	ctg	gtt	ctg	cac	ggt	cgt	tcc	ctg	ctg	ttc	gtc	cgc	aac	1171
Gly	Thr	Glu	Leu	Val 345	Leu	His	Gly	Arg	Ser 350	Leu	Leu	Phe	Val	Arg	Asn 355	
gtt	ggt	cac	ctc	atg	caa	aac	cca	tcc	atc	ttg	att	gat	ggc	gag	gag	1219
Val	Gly	His	Leu	Met 360	Gln	Asn	Pro	Ser	Ile 365	Leu	Ile	Asp	Gly	Glu	Glu 370	
atc	ttc	gaa	ggc	atc	atg	gat	gct	gtc	ttg	acc	act	gtt	tgt	gcc	atc	1267
Ile	Phe	Glu	Gly	Ile 375	Met	Asp	Ala	Val	Leu	Thr	Thr	Val	Cys	Ala	Ile 380	
cca	gga	att	gct	ccg	cag	aac	aag	atg	cgc	aat	tcc	cgc	aag	ggc	tcc	1315
Pro	Gly	Ile	Ala	Pro 390	Gln	Asn	Lys	Met	Arg 400	Asn	Ser	Arg	Lys	Gly	Ser 405	
atc	tac	atc	gtg	aag	cct	aag	cag	cac	ggc	cct	gaa	gaa	gtc	gcg	ttc	1363
Ile	Tyr	Ile	Val	Lys 410	Pro	Lys	Gln	His	Gly 415	Pro	Glu	Glu	Val	Ala	Phe 420	
acc	aac	gag	ctc	ttc	ggc	cgc	gtt	gag	gat	ctg	ctt	gat	ctg	cca	cgc	1411
Thr	Asn	Glu	Leu	Phe 425	Gly	Arg	Val	Glu	Asp 430	Leu	Leu	Asp	Leu	Pro	Arg 435	
cac	acc	ttg	aag	gtt	ggt	gtt	atg	gat	gag	gag	cgt	cgc	acg	tcc	gtg	1459
His	Thr	Leu	Lys	Val 440	Gly	Val	Met	Asp	Glu	Glu	Arg	Arg	Thr	Ser	Val 445	
aac	ctg	gat	gcc	agc	atc	atg	gaa	gtt	gct	gac	cgc	ttg	gca	ttc	atc	1507
Asn	Leu	Asp	Ala	Ser 455	Ile	Met	Glu	Val	Ala	Asp	Arg	Leu	Ala	Phe	Ile 460	
aac	act	ggc	ttc	ctg	gac	cgc	acc	ggc	gat	gaa	atc	cac	acc	tcc	atg	1555
Asn	Thr	Gly	Phe	Leu 470	Asp	Arg	Thr	Gly	Asp	Glu	Ile	His	Thr	Ser	Met 475	
gaa	gca	ggc	gcc	atg	gtg	cgc	aag	gct	gat	atg	cag	acc	gca	ccg	tgg	1603
Glu	Ala	Gly	Ala	Met 490	Val	Arg	Lys	Ala	Asp	Met	Gln	Thr	Ala	Pro	Trp 500	
aag	cag	gcc	tac	gag	aac	aac	aac	gtt	gat	gca	ggt	att	cag	cgt	ggt	1651
Lys	Gln	Ala	Tyr	Glu 505	Asn	Asn	Asn	Val	Asp	Ala	Gly	Ile	Gln	Arg	Gly 510	
ctt	cct	ggc	aag	gct	cag	atc	ggt	aag	ggc	atg	tgg	gcg	atg	act	gaa	1699
Leu	Pro	Gly	Lys	Ala 520	Gln	Ile	Gly	Lys	Gly	Met	Trp	Ala	Met	Thr	Glu 525	
ctc	atg	gca	gaa	atg	ctg	gag	aag	aag	atc	ggc	cag	cca	cgc	gaa	ggc	1747
Leu	Met	Ala	Glu	Met 535	Leu	Glu	Lys	Lys	Ile	Gly	Gln	Pro	Arg	Glu	Gly 540	
gcc	aac	act	gca	tgg	gtt	cct	tca	cca	act	ggt	gcg	acg	ctg	cac	gca	1795
Ala	Asn	Thr	Ala	Trp	Val	Pro	Ser	Pro	Thr	Gly	Ala	Thr	Leu	His	Ala 545	

550	555	560	565	
acg cac tac cac ttg gtt gat gtg ttc aag gtt caa gac gaa ctg cgt				1843
Thr His Tyr His Leu Val Asp Val Phe Lys Val Gln Asp Glu Leu Arg				
570		575	580	
gct gcc ggc cgc cgc gac agc ctg cgc aac att ctc acc att tca acc				1891
Ala Ala Gly Arg Arg Asp Ser Leu Arg Asn Ile Leu Thr Ile Ser Thr				
585		590	595	
gca cca aac acc aat tgg tct gag gaa gag aag aag gaa gag atg gac				1939
Ala Pro Asn Thr Asn Trp Ser Glu Glu Glu Lys Lys Glu Glu Met Asp				
600		605	610	
aac aac tgc cag tcc atc ctc gga tac gtt gtg cgc tgg gtt gag cac				1987
Asn Asn Cys Gln Ser Ile Leu Gly Tyr Val Val Arg Trp Val Glu His				
615		620	625	
ggt gtt ggt tgc tcc aag gtt cca gac atc cat gac atc gac ctc atg				2035
Gly Val Gly Cys Ser Lys Val Pro Asp Ile His Asp Ile Asp Leu Met				
630		635	640	645
gaa gac cgc gca acg ctg cgt att tcc tcg cag atg ctg gcc aac tgg				2083
Glu Asp Arg Ala Thr Leu Arg Ile Ser Ser Gln Met Leu Ala Asn Trp				
650		655	660	
atc cgc cat gat gtt gtc tcg aag gag cag gtc ttg gag tca ctg gaa				2131
Ile Arg His Asp Val Val Ser Lys Glu Gln Val Leu Glu Ser Leu Glu				
665		670	675	
cga atg gca gtg gtc gtc gac aag caa aat gcg ggc gac gag gcc tac				2179
Arg Met Ala Val Val Val Asp Lys Gln Asn Ala Gly Asp Glu Ala Tyr				
680		685	690	
cgc gat atg gcg ccg aag tac gac gcc tcc ctc gcc ttc cag gcg gct				2227
Arg Asp Met Ala Pro Lys Tyr Asp Ala Ser Leu Ala Phe Gln Ala Ala				
695		700	705	
aag gac ttg att ttc gaa ggc acc aag tcc cca tcg ggc tac acc gag				2275
Lys Asp Leu Ile Phe Glu Gly Thr Lys Ser Pro Ser Gly Tyr Thr Glu				
710		715	720	725
ccc atc ttg cac gca cgc cgc cgc gag ttc aaa gca aaa aac				2317
Pro Ile Leu His Ala Arg Arg Arg Glu Phe Lys Ala Lys Asn				
730		735		
taagcacgct ttctgacgct tac				2340

<210> 594

<211> 739

<212> PRT

<213> Corynebacterium glutamicum

<400> 594

Met	Thr	Glu	Gln	Glu	Leu	Leu	Ser	Ala	Gln	Thr	Ala	Asp	Asn	Ala	Gly
1				5					10					15	

Thr	Asp	Ser	Thr	Glu	Arg	Val	Asp	Ala	Gly	Gly	Met	Gln	Val	Ala	Lys
			20					25					30		

Val Leu Tyr Asp Phe Val Thr Glu Ala Val Leu Pro Arg Val Gly Val
 35 40 45
 Asp Ala Glu Lys Phe Trp Ser Gly Phe Ala Ala Ile Ala Arg Asp Leu
 50 55 60
 Thr Pro Arg Asn Arg Glu Leu Leu Ala Arg Arg Asp Glu Leu Gln Met
 65 70 75 80
 Leu Ile Asp Asp Tyr His Arg Asn Asn Ser Gly Thr Ile Asp Gln Glu
 85 90 95
 Ala Tyr Glu Asp Phe Leu Lys Glu Ile Gly Tyr Leu Val Glu Glu Pro
 100 105 110
 Glu Ala Ala Glu Ile Arg Thr Gln Asn Val Asp Thr Glu Ile Ser Ser
 115 120 125
 Thr Ala Gly Pro Gln Leu Val Val Pro Ile Leu Asn Ala Arg Phe Ala
 130 135 140
 Leu Asn Ala Ala Asn Ala Arg Trp Gly Ser Leu Tyr Asp Ala Leu Tyr
 145 150 155 160
 Gly Thr Asn Ala Ile Pro Glu Thr Asp Gly Ala Glu Lys Gly Lys Glu
 165 170 175
 Tyr Asn Pro Val Arg Gly Gln Lys Val Ile Glu Trp Gly Arg Glu Phe
 180 185 190
 Leu Asp Ser Val Val Pro Leu Asp Gly Ala Ser His Ala Asp Val Glu
 195 200 205
 Lys Tyr Asn Ile Thr Asp Gly Lys Leu Ala Ala His Ile Gly Asp Ser
 210 215 220
 Val Tyr Arg Leu Lys Asn Arg Glu Ser Tyr Arg Gly Phe Thr Gly Asn
 225 230 235 240
 Phe Leu Asp Pro Glu Ala Ile Leu Leu Glu Thr Asn Gly Leu His Ile
 245 250 255
 Glu Leu Gln Ile Asp Pro Val His Pro Ile Gly Lys Ala Asp Lys Thr
 260 265 270
 Gly Leu Lys Asp Ile Val Leu Glu Ser Ala Ile Thr Thr Ile Met Asp
 275 280 285
 Phe Glu Asp Ser Val Ala Ala Val Asp Ala Glu Asp Lys Thr Leu Gly
 290 295 300
 Tyr Ser Asn Trp Phe Gly Leu Asn Thr Gly Glu Leu Lys Glu Glu Met
 305 310 315 320
 Ser Lys Asn Gly Arg Ile Phe Thr Arg Glu Leu Asn Lys Asp Arg Val
 325 330 335
 Tyr Ile Gly Arg Asn Gly Thr Glu Leu Val Leu His Gly Arg Ser Leu
 340 345 350
 Leu Phe Val Arg Asn Val Gly His Leu Met Gln Asn Pro Ser Ile Leu

355					360					365					
Ile	Asp	Gly	Glu	Glu	Ile	Phe	Glu	Gly	Ile	Met	Asp	Ala	Val	Leu	Thr
370					375					380					
Thr	Val	Cys	Ala	Ile	Pro	Gly	Ile	Ala	Pro	Gln	Asn	Lys	Met	Arg	Asn
385					390					395					400
Ser	Arg	Lys	Gly	Ser	Ile	Tyr	Ile	Val	Lys	Pro	Lys	Gln	His	Gly	Pro
				405					410					415	
Glu	Glu	Val	Ala	Phe	Thr	Asn	Glu	Leu	Phe	Gly	Arg	Val	Glu	Asp	Leu
			420					425					430		
Leu	Asp	Leu	Pro	Arg	His	Thr	Leu	Lys	Val	Gly	Val	Met	Asp	Glu	Glu
		435					440					445			
Arg	Arg	Thr	Ser	Val	Asn	Leu	Asp	Ala	Ser	Ile	Met	Glu	Val	Ala	Asp
		450					455					460			
Arg	Leu	Ala	Phe	Ile	Asn	Thr	Gly	Phe	Leu	Asp	Arg	Thr	Gly	Asp	Glu
465					470					475					480
Ile	His	Thr	Ser	Met	Glu	Ala	Gly	Ala	Met	Val	Arg	Lys	Ala	Asp	Met
				485					490					495	
Gln	Thr	Ala	Pro	Trp	Lys	Gln	Ala	Tyr	Glu	Asn	Asn	Asn	Val	Asp	Ala
			500					505					510		
Gly	Ile	Gln	Arg	Gly	Leu	Pro	Gly	Lys	Ala	Gln	Ile	Gly	Lys	Gly	Met
		515					520					525			
Trp	Ala	Met	Thr	Glu	Leu	Met	Ala	Glu	Met	Leu	Glu	Lys	Lys	Ile	Gly
		530					535					540			
Gln	Pro	Arg	Glu	Gly	Ala	Asn	Thr	Ala	Trp	Val	Pro	Ser	Pro	Thr	Gly
545					550					555					560
Ala	Thr	Leu	His	Ala	Thr	His	Tyr	His	Leu	Val	Asp	Val	Phe	Lys	Val
			565						570					575	
Gln	Asp	Glu	Leu	Arg	Ala	Ala	Gly	Arg	Arg	Asp	Ser	Leu	Arg	Asn	Ile
			580					585					590		
Leu	Thr	Ile	Ser	Thr	Ala	Pro	Asn	Thr	Asn	Trp	Ser	Glu	Glu	Glu	Lys
		595					600					605			
Lys	Glu	Glu	Met	Asp	Asn	Asn	Cys	Gln	Ser	Ile	Leu	Gly	Tyr	Val	Val
		610					615					620			
Arg	Trp	Val	Glu	His	Gly	Val	Gly	Cys	Ser	Lys	Val	Pro	Asp	Ile	His
625					630					635					640
Asp	Ile	Asp	Leu	Met	Glu	Asp	Arg	Ala	Thr	Leu	Arg	Ile	Ser	Ser	Gln
			645						650				655		
Met	Leu	Ala	Asn	Trp	Ile	Arg	His	Asp	Val	Val	Ser	Lys	Glu	Gln	Val
			660					665					670		
Leu	Glu	Ser	Leu	Glu	Arg	Met	Ala	Val	Val	Val	Asp	Lys	Gln	Asn	Ala
		675					680						685		

Gly Asp Glu Ala Tyr Arg Asp Met Ala Pro Lys Tyr Asp Ala Ser Leu
 690 695 700

Ala Phe Gln Ala Ala Lys Asp Leu Ile Phe Glu Gly Thr Lys Ser Pro
 705 710 715 720

Ser Gly Tyr Thr Glu Pro Ile Leu His Ala Arg Arg Arg Glu Phe Lys
 725 730 735

Ala Lys Asn

<210> 595

<211> 2159

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(2136)

<223> FRXA02404

<400> 595

atg cag gtt gca aaa gtt ctc tac gac ttt gta acc gaa gcg gta ctc 48
 Met Gln Val Ala Lys Val Leu Tyr Asp Phe Val Thr Glu Ala Val Leu
 1 5 10 15

cct cgc gtg ggt gtg gat gcg gaa aag ttc tgg tcc gga ttc gcc gcc 96
 Pro Arg Val Gly Val Asp Ala Glu Lys Phe Trp Ser Gly Phe Ala Ala
 20 25 30

atc gcc cgg gac ctc acc cca cgc aac cgc gag ctg ctt gct cgc cgc 144
 Ile Ala Arg Asp Leu Thr Pro Arg Asn Arg Glu Leu Leu Ala Arg Arg
 35 40 45

gat gaa ctg cag atg ctt atc gac gac tac cac cgc aac aac tcc ggc 192
 Asp Glu Leu Gln Met Leu Ile Asp Asp Tyr His Arg Asn Asn Ser Gly
 50 55 60

acc atc gac caa gag gcg tac gag gat ttc ctc aaa gaa atc gga tac 240
 Thr Ile Asp Gln Glu Ala Tyr Glu Asp Phe Leu Lys Glu Ile Gly Tyr
 65 70 75 80

ttg gtt gag gag cca gaa gct gca gaa atc cgt acc caa aac gtc gat 288
 Leu Val Glu Glu Pro Glu Ala Ala Glu Ile Arg Thr Gln Asn Val Asp
 85 90 95

acg gaa atc tcc agc acc gca gga cct cag ctg gtt gtt cca att ctg 336
 Thr Glu Ile Ser Ser Thr Ala Gly Pro Gln Leu Val Val Pro Ile Leu
 100 105 110

aac gca cgc ttc gcg ctg aac gct gcc aat gct cgc tgg ggt tcc ctc 384
 Asn Ala Arg Phe Ala Leu Asn Ala Ala Asn Ala Arg Trp Gly Ser Leu
 115 120 125

tac gat gcg ttg tac ggc acc aac gcc atc cca gaa act gat ggc gct 432
 Tyr Asp Ala Leu Tyr Gly Thr Asn Ala Ile Pro Glu Thr Asp Gly Ala
 130 135 140

gaa aag ggc aag gag tac aac ccg gtc cgc ggc cag aag gtc atc gag	480
Glu Lys Gly Lys Glu Tyr Asn Pro Val Arg Gly Gln Lys Val Ile Glu	
145 150 155 160	
tgg ggt cgt gaa ttc ctc gac agc gtt gtc cca ctg gac ggt gct tcg	528
Trp Gly Arg Glu Phe Leu Asp Ser Val Val Pro Leu Asp Gly Ala Ser	
165 170 175	
cat gcc gat gtt gag aag tac aac atc acc gat gga aag ctt gca gcc	576
His Ala Asp Val Glu Lys Tyr Asn Ile Thr Asp Gly Lys Leu Ala Ala	
180 185 190	
cac att gga gat agc gtc tac cga ctg aaa aac cgt gaa tcc tac cgt	624
His Ile Gly Asp Ser Val Tyr Arg Leu Lys Asn Arg Glu Ser Tyr Arg	
195 200 205	
ggc ttc acc ggc aac ttc ctt gat cca gaa gca atc ctg ctg gaa acc	672
Gly Phe Thr Gly Asn Phe Leu Asp Pro Glu Ala Ile Leu Leu Glu Thr	
210 215 220	
aac ggc ctg cac atc gag ctg cag atc gat cct gtc cac cca atc ggc	720
Asn Gly Leu His Ile Glu Leu Gln Ile Asp Pro Val His Pro Ile Gly	
225 230 235 240	
aag gca gac aag act ggt ctc aaa gac atc gtt ttg gaa tct gcg atc	768
Lys Ala Asp Lys Thr Gly Leu Lys Asp Ile Val Leu Glu Ser Ala Ile	
245 250 255	
acc acg atc atg gac ttc gaa gac tcc gtt gca gct gtt gat gct gaa	816
Thr Thr Ile Met Asp Phe Glu Asp Ser Val Ala Ala Val Asp Ala Glu	
260 265 270	
gac aag acc tta ggt tac tct aac tgg ttc gga ctc aac acc ggc gaa	864
Asp Lys Thr Leu Gly Tyr Ser Asn Trp Phe Gly Leu Asn Thr Gly Glu	
275 280 285	
ctg aaa gaa gag atg tcc aag aac gga cgc atc ttc acc cgt gag ctc	912
Leu Lys Glu Glu Met Ser Lys Asn Gly Arg Ile Phe Thr Arg Glu Leu	
290 295 300	
aac aag gac cgc gtc tac att ggc cgc aat ggt acc gag ctg gtt ctg	960
Asn Lys Asp Arg Val Tyr Ile Gly Arg Asn Gly Thr Glu Leu Val Leu	
305 310 315 320	
cac ggt cgt tcc ctg ctg ttc gtc cgc aac gtt ggt cac ctc atg caa	1008
His Gly Arg Ser Leu Leu Phe Val Arg Asn Val Gly His Leu Met Gln	
325 330 335	
aac cca tcc atc ttg att gat ggc gag gag atc ttc gaa ggc atc atg	1056
Asn Pro Ser Ile Leu Ile Asp Gly Glu Glu Ile Phe Glu Gly Ile Met	
340 345 350	
gat gct gtc ttg acc act gtt tgt gcc atc cca gga att gct ccg cag	1104
Asp Ala Val Leu Thr Thr Val Cys Ala Ile Pro Gly Ile Ala Pro Gln	
355 360 365	
aac aag atg cgc aat tcc cgc aag ggc tcc atc tac atc gtg aag cct	1152
Asn Lys Met Arg Asn Ser Arg Lys Gly Ser Ile Tyr Ile Val Lys Pro	
370 375 380	
aag cag cac ggc cct gaa gaa gtc gcg ttc acc aac gag ctc ttc ggc	1200

Lys	Gln	His	Gly	Pro	Glu	Glu	Val	Ala	Phe	Thr	Asn	Glu	Leu	Phe	Gly		
385					390					395					400		
cgc	gtt	gag	gat	ctg	ctt	gat	ctg	cca	cgc	cac	acc	ttg	aag	gtt	ggt	1248	
Arg	Val	Glu	Asp	Leu	Leu	Asp	Leu	Pro	Arg	His	Thr	Leu	Lys	Val	Gly		
				405					410					415			
gtt	atg	gat	gag	gag	cgt	cgc	acg	tcc	gtg	aac	ctg	gat	gcc	agc	atc	1296	
Val	Met	Asp	Glu	Glu	Arg	Arg	Thr	Ser	Val	Asn	Leu	Asp	Ala	Ser	Ile		
				420				425					430				
atg	gaa	gtt	gct	gac	cgc	ttg	gca	ttc	atc	aac	act	ggc	ttc	ctg	gac	1344	
Met	Glu	Val	Ala	Asp	Arg	Leu	Ala	Phe	Ile	Asn	Thr	Gly	Phe	Leu	Asp		
		435					440					445					
cgc	acc	ggc	gat	gaa	atc	cac	acc	tcc	atg	gaa	gca	ggc	gcc	atg	gtg	1392	
Arg	Thr	Gly	Asp	Glu	Ile	His	Thr	Ser	Met	Glu	Ala	Gly	Ala	Met	Val		
	450					455					460						
cgc	aag	gct	gat	atg	cag	acc	gca	ccg	tgg	aag	cag	gcc	tac	gag	aac	1440	
Arg	Lys	Ala	Asp	Met	Gln	Thr	Ala	Pro	Trp	Lys	Gln	Ala	Tyr	Glu	Asn		
465					470					475					480		
aac	aac	gtt	gat	gca	ggc	att	cag	cgt	ggc	ctt	cct	ggc	aag	gct	cag	1488	
Asn	Asn	Val	Asp	Ala	Gly	Ile	Gln	Arg	Gly	Leu	Pro	Gly	Lys	Ala	Gln		
				485					490					495			
atc	ggc	aag	ggc	atg	tgg	gcg	atg	act	gaa	ctc	atg	gca	gaa	atg	ctg	1536	
Ile	Gly	Lys	Gly	Met	Trp	Ala	Met	Thr	Glu	Leu	Met	Ala	Glu	Met	Leu		
			500					505					510				
gag	aag	aag	atc	ggc	cag	cca	cgc	gaa	ggc	gcc	aac	act	gca	tgg	gtt	1584	
Glu	Lys	Lys	Ile	Gly	Gln	Pro	Arg	Glu	Gly	Ala	Asn	Thr	Ala	Trp	Val		
		515					520					525					
cct	tca	cca	act	ggc	gcg	acg	ctg	cac	gca	acg	cac	tac	cac	ttg	gtt	1632	
Pro	Ser	Pro	Thr	Gly	Ala	Thr	Leu	His	Ala	Thr	His	Tyr	His	Leu	Val		
		530				535					540						
gat	gtg	ttc	aag	gtt	caa	gac	gaa	ctg	cgt	gct	gcc	ggc	cgc	cgc	gac	1680	
Asp	Val	Phe	Lys	Val	Gln	Asp	Glu	Leu	Arg	Ala	Ala	Gly	Arg	Arg	Asp		
545					550					555					560		
agc	ctg	cgc	aac	att	ctc	acc	att	tca	acc	gca	cca	aac	acc	aat	tgg	1728	
Ser	Leu	Arg	Asn	Ile	Leu	Thr	Ile	Ser	Thr	Ala	Pro	Asn	Thr	Asn	Trp		
				565					570					575			
tct	gag	gaa	gag	aag	aag	gaa	gag	atg	gac	aac	aac	tgc	cag	tcc	atc	1776	
Ser	Glu	Glu	Glu	Lys	Lys	Glu	Glu	Met	Asp	Asn	Asn	Cys	Gln	Ser	Ile		
				580				585					590				
ctc	gga	tac	gtt	gtg	cgc	tgg	gtt	gag	cac	ggc	gtt	ggc	tgc	tcc	aag	1824	
Leu	Gly	Tyr	Val	Val	Arg	Trp	Val	Glu	His	Gly	Val	Gly	Cys	Ser	Lys		
		595				600						605					
gtt	cca	gac	atc	cat	gac	atc	gac	ctc	atg	gaa	gac	cgc	gca	acg	ctg	1872	
Val	Pro	Asp	Ile	His	Asp	Ile	Asp	Leu	Met	Glu	Asp	Arg	Ala	Thr	Leu		
		610				615					620						
cgt	att	tcc	tcg	cag	atg	ctg	gcc	aac	tgg	atc	cgc	cat	gat	gtt	gtc	1920	
Arg	Ile	Ser	Ser	Gln	Met	Leu	Ala	Asn	Trp	Ile	Arg	His	Asp	Val	Val		

625	630	635	640	
tcg aag gag cag gtc ttg gag tca ctg gaa cga atg gca gtg gtc gtc				1968
Ser Lys Glu Gln Val Leu Glu Ser Leu Glu Arg Met Ala Val Val Val	645	650	655	
gac aag caa aat gcg ggc gac gag gcc tac cgc gat atg gcg ccg aag				2016
Asp Lys Gln Asn Ala Gly Asp Glu Ala Tyr Arg Asp Met Ala Pro Lys	660	665	670	
tac gac gcc tcc ctc gcc ttc cag gcg gct aag gac ttg att ttc gaa				2064
Tyr Asp Ala Ser Leu Ala Phe Gln Ala Ala Lys Asp Leu Ile Phe Glu	675	680	685	
ggc acc aag tcc cca tcg ggc tac acc gag ccc atc ttg cac gca cgc				2112
Gly Thr Lys Ser Pro Ser Gly Tyr Thr Glu Pro Ile Leu His Ala Arg	690	695	700	
cgc cgc gag ttc aaa gca aaa aac taagcacgct tttcgacgct tac				2159
Arg Arg Glu Phe Lys Ala Lys Asn	705	710		
<210> 596				
<211> 712				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 596				
Met Gln Val Ala Lys Val Leu Tyr Asp Phe Val Thr Glu Ala Val Leu				
1 5 10 15				
Pro Arg Val Gly Val Asp Ala Glu Lys Phe Trp Ser Gly Phe Ala Ala				
20 25 30				
Ile Ala Arg Asp Leu Thr Pro Arg Asn Arg Glu Leu Leu Ala Arg Arg				
35 40 45				
Asp Glu Leu Gln Met Leu Ile Asp Asp Tyr His Arg Asn Asn Ser Gly				
50 55 60				
Thr Ile Asp Gln Glu Ala Tyr Glu Asp Phe Leu Lys Glu Ile Gly Tyr				
65 70 75 80				
Leu Val Glu Glu Pro Glu Ala Ala Glu Ile Arg Thr Gln Asn Val Asp				
85 90 95				
Thr Glu Ile Ser Ser Thr Ala Gly Pro Gln Leu Val Val Pro Ile Leu				
100 105 110				
Asn Ala Arg Phe Ala Leu Asn Ala Ala Asn Ala Arg Trp Gly Ser Leu				
115 120 125				
Tyr Asp Ala Leu Tyr Gly Thr Asn Ala Ile Pro Glu Thr Asp Gly Ala				
130 135 140				
Glu Lys Gly Lys Glu Tyr Asn Pro Val Arg Gly Gln Lys Val Ile Glu				
145 150 155 160				
Trp Gly Arg Glu Phe Leu Asp Ser Val Val Pro Leu Asp Gly Ala Ser				
165 170 175				

His Ala Asp Val Glu Lys Tyr Asn Ile Thr Asp Gly Lys Leu Ala Ala
 180 185 190
 His Ile Gly Asp Ser Val Tyr Arg Leu Lys Asn Arg Glu Ser Tyr Arg
 195 200 205
 Gly Phe Thr Gly Asn Phe Leu Asp Pro Glu Ala Ile Leu Leu Glu Thr
 210 215 220
 Asn Gly Leu His Ile Glu Leu Gln Ile Asp Pro Val His Pro Ile Gly
 225 230 235 240
 Lys Ala Asp Lys Thr Gly Leu Lys Asp Ile Val Leu Glu Ser Ala Ile
 245 250 255
 Thr Thr Ile Met Asp Phe Glu Asp Ser Val Ala Ala Val Asp Ala Glu
 260 265 270
 Asp Lys Thr Leu Gly Tyr Ser Asn Trp Phe Gly Leu Asn Thr Gly Glu
 275 280 285
 Leu Lys Glu Glu Met Ser Lys Asn Gly Arg Ile Phe Thr Arg Glu Leu
 290 295 300
 Asn Lys Asp Arg Val Tyr Ile Gly Arg Asn Gly Thr Glu Leu Val Leu
 305 310 315 320
 His Gly Arg Ser Leu Leu Phe Val Arg Asn Val Gly His Leu Met Gln
 325 330 335
 Asn Pro Ser Ile Leu Ile Asp Gly Glu Glu Ile Phe Glu Gly Ile Met
 340 345 350
 Asp Ala Val Leu Thr Thr Val Cys Ala Ile Pro Gly Ile Ala Pro Gln
 355 360 365
 Asn Lys Met Arg Asn Ser Arg Lys Gly Ser Ile Tyr Ile Val Lys Pro
 370 375 380
 Lys Gln His Gly Pro Glu Glu Val Ala Phe Thr Asn Glu Leu Phe Gly
 385 390 395 400
 Arg Val Glu Asp Leu Leu Asp Leu Pro Arg His Thr Leu Lys Val Gly
 405 410 415
 Val Met Asp Glu Glu Arg Arg Thr Ser Val Asn Leu Asp Ala Ser Ile
 420 425 430
 Met Glu Val Ala Asp Arg Leu Ala Phe Ile Asn Thr Gly Phe Leu Asp
 435 440 445
 Arg Thr Gly Asp Glu Ile His Thr Ser Met Glu Ala Gly Ala Met Val
 450 455 460
 Arg Lys Ala Asp Met Gln Thr Ala Pro Trp Lys Gln Ala Tyr Glu Asn
 465 470 475 480
 Asn Asn Val Asp Ala Gly Ile Gln Arg Gly Leu Pro Gly Lys Ala Gln
 485 490 495

Ile Gly Lys Gly Met Trp Ala Met Thr Glu Leu Met Ala Glu Met Leu
 500 505 510
 Glu Lys Lys Ile Gly Gln Pro Arg Glu Gly Ala Asn Thr Ala Trp Val
 515 520 525
 Pro Ser Pro Thr Gly Ala Thr Leu His Ala Thr His Tyr His Leu Val
 530 535 540
 Asp Val Phe Lys Val Gln Asp Glu Leu Arg Ala Ala Gly Arg Arg Asp
 545 550 555 560
 Ser Leu Arg Asn Ile Leu Thr Ile Ser Thr Ala Pro Asn Thr Asn Trp
 565 570 575
 Ser Glu Glu Glu Lys Lys Glu Glu Met Asp Asn Asn Cys Gln Ser Ile
 580 585 590
 Leu Gly Tyr Val Val Arg Trp Val Glu His Gly Val Gly Cys Ser Lys
 595 600 605
 Val Pro Asp Ile His Asp Ile Asp Leu Met Glu Asp Arg Ala Thr Leu
 610 615 620
 Arg Ile Ser Ser Gln Met Leu Ala Asn Trp Ile Arg His Asp Val Val
 625 630 635 640
 Ser Lys Glu Gln Val Leu Glu Ser Leu Glu Arg Met Ala Val Val Val
 645 650 655
 Asp Lys Gln Asn Ala Gly Asp Glu Ala Tyr Arg Asp Met Ala Pro Lys
 660 665 670
 Tyr Asp Ala Ser Leu Ala Phe Gln Ala Ala Lys Asp Leu Ile Phe Glu
 675 680 685
 Gly Thr Lys Ser Pro Ser Gly Tyr Thr Glu Pro Ile Leu His Ala Arg
 690 695 700
 Arg Arg Glu Phe Lys Ala Lys Asn
 705 710

<210> 597
 <211> 873
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(850)
 <223> RXA01089

<400> 597
 aaaaattcgg ttcacaaaag gtttatcagt ccagcttaaa cccatcgacac gggcgggaga 60
 attagactca aggcacatca cattgaagga gcttcttata ttg tct cga ttt gct 115
 Leu Ser Arg Phe Ala
 1 5
 gcc aac ctg tca ttg act ttt act gag cta gat ttc ctg gat cgt ttt 163

Ala	Asn	Leu	Ser	Leu	Thr	Phe	Thr	Glu	Leu	Asp	Phe	Leu	Asp	Arg	Phe		
				10					15					20			
gat	gcc	gct	tcg	aag	cat	gct	ttc	agt	gcc	gtg	gag	ttt	cag	tac	cct	211	
Asp	Ala	Ala	Ser	Lys	His	Ala	Phe	Ser	Ala	Val	Glu	Phe	Gln	Tyr	Pro		
			25					30					35				
tac	gat	ttc	gat	gtt	caa	gag	att	aaa	cag	cgt	gct	gat	tcc	gca	ggc	259	
Tyr	Asp	Phe	Asp	Val	Gln	Glu	Ile	Lys	Gln	Arg	Ala	Asp	Ser	Ala	Gly		
			40				45					50					
ctg	ccc	att	gaa	ctg	ttc	aat	gcc	cca	cct	ggg	gat	act	ttt	ggc	ctt	307	
Leu	Pro	Ile	Glu	Leu	Phe	Asn	Ala	Pro	Pro	Gly	Asp	Thr	Phe	Gly	Leu		
	55					60					65						
gcg	gca	ctg	gct	tcc	cct	gaa	gac	ttt	caa	caa	tcc	atc	gag	cag	gcc	355	
Ala	Ala	Leu	Ala	Ser	Pro	Glu	Asp	Phe	Gln	Gln	Ser	Ile	Glu	Gln	Ala		
	70				75				80						85		
atc	acg	tac	gcc	aca	gtg	ttg	aag	cca	aag	aag	atg	cat	gtc	atg	gct	403	
Ile	Thr	Tyr	Ala	Thr	Val	Leu	Lys	Pro	Lys	Lys	Met	His	Val	Met	Ala		
				90				95						100			
ggc	atc	gcg	gac	gta	acc	tca	gaa	acc	acg	gcg	cgc	tat	gtg	gag	aat	451	
Gly	Ile	Ala	Asp	Val	Thr	Ser	Glu	Thr	Thr	Ala	Arg	Tyr	Val	Glu	Asn		
			105					110					115				
att	cgc	tgg	gct	gcg	cag	caa	cta	gac	aag	ctc	gac	gtt	gtc	gtt	gtt	499	
Ile	Arg	Trp	Ala	Ala	Gln	Gln	Leu	Asp	Lys	Leu	Asp	Val	Val	Val	Val		
		120					125					130					
att	gaa	cca	att	aat	cac	tat	tcg	gtt	ccc	ggc	tat	ttc	ctg	cac	act	547	
Ile	Glu	Pro	Ile	Asn	His	Tyr	Ser	Val	Pro	Gly	Tyr	Phe	Leu	His	Thr		
	135					140					145						
tta	gag	cag	gcg	tat	tgg	ctt	atc	gac	agc	att	gcc	cac	ccc	aat	gtg	595	
Leu	Glu	Gln	Ala	Tyr	Trp	Leu	Ile	Asp	Ser	Ile	Ala	His	Pro	Asn	Val		
	150				155					160					165		
aag	atc	tta	ttc	gat	act	ttc	cac	ctt	cag	cag	att	cat	ggc	aat	ctc	643	
Lys	Ile	Leu	Phe	Asp	Thr	Phe	His	Leu	Gln	Gln	Ile	His	Gly	Asn	Leu		
			170					175					180				
acc	cgc	cgc	ctg	cgc	gag	gtt	cat	ggc	gca	ggc	ctt	ttg	gga	cac	gtg	691	
Thr	Arg	Arg	Leu	Arg	Glu	Val	His	Gly	Ala	Gly	Leu	Leu	Gly	His	Val		
			185					190					195				
caa	gtg	gcc	tca	gtt	cct	gat	cga	cac	gaa	cct	ggc	act	ggc	gaa	gtc	739	
Gln	Val	Ala	Ser	Val	Pro	Asp	Arg	His	Glu	Pro	Gly	Thr	Gly	Glu	Val		
		200					205					210					
aat	gcg	gcg	tat	atc	ttc	caa	ctc	cta	agc	gaa	ctg	gga	tat	gac	ggc	787	
Asn	Ala	Ala	Tyr	Ile	Phe	Gln	Leu	Leu	Ser	Glu	Leu	Gly	Tyr	Asp	Gly		
	215					220					225						
gtc	atc	gct	ggc	gaa	tac	cac	cct	gct	ggc	gaa	act	aca	gcc	ggc	ttg	835	
Val	Ile	Ala	Gly	Glu	Tyr	His	Pro	Ala	Gly	Glu	Thr	Thr	Ala	Gly	Leu		
	230				235				240						245		
ggc	tgg	ttg	gag	ctc	tagatcgtaa	gtggtgtcgt	acc									873	
Gly	Trp	Leu	Glu	Leu													

250

<210> 598

<211> 250

<212> PRT

<213> Corynebacterium glutamicum

<400> 598

Leu Ser Arg Phe Ala Ala Asn Leu Ser Leu Thr Phe Thr Glu Leu Asp
 1 5 10 15

Phe Leu Asp Arg Phe Asp Ala Ala Ser Lys His Ala Phe Ser Ala Val
 20 25 30

Glu Phe Gln Tyr Pro Tyr Asp Phe Asp Val Gln Glu Ile Lys Gln Arg
 35 40 45

Ala Asp Ser Ala Gly Leu Pro Ile Glu Leu Phe Asn Ala Pro Pro Gly
 50 55 60

Asp Thr Phe Gly Leu Ala Ala Leu Ala Ser Pro Glu Asp Phe Gln Gln
 65 70 75 80

Ser Ile Glu Gln Ala Ile Thr Tyr Ala Thr Val Leu Lys Pro Lys Lys
 85 90 95

Met His Val Met Ala Gly Ile Ala Asp Val Thr Ser Glu Thr Thr Ala
 100 105 110

Arg Tyr Val Glu Asn Ile Arg Trp Ala Ala Gln Gln Leu Asp Lys Leu
 115 120 125

Asp Val Val Val Val Ile Glu Pro Ile Asn His Tyr Ser Val Pro Gly
 130 135 140

Tyr Phe Leu His Thr Leu Glu Gln Ala Tyr Trp Leu Ile Asp Ser Ile
 145 150 155 160

Ala His Pro Asn Val Lys Ile Leu Phe Asp Thr Phe His Leu Gln Gln
 165 170 175

Ile His Gly Asn Leu Thr Arg Arg Leu Arg Glu Val His Gly Ala Gly
 180 185 190

Leu Leu Gly His Val Gln Val Ala Ser Val Pro Asp Arg His Glu Pro
 195 200 205

Gly Thr Gly Glu Val Asn Ala Ala Tyr Ile Phe Gln Leu Leu Ser Glu
 210 215 220

Leu Gly Tyr Asp Gly Val Ile Ala Gly Glu Tyr His Pro Ala Gly Glu
 225 230 235 240

Thr Thr Ala Gly Leu Gly Trp Leu Glu Leu
 245 250

<210> 599

<211> 897

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(874)

<223> RXA01886

<400> 599

```

gcgaagctgc acgcaccgca ctactcatcg cactcggcgc catccgaagc gtagaaaccg 60
gogcaaccat caaccttgct gaaagcatcg aggtttaacc atg act ttt aaa ctc 115
                                         Met Thr Phe Lys Leu
                                         1                               5

gca gca tgc gca gag atg atc tac cag gac ctg cct ttc gag gag agg 163
Ala Ala Cys Ala Glu Met Ile Tyr Gln Asp Leu Pro Phe Glu Glu Arg
                        10                        15                        20

gtc aag acg atc tct gat cag gga ttc ctc gtg gaa att tgg gac tgg 211
Val Lys Thr Ile Ser Asp Gln Gly Phe Leu Val Glu Ile Trp Asp Trp
                        25                        30                        35

tcc aca aaa gac atc gat gcg ctc gtg gca aca ggc gcg gaa ttt tcc 259
Ser Thr Lys Asp Ile Asp Ala Leu Val Ala Thr Gly Ala Glu Phe Ser
                        40                        45                        50

tcc atg acg ggc tac ctg cgc ggg gat ctg att act gaa cag ggc cgc 307
Ser Met Thr Gly Tyr Leu Arg Gly Asp Leu Ile Thr Glu Gln Gly Arg
                        55                        60                        65

gcg gag ctc ttg gca acc gct tcg gag tcc ttg gcg gtg gcg gaa aag 355
Ala Glu Leu Leu Ala Thr Ala Ser Glu Ser Leu Ala Val Ala Glu Lys
70                        75                        80                        85

ctc aac tgc ccc cgg ctg aat ctg cat gga act ggc ctt gga ccg cag 403
Leu Asn Cys Pro Arg Leu Asn Leu His Gly Thr Gly Leu Gly Pro Gln
                        90                        95                        100

gga cta cct gtt act ccc att gaa gtg gtt acc cca gaa atg tgg ctc 451
Gly Leu Pro Val Thr Pro Ile Glu Val Val Thr Pro Glu Met Trp Leu
                        105                        110                        115

tac gct gct gaa acg ctc cgc cag atc gct gag ctg ggg gag cgc gca 499
Tyr Ala Ala Glu Thr Leu Arg Gln Ile Ala Glu Leu Gly Glu Arg Ala
                        120                        125                        130

ggc aag gtt ttc gtg ctg gaa aac ctc aac ctc gca gtc gat cac ccc 547
Gly Lys Val Phe Val Leu Glu Asn Leu Asn Leu Ala Val Asp His Pro
                        135                        140                        145

ggc act cct ttt gcc aag gcc act gac act ttg gcg ctg gtc aag gct 595
Gly Thr Pro Phe Ala Lys Ala Thr Asp Thr Leu Ala Leu Val Lys Ala
150                        155                        160                        165

gtc aat cac ccg aat ctg cgc ctc aac ctg gat ttg tac cac gcc cag 643
Val Asn His Pro Asn Leu Arg Leu Asn Leu Asp Leu Tyr His Ala Gln
                        170                        175                        180

att ggc gaa gga aac ctc att gag ctg ctc cgt gag gcg cag cca ttc 691
Ile Gly Glu Gly Asn Leu Ile Glu Leu Leu Arg Glu Ala Gln Pro Phe
                        185                        190                        195

```

atc ggc gaa atc cag gtt gcc gat gtc ccc ggc cgc atg gaa ccc ggc 739
 Ile Gly Glu Ile Gln Val Ala Asp Val Pro Gly Arg Met Glu Pro Gly
 200 205 210

acc ggc gag atc aac tac cag ggc gtc gcg aaa gct ctc gcc gcg atg 787
 Thr Gly Glu Ile Asn Tyr Gln Gly Val Ala Lys Ala Leu Ala Ala Met
 215 220 225

ggc tac gac ggc gtc atc ggc atg gag gcg tgg gca tcg ggc gac tcc 835
 Gly Tyr Asp Gly Val Ile Gly Met Glu Ala Trp Ala Ser Gly Asp Ser
 230 235 240 245

agc gac gcg ctg cag gcg ttg aag tca gcg ttc acg gtc taaattgctt 884
 Ser Asp Ala Leu Gln Ala Leu Lys Ser Ala Phe Thr Val
 250 255

atcgacgcac ccc 897

<210> 600

<211> 258

<212> PRT

<213> Corynebacterium glutamicum

<400> 600

Met Thr Phe Lys Leu Ala Ala Cys Ala Glu Met Ile Tyr Gln Asp Leu
 1 5 10 15

Pro Phe Glu Glu Arg Val Lys Thr Ile Ser Asp Gln Gly Phe Leu Val
 20 25 30

Glu Ile Trp Asp Trp Ser Thr Lys Asp Ile Asp Ala Leu Val Ala Thr
 35 40 45

Gly Ala Glu Phe Ser Ser Met Thr Gly Tyr Leu Arg Gly Asp Leu Ile
 50 55 60

Thr Glu Gln Gly Arg Ala Glu Leu Leu Ala Thr Ala Ser Glu Ser Leu
 65 70 75 80

Ala Val Ala Glu Lys Leu Asn Cys Pro Arg Leu Asn Leu His Gly Thr
 85 90 95

Gly Leu Gly Pro Gln Gly Leu Pro Val Thr Pro Ile Glu Val Val Thr
 100 105 110

Pro Glu Met Trp Leu Tyr Ala Ala Glu Thr Leu Arg Gln Ile Ala Glu
 115 120 125

Leu Gly Glu Arg Ala Gly Lys Val Phe Val Leu Glu Asn Leu Asn Leu
 130 135 140

Ala Val Asp His Pro Gly Thr Pro Phe Ala Lys Ala Thr Asp Thr Leu
 145 150 155 160

Ala Leu Val Lys Ala Val Asn His Pro Asn Leu Arg Leu Asn Leu Asp
 165 170 175

Leu Tyr His Ala Gln Ile Gly Glu Gly Asn Leu Ile Glu Leu Leu Arg
 180 185 190

Glu Ala Gln Pro Phe Ile Gly Glu Ile Gln Val Ala Asp Val Pro Gly
 195 200 205

Arg Met Glu Pro Gly Thr Gly Glu Ile Asn Tyr Gln Gly Val Ala Lys
 210 215 220

Ala Leu Ala Ala Met Gly Tyr Asp Gly Val Ile Gly Met Glu Ala Trp
 225 230 235 240

Ala Ser Gly Asp Ser Ser Asp Ala Leu Gln Ala Leu Lys Ser Ala Phe
 245 250 255

Thr Val

<210> 601
 <211> 1575
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (41)..(1552)
 <223> RXN03117

<400> 601
 tgtgcaacat tagttcgtta agaagagtca cattccagcc atg att acc cac gaa 55
 Met Ile Thr His Glu
 1 5

gtg cgc acc cac cgt tct gcg gaa gag ttc ccg tac aag aag cac ctg 103
 Val Arg Thr His Arg Ser Ala Glu Glu Phe Pro Tyr Lys Lys His Leu
 10 15 20

gct cac aag atg gct cgc gtt gca gcc gac cca gtt gag gtt gct gcg 151
 Ala His Lys Met Ala Arg Val Ala Ala Asp Pro Val Glu Val Ala Ala
 25 30 35

gac act cag gaa atg atc atc acc cgc atc atc gac aat gca tcg gtg 199
 Asp Thr Gln Glu Met Ile Ile Thr Arg Ile Ile Asp Asn Ala Ser Val
 40 45 50

cag gca gct tcc gtg ttg cgt cga cca gtt agc tct gcc cgt gcg atg 247
 Gln Ala Ala Ser Val Leu Arg Arg Pro Val Ser Ser Ala Arg Ala Met
 55 60 65

gca cag gtc agg cca gtt acc gat ggt cgg ggt gca tct gtt ttc ggt 295
 Ala Gln Val Arg Pro Val Thr Asp Gly Arg Gly Ala Ser Val Phe Gly
 70 75 80 85

ctg cca gga cgt tat gcc gcg gaa tgg gct gcg ctt gct aac ggc act 343
 Leu Pro Gly Arg Tyr Ala Ala Glu Trp Ala Ala Leu Ala Asn Gly Thr
 90 95 100

gcg gtg cgt gag ctt gat ttc cat gac acg ttc ctc gct gcg gaa tac 391
 Ala Val Arg Glu Leu Asp Phe His Asp Thr Phe Leu Ala Ala Glu Tyr
 105 110 115

tcc cac cca gga gat aac att cct ccg att ttg gct gca gca cag cag 439

Ser His Pro Gly Asp Asn Ile Pro Pro Ile Leu Ala Ala Ala Gln Gln	
120 125 130	
gct gga aaa ggt ggc aag gat ctg atc cgt ggc atc gct act ggg tat	487
Ala Gly Lys Gly Gly Lys Asp Leu Ile Arg Gly Ile Ala Thr Gly Tyr	
135 140 145	
gag att cag gtt aac ttg gtg cgt gga atg tgc ctg cat gag cac aag	535
Glu Ile Gln Val Asn Leu Val Arg Gly Met Cys Leu His Glu His Lys	
150 155 160 165	
att gat cac gtt gct cat ctt gga cca tca gcg gct gct ggt atc gga	583
Ile Asp His Val Ala His Leu Gly Pro Ser Ala Ala Ala Gly Ile Gly	
170 175 180	
acc ttg cta gac cta gat gtg gac acc atc tac cag gca att ggt cag	631
Thr Leu Leu Asp Leu Asp Val Asp Thr Ile Tyr Gln Ala Ile Gly Gln	
185 190 195	
gca ttg cac acc acc acg gcg acg agg cag tcc cgt aaa ggt gcg att	679
Ala Leu His Thr Thr Thr Ala Thr Arg Gln Ser Arg Lys Gly Ala Ile	
200 205 210	
tct tca tgg aag gca ttt gct cct gcg ttt gcg ggc aag atg tcc atc	727
Ser Ser Trp Lys Ala Phe Ala Pro Ala Phe Ala Gly Lys Met Ser Ile	
215 220 225	
gag gca gta gat cgc gca atg cgt ggc gag ggc gca ccg tca cca atc	775
Glu Ala Val Asp Arg Ala Met Arg Gly Glu Gly Ala Pro Ser Pro Ile	
230 235 240 245	
tgg gaa ggc gaa gac ggc gta atc gcg tgg ctg ctg tcc ggt ctt gat	823
Trp Glu Gly Glu Asp Gly Val Ile Ala Trp Leu Leu Ser Gly Leu Asp	
250 255 260	
cac atc tac acc att cct ttg cct gca gaa ggt gaa gcc aaa cga gca	871
His Ile Tyr Thr Ile Pro Leu Pro Ala Glu Gly Glu Ala Lys Arg Ala	
265 270 275	
atc ttg gat acc tac acc aag gaa cac tcg gcg gaa tac cag tca cag	919
Ile Leu Asp Thr Tyr Thr Lys Glu His Ser Ala Glu Tyr Gln Ser Gln	
280 285 290	
gca ccg atc gac ttg gcg cgc agc atg ggg gag aag ctg gca gca cag	967
Ala Pro Ile Asp Leu Ala Arg Ser Met Gly Glu Lys Leu Ala Ala Gln	
295 300 305	
ggc ttg gac ctg cgt gat gtg gac tcc atc gtt ttg cac acc tcc cac	1015
Gly Leu Asp Leu Arg Asp Val Asp Ser Ile Val Leu His Thr Ser His	
310 315 320 325	
cac act cac tac gtg atc ggc acc gga tct aat gat cca cag aag ttc	1063
His Thr His Tyr Val Ile Gly Thr Gly Ser Asn Asp Pro Gln Lys Phe	
330 335 340	
gat cca gat gca tcg cga gaa acc ctt gat cac tcc atc atg tac att	1111
Asp Pro Asp Ala Ser Arg Glu Thr Leu Asp His Ser Ile Met Tyr Ile	
345 350 355	
ttc gct gtc gcg ctg aag gat cgc gcg tgg cac cac gag cgt tcc tat	1159
Phe Ala Val Ala Leu Lys Asp Arg Ala Trp His His Glu Arg Ser Tyr	

360	365	370	
gct cct gag cga gcc cac cgc cga gag acc atc gag ctg tgg aac aag Ala Pro Glu Arg Ala His Arg Arg Glu Thr Ile Glu Leu Trp Asn Lys 375 380 385			1207
att tcc acg gtg gag gat cct gaa tgg acc agg cgt tac cac tcc gtt Ile Ser Thr Val Glu Asp Pro Glu Trp Thr Arg Arg Tyr His Ser Val 390 395 400 405			1255
gat cct gca gaa aag gcc ttc ggc gca cgc gca gtg atc acc ttc aag Asp Pro Ala Glu Lys Ala Phe Gly Ala Arg Ala Val Ile Thr Phe Lys 410 415 420			1303
gat gga acc gtc gtg gaa gat gaa ctg gct gtg gcg aat gcg cat cct Asp Gly Thr Val Val Glu Asp Glu Leu Ala Val Ala Asn Ala His Pro 425 430 435			1351
ctg gga gca cgg cct ttc gct agg gag cag tac att cag aaa ttc cgc Leu Gly Ala Arg Pro Phe Ala Arg Glu Gln Tyr Ile Gln Lys Phe Arg 440 445 450			1399
acc ttg gct gaa ggt gtt gtg tcc gaa aag gaa cag gat cgc ttc ttg Thr Leu Ala Glu Gly Val Val Ser Glu Lys Glu Gln Asp Arg Phe Leu 455 460 465			1447
gat gcg gca cag cgt acg cac gag ctt gag gat ctt tca gaa ctc aac Asp Ala Ala Gln Arg Thr His Glu Leu Glu Asp Leu Ser Glu Leu Asn 470 475 480 485			1495
att gaa ttg gat gcc gat att ttg gcc aag gct cct gtg att ccg gaa Ile Glu Leu Asp Ala Asp Ile Leu Ala Lys Ala Pro Val Ile Pro Glu 490 495 500			1543
gga ctg ttc tgatggcggg tttgttttcc tct Gly Leu Phe			1575

<210> 602

<211> 504

<212> PRT

<213> Corynebacterium glutamicum

<400> 602

Met Ile Thr His Glu Val Arg Thr His Arg Ser Ala Glu Glu Phe Pro 1 5 10 15
Tyr Lys Lys His Leu Ala His Lys Met Ala Arg Val Ala Ala Asp Pro 20 25 30
Val Glu Val Ala Ala Asp Thr Gln Glu Met Ile Ile Thr Arg Ile Ile 35 40 45
Asp Asn Ala Ser Val Gln Ala Ala Ser Val Leu Arg Arg Pro Val Ser 50 55 60
Ser Ala Arg Ala Met Ala Gln Val Arg Pro Val Thr Asp Gly Arg Gly 65 70 75 80
Ala Ser Val Phe Gly Leu Pro Gly Arg Tyr Ala Ala Glu Trp Ala Ala

Val Ile Thr Phe Lys Asp Gly Thr Val Val Glu Asp Glu Leu Ala Val
 420 425 430

Ala Asn Ala His Pro Leu Gly Ala Arg Pro Phe Ala Arg Glu Gln Tyr
 435 440 445

Ile Gln Lys Phe Arg Thr Leu Ala Glu Gly Val Val Ser Glu Lys Glu
 450 455 460

Gln Asp Arg Phe Leu Asp Ala Ala Gln Arg Thr His Glu Leu Glu Asp
 465 470 475 480

Leu Ser Glu Leu Asn Ile Glu Leu Asp Ala Asp Ile Leu Ala Lys Ala
 485 490 495

Pro Val Ile Pro Glu Gly Leu Phe
 500

<210> 603
 <211> 975
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(975)
 <223> FRXA00406

<400> 603
 gac cca gtt gag gtt gct gcg gac act cag gaa atg atc atc acc cgc 48
 Asp Pro Val Glu Val Ala Ala Asp Thr Gln Glu Met Ile Ile Thr Arg
 1 5 10 15

atc atc gac aat gca tcg gtg cag gca gct tcc gtg ttg cgt cga cca 96
 Ile Ile Asp Asn Ala Ser Val Gln Ala Ala Ser Val Leu Arg Arg Pro
 20 25 30

gtt agc tct gcc cgt gcg atg gca cag gtc agg cca gtt acc gat ggt 144
 Val Ser Ser Ala Arg Ala Met Ala Gln Val Arg Pro Val Thr Asp Gly
 35 40 45

cgg ggt gca tct gtt ttc ggt ctg cca gga cgt tat gcc gcg gaa tgg 192
 Arg Gly Ala Ser Val Phe Gly Leu Pro Gly Arg Tyr Ala Ala Glu Trp
 50 55 60

gct gcg ctt gct aac ggc act gcg gtg cgt gag ctt gat ttc cat gac 240
 Ala Ala Leu Ala Asn Gly Thr Ala Val Arg Glu Leu Asp Phe His Asp
 65 70 75 80

acg ttc ctc gct gcg gaa tac tcc cac cca gga gat aac att cct ccg 288
 Thr Phe Leu Ala Ala Glu Tyr Ser His Pro Gly Asp Asn Ile Pro Pro
 85 90 95

att ttg gct gca gca cag cag gct gga aaa ggt ggc aag gat ctg atc 336
 Ile Leu Ala Ala Ala Gln Gln Ala Gly Lys Gly Gly Lys Asp Leu Ile
 100 105 110

cgt ggc atc gct act ggg tat gag att cag gtt aac ttg gtg cgt gga 384
 Arg Gly Ile Ala Thr Gly Tyr Glu Ile Gln Val Asn Leu Val Arg Gly

115	120	125	
atg tgc ctg cat gag cac aag att gat cac gtt gct cat ctt gga cca			432
Met Cys Leu His Glu His Lys Ile Asp His Val Ala His Leu Gly Pro			
130	135	140	
tca gcg gct gct ggt atc gga acc ttg cta gac cta gat gtg gac acc			480
Ser Ala Ala Ala Gly Ile Gly Thr Leu Leu Asp Leu Asp Val Asp Thr			
145	150	155	160
atc tac cag gca att ggt cag gca ttg cac acc acc acg gcg acg agg			528
Ile Tyr Gln Ala Ile Gly Gln Ala Leu His Thr Thr Thr Ala Thr Arg			
	165	170	175
cag tcc cgt aaa ggt gcg att tct tca tgg aag gca ttt gct cct gcg			576
Gln Ser Arg Lys Gly Ala Ile Ser Ser Trp Lys Ala Phe Ala Pro Ala			
	180	185	190
ttt gcg ggc aag atg tcc atc gag gca gta gat cgc gca atg cgt ggc			624
Phe Ala Gly Lys Met Ser Ile Glu Ala Val Asp Arg Ala Met Arg Gly			
	195	200	205
gag ggc gca ccg tca cca atc tgg gaa ggc gaa gac ggc gta atc gcg			672
Glu Gly Ala Pro Ser Pro Ile Trp Glu Gly Glu Asp Gly Val Ile Ala			
	210	215	220
tgg ctg ctg tcc ggt ctt gat cac atc tac acc att cct ttg cct gca			720
Trp Leu Leu Ser Gly Leu Asp His Ile Tyr Thr Ile Pro Leu Pro Ala			
	225	230	235
gaa ggt gaa gcc aaa cga gca atc ttg gat acc tac acc aag gaa cac			768
Glu Gly Glu Ala Lys Arg Ala Ile Leu Asp Thr Tyr Thr Lys Glu His			
	245	250	255
tcg gcg gaa tac cag tca cag gca ccg atc gac ttg gcg cgc agc atg			816
Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile Asp Leu Ala Arg Ser Met			
	260	265	270
ggg gag aag ctg gca gca cag ggc ttg gac ctg cgt gat gtg gac tcc			864
Gly Glu Lys Leu Ala Ala Gln Gly Leu Asp Leu Arg Asp Val Asp Ser			
	275	280	285
atc gtt ttg cac acc tcc cac cac act cac tac gtg atc ggc acc gga			912
Ile Val Leu His Thr Ser His His Thr His Tyr Val Ile Gly Thr Gly			
	290	295	300
tct aat gat cca cag aag ttc gat cca gat gca tcg cga gaa acc ctt			960
Ser Asn Asp Pro Gln Lys Phe Asp Pro Asp Ala Ser Arg Glu Thr Leu			
	305	310	315
gat cac tcc atc atg			975
Asp His Ser Ile Met			
	325		

<210> 604

<211> 325

<212> PRT

<213> Corynebacterium glutamicum

<400> 604

Asp Pro Val Glu Val Ala Ala Asp Thr Gln Glu Met Ile Ile Thr Arg
 1 5 10 15
 Ile Ile Asp Asn Ala Ser Val Gln Ala Ala Ser Val Leu Arg Arg Pro
 20 25 30
 Val Ser Ser Ala Arg Ala Met Ala Gln Val Arg Pro Val Thr Asp Gly
 35 40 45
 Arg Gly Ala Ser Val Phe Gly Leu Pro Gly Arg Tyr Ala Ala Glu Trp
 50 55 60
 Ala Ala Leu Ala Asn Gly Thr Ala Val Arg Glu Leu Asp Phe His Asp
 65 70 75 80
 Thr Phe Leu Ala Ala Glu Tyr Ser His Pro Gly Asp Asn Ile Pro Pro
 85 90 95
 Ile Leu Ala Ala Ala Gln Gln Ala Gly Lys Gly Gly Lys Asp Leu Ile
 100 105 110
 Arg Gly Ile Ala Thr Gly Tyr Glu Ile Gln Val Asn Leu Val Arg Gly
 115 120 125
 Met Cys Leu His Glu His Lys Ile Asp His Val Ala His Leu Gly Pro
 130 135 140
 Ser Ala Ala Ala Gly Ile Gly Thr Leu Leu Asp Leu Asp Val Asp Thr
 145 150 155 160
 Ile Tyr Gln Ala Ile Gly Gln Ala Leu His Thr Thr Thr Ala Thr Arg
 165 170 175
 Gln Ser Arg Lys Gly Ala Ile Ser Ser Trp Lys Ala Phe Ala Pro Ala
 180 185 190
 Phe Ala Gly Lys Met Ser Ile Glu Ala Val Asp Arg Ala Met Arg Gly
 195 200 205
 Glu Gly Ala Pro Ser Pro Ile Trp Glu Gly Glu Asp Gly Val Ile Ala
 210 215 220
 Trp Leu Leu Ser Gly Leu Asp His Ile Tyr Thr Ile Pro Leu Pro Ala
 225 230 235 240
 Glu Gly Glu Ala Lys Arg Ala Ile Leu Asp Thr Tyr Thr Lys Glu His
 245 250 255
 Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile Asp Leu Ala Arg Ser Met
 260 265 270
 Gly Glu Lys Leu Ala Ala Gln Gly Leu Asp Leu Arg Asp Val Asp Ser
 275 280 285
 Ile Val Leu His Thr Ser His His Thr His Tyr Val Ile Gly Thr Gly
 290 295 300
 Ser Asn Asp Pro Gln Lys Phe Asp Pro Asp Ala Ser Arg Glu Thr Leu
 305 310 315 320
 Asp His Ser Ile Met

325

<210> 605
 <211> 431
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(408)
 <223> FRXA00514

<400> 605
 cac gag cgt tcc tat gct cct gag cga gcc ctc cgc cga gag acc atc 48
 His Glu Arg Ser Tyr Ala Pro Glu Arg Ala Leu Arg Arg Glu Thr Ile
 1 5 10 15
 gag ctg tgg aac aag att tcc acg gtg gag gat cct gaa tgg acc agg 96
 Glu Leu Trp Asn Lys Ile Ser Thr Val Glu Asp Pro Glu Trp Thr Arg
 20 25 30
 cgt tac cac tcc gtt gat cct gca gaa aag gcc ttc ggc gca cgc gca 144
 Arg Tyr His Ser Val Asp Pro Ala Glu Lys Ala Phe Gly Ala Arg Ala
 35 40 45
 gtg atc acc ttc aag gat gga acc gtc gtg gaa gat gaa ctg gct gtg 192
 Val Ile Thr Phe Lys Asp Gly Thr Val Val Glu Asp Glu Leu Ala Val
 50 55 60
 gcg aat gcg cat cct ctg gga gca cgg cct ttc gct agg gag cag tac 240
 Ala Asn Ala His Pro Leu Gly Ala Arg Pro Phe Ala Arg Glu Gln Tyr
 65 70 75 80
 att cag aaa ttc cgc acc ttg gct gaa ggt gtt gtg tcc gaa aag gaa 288
 Ile Gln Lys Phe Arg Thr Leu Ala Glu Gly Val Val Ser Glu Lys Glu
 85 90 95
 cag gat cgc ttc ttg gat gcg gca cag cgt acg cac gag ctt gag gat 336
 Gln Asp Arg Phe Leu Asp Ala Ala Gln Arg Thr His Glu Leu Glu Asp
 100 105 110
 ctt tca gaa ctc aac att gaa ttg gat gcc gat att ttg gcc aag gct 384
 Leu Ser Glu Leu Asn Ile Glu Leu Asp Ala Asp Ile Leu Ala Lys Ala
 115 120 125
 cct gtg att ccg gaa gga ctg ttc tgatggcggg tttgttttcc tct 431
 Pro Val Ile Pro Glu Gly Leu Phe
 130 135

<210> 606
 <211> 136
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 606
 His Glu Arg Ser Tyr Ala Pro Glu Arg Ala Leu Arg Arg Glu Thr Ile
 1 5 10 15
 Glu Leu Trp Asn Lys Ile Ser Thr Val Glu Asp Pro Glu Trp Thr Arg

20 25 30
 Arg Tyr His Ser Val Asp Pro Ala Glu Lys Ala Phe Gly Ala Arg Ala
 35 40 45
 Val Ile Thr Phe Lys Asp Gly Thr Val Val Glu Asp Glu Leu Ala Val
 50 55 60
 Ala Asn Ala His Pro Leu Gly Ala Arg Pro Phe Ala Arg Glu Gln Tyr
 65 70 75 80
 Ile Gln Lys Phe Arg Thr Leu Ala Glu Gly Val Val Ser Glu Lys Glu
 85 90 95
 Gln Asp Arg Phe Leu Asp Ala Ala Gln Arg Thr His Glu Leu Glu Asp
 100 105 110
 Leu Ser Glu Leu Asn Ile Glu Leu Asp Ala Asp Ile Leu Ala Lys Ala
 115 120 125
 Pro Val Ile Pro Glu Gly Leu Phe
 130 135

<210> 607
 <211> 718
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(718)
 <223> RXA00512

<400> 607
 tacaacgagt acaacgcttt cgaccagcaa gtattcacct attccgctga cagctacaag 60
 cccatcttct aaccgccta tatataagga gtgaatcacc atg tcc agc gcc aca 115
 Met Ser Ser Ala Thr
 1 5
 acc act gat gtt cgc aaa ggg ctc tac gga gtc atc gcc gat tac acg 163
 Thr Thr Asp Val Arg Lys Gly Leu Tyr Gly Val Ile Ala Asp Tyr Thr
 10 15 20
 gcc gtt tcc aaa gtc atg cca gag acc aat tca ctg acc tac cgt ggc 211
 Ala Val Ser Lys Val Met Pro Glu Thr Asn Ser Leu Thr Tyr Arg Gly
 25 30 35
 tac gcg gtg gaa gat ttg gtg gaa aac tgc agc ttc gag gag gtg ttt 259
 Tyr Ala Val Glu Asp Leu Val Glu Asn Cys Ser Phe Glu Glu Val Phe
 40 45 50
 tac ctc ctg tgg cac ggc gag ctg ccc act gcg caa caa ctt gcg gag 307
 Tyr Leu Leu Trp His Gly Glu Leu Pro Thr Ala Gln Gln Leu Ala Glu
 55 60 65
 ttc aat gag cgt ggc cgt tcc tac cgc tcc ctg gat gcc ggt ttg atc 355
 Phe Asn Glu Arg Gly Arg Ser Tyr Arg Ser Leu Asp Ala Gly Leu Ile
 70 75 80 85

tcc ctg atc cac tct ttg ccc aaa gaa gcc cac ccg atg gat gtt atg 403
 Ser Leu Ile His Ser Leu Pro Lys Glu Ala His Pro Met Asp Val Met
 90 95 100

cgc acc gcg gtg tcc tac atg ggc acc aag gat tcc gag tat ttc acc 451
 Arg Thr Ala Val Ser Tyr Met Gly Thr Lys Asp Ser Glu Tyr Phe Thr
 105 110 115

acc gat tct gag cac atc cgc aaa gtt ggc cac acc ttg ttg gcg cag 499
 Thr Asp Ser Glu His Ile Arg Lys Val Gly His Thr Leu Leu Ala Gln
 120 125 130

ctt ccg atg gtg cta gcc atg gat att cgt cgc cgc aag ggc ctc gat 547
 Leu Pro Met Val Leu Ala Met Asp Ile Arg Arg Arg Lys Gly Leu Asp
 135 140 145

atc atc gcc cct gac tcc agc aag tca gtc gcc gaa aac ctg ctg tct 595
 Ile Ile Ala Pro Asp Ser Ser Lys Ser Val Ala Glu Asn Leu Leu Ser
 150 155 160 165

atg gtg ttt ggt act ggc ccg gaa tca cct gca tcc aac cca gct gac 643
 Met Val Phe Gly Thr Gly Pro Glu Ser Pro Ala Ser Asn Pro Ala Asp
 170 175 180

gtc cgc gat ttt gag aaa tca ctg atc ctc tac gcc gag cac tcc ttc 691
 Val Arg Asp Phe Glu Lys Ser Leu Ile Leu Tyr Ala Glu His Ser Phe
 185 190 195

aac gcc tcc acc ttc acc gcc cgc gtg 718
 Asn Ala Ser Thr Phe Thr Ala Arg Val
 200 205

<210> 608

<211> 206

<212> PRT

<213> Corynebacterium glutamicum

<400> 608

Met Ser Ser Ala Thr Thr Thr Asp Val Arg Lys Gly Leu Tyr Gly Val
 1 5 10 15

Ile Ala Asp Tyr Thr Ala Val Ser Lys Val Met Pro Glu Thr Asn Ser
 20 25 30

Leu Thr Tyr Arg Gly Tyr Ala Val Glu Asp Leu Val Glu Asn Cys Ser
 35 40 45

Phe Glu Glu Val Phe Tyr Leu Leu Trp His Gly Glu Leu Pro Thr Ala
 50 55 60

Gln Gln Leu Ala Glu Phe Asn Glu Arg Gly Arg Ser Tyr Arg Ser Leu
 65 70 75 80

Asp Ala Gly Leu Ile Ser Leu Ile His Ser Leu Pro Lys Glu Ala His
 85 90 95

Pro Met Asp Val Met Arg Thr Ala Val Ser Tyr Met Gly Thr Lys Asp
 100 105 110

Ser Glu Tyr Phe Thr Thr Asp Ser Glu His Ile Arg Lys Val Gly His

115	120	125
Thr Leu Leu Ala Gln Leu Pro Met Val Leu Ala Met Asp Ile Arg Arg		
130	135	140
Arg Lys Gly Leu Asp Ile Ile Ala Pro Asp Ser Ser Lys Ser Val Ala		
145	150	155
Glu Asn Leu Leu Ser Met Val Phe Gly Thr Gly Pro Glu Ser Pro Ala		
165	170	175
Ser Asn Pro Ala Asp Val Arg Asp Phe Glu Lys Ser Leu Ile Leu Tyr		
180	185	190
Ala Glu His Ser Phe Asn Ala Ser Thr Phe Thr Ala Arg Val		
195	200	205

<210> 609

<211> 320

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(297)

<223> RXA00518

<400> 609

gtc ctt ccg gta tta gct gcc cgc cac gac ggc gaa aag tgg gtt gcc	48
Val Leu Pro Val Leu Ala Ala Arg His Asp Gly Glu Lys Trp Val Ala	
1 5 10 15	
atg tat gaa aac atg cgc gac gcc atg gac gcc cgc acc ggc atc aag	96
Met Tyr Glu Asn Met Arg Asp Ala Met Asp Ala Arg Thr Gly Ile Lys	
20 25 30	
ccg aat ctc gat ttc cct gct ggc cct gcc tac cac ctg ctc ggt ttc	144
Pro Asn Leu Asp Phe Pro Ala Gly Pro Ala Tyr His Leu Leu Gly Phe	
35 40 45	
ccg gtc gat ttc ttc acc ccg ctg ttc gtc atc gcc cgc gtc gcc ggc	192
Pro Val Asp Phe Phe Thr Pro Leu Phe Val Ile Ala Arg Val Ala Gly	
50 55 60	
tgg acg gcc cac atc gtg gag cag tac gaa aac aac tcg ctc atc cgc	240
Trp Thr Ala His Ile Val Glu Gln Tyr Glu Asn Asn Ser Leu Ile Arg	
65 70 75 80	
cca ctg tcc gag tac aac ggc gag gag cag cgc gag gtc gcg ccc att	288
Pro Leu Ser Glu Tyr Asn Gly Glu Glu Gln Arg Glu Val Ala Pro Ile	
85 90 95	
gaa aag cgc taaaagattt tcgcttttcg acg	320
Glu Lys Arg	

<210> 610

<211> 99

<212> PRT

<213> Corynebacterium glutamicum

<400> 610

Val Leu Pro Val Leu Ala Ala Arg His Asp Gly Glu Lys Trp Val Ala
 1 5 10 15

Met Tyr Glu Asn Met Arg Asp Ala Met Asp Ala Arg Thr Gly Ile Lys
 20 25 30

Pro Asn Leu Asp Phe Pro Ala Gly Pro Ala Tyr His Leu Leu Gly Phe
 35 40 45

Pro Val Asp Phe Phe Thr Pro Leu Phe Val Ile Ala Arg Val Ala Gly
 50 55 60

Trp Thr Ala His Ile Val Glu Gln Tyr Glu Asn Asn Ser Leu Ile Arg
 65 70 75 80

Pro Leu Ser Glu Tyr Asn Gly Glu Glu Gln Arg Glu Val Ala Pro Ile
 85 90 95

Glu Lys Arg

<210> 611

<211> 1494

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1471)

<223> RXA01077

<400> 611

tctatgactt gatccacaat gtgatgcaaa tcattgaccc tcaccccggga ccaagcgctt 60

aatgaaggca agccaaactt aactagtaga taggattgca atg acc gaa tcg caa 115
 Met Thr Glu Ser Gln
 1 5

gat ctc gcc gca ttc gtg gaa gct gcc aaa ctc aat gat gca agc ccc 163
 Asp Leu Ala Ala Phe Val Glu Ala Ala Lys Leu Asn Asp Ala Ser Pro
 10 15 20

gaa gcc gta gag caa ttg aaa atc aga gtg cta gac acc gta ggc gtt 211
 Glu Ala Val Glu Gln Leu Lys Ile Arg Val Leu Asp Thr Val Gly Val
 25 30 35

gcc att ggc gca ctg gat gcc gaa ccg att gtc gcc att cga gga ctc 259
 Ala Ile Gly Ala Leu Asp Ala Glu Pro Ile Val Ala Ile Arg Gly Leu
 40 45 50

ctg gaa gac ctc ggg gga acc gaa cag tca aca ctt att ggt ggt ggc 307
 Leu Glu Asp Leu Gly Gly Thr Glu Gln Ser Thr Leu Ile Gly Gly Gly
 55 60 65

aaa acc agt ccg gaa cgt gca gca ttt ttc aac agc gca tta agc cgc 355
 Lys Thr Ser Pro Glu Arg Ala Ala Phe Phe Asn Ser Ala Leu Ser Arg
 70 75 80 85

tac ctc gac ttc atg gac gcc tac cta gca aag ggc gaa acc aac cac	403
Tyr Leu Asp Phe Met Asp Ala Tyr Leu Ala Lys Gly Glu Thr Asn His	
90 95 100	
ccc tcg gat aac ttc gga gca gtg ctc gct gca gcc gaa agc gtt ggc	451
Pro Ser Asp Asn Phe Gly Ala Val Leu Ala Ala Ala Glu Ser Val Gly	
105 110 115	
gcc tct gga aaa gac ctg ctc acc gca ttc gcc gtg gcc tac cag gta	499
Ala Ser Gly Lys Asp Leu Leu Thr Ala Phe Ala Val Ala Tyr Gln Val	
120 125 130	
cac acc aga ctt tca gat gtc gca cca gtt cgc gcc aaa ggt ttc gat	547
His Thr Arg Leu Ser Asp Val Ala Pro Val Arg Ala Lys Gly Phe Asp	
135 140 145	
cac acc acc caa gga gca ttc gca gcg ggc gca tct gct gcc aag gca	595
His Thr Thr Gln Gly Ala Phe Ala Ala Gly Ala Ser Ala Ala Lys Ala	
150 155 160 165	
ctg ggt ttg cca gct gat caa atc gcc aac gca ctg gcc atc gca gga	643
Leu Gly Leu Pro Ala Asp Gln Ile Ala Asn Ala Leu Ala Ile Ala Gly	
170 175 180	
aca gcc aat gtt gca ctt cgt gtc act cgc act gga aac ttg agc cac	691
Thr Ala Asn Val Ala Leu Arg Val Thr Arg Thr Gly Asn Leu Ser His	
185 190 195	
tgg aaa ggc ctt gcc tac cca cac gtg tcc aaa gaa gga acc tgg gca	739
Trp Lys Gly Leu Ala Tyr Pro His Val Ser Lys Glu Gly Thr Trp Ala	
200 205 210	
gca ctg ctc gca agc cga ggt att acc ggt ccg gaa gaa gtc ttc gaa	787
Ala Leu Leu Ala Ser Arg Gly Ile Thr Gly Pro Glu Glu Val Phe Glu	
215 220 225	
ggc aac aag gga ttc aaa gag tcc gtc tcc gga ccg ttc gag atc gat	835
Gly Asn Lys Gly Phe Lys Glu Ser Val Ser Gly Pro Phe Glu Ile Asp	
230 235 240 245	
tgg tcc aag gaa gac ttg gaa agc gtt aag cgc acc atc atc aag aaa	883
Trp Ser Lys Glu Asp Leu Glu Ser Val Lys Arg Thr Ile Ile Lys Lys	
250 255 260	
cac aac gcg gaa att cac tcg cag tca gcg ctt gat gca gcc caa gaa	931
His Asn Ala Glu Ile His Ser Gln Ser Ala Leu Asp Ala Ala Gln Glu	
265 270 275	
ata cgc gca caa gaa ggc ttc aat gtg gac aac att gaa aag att cac	979
Ile Arg Ala Gln Glu Gly Phe Asn Val Asp Asn Ile Glu Lys Ile His	
280 285 290	
ctg act act ttc gac gtt gcc tac tcc atc att ggc ggc ggc gaa gaa	1027
Leu Thr Thr Phe Asp Val Ala Tyr Ser Ile Ile Gly Gly Gly Glu Glu	
295 300 305	
ggc gac aaa cag ctt att cgc acc aaa gaa gaa gcc gat cac tca ctg	1075
Gly Asp Lys Gln Leu Ile Arg Thr Lys Glu Glu Ala Asp His Ser Leu	
310 315 320 325	

ccg tgg atg ctc gct gta gtt ctg ctg gat ggt cag ctc aat ccc gaa 1123
 Pro Trp Met Leu Ala Val Val Leu Leu Asp Gly Gln Leu Asn Pro Glu
 330 335 340

cag tac gaa cca tca cgc atc gtt gct gat gat gta caa acc ttg atg 1171
 Gln Tyr Glu Pro Ser Arg Ile Val Ala Asp Asp Val Gln Thr Leu Met
 345 350 355

aag aaa atc gaa atc aca ccg tca gat gaa ttc tct gat cgc ttc cct 1219
 Lys Lys Ile Glu Ile Thr Pro Ser Asp Glu Phe Ser Asp Arg Phe Pro
 360 365 370

gac cac atg cca gct gat cta gaa gtc aca cta aac gat ggc tcg gtg 1267
 Asp His Met Pro Ala Asp Leu Glu Val Thr Leu Asn Asp Gly Ser Val
 375 380 385

ttc aaa gct tca caa gat agc tac tta ggc ttc cac gac aat ccc cta 1315
 Phe Lys Ala Ser Gln Asp Ser Tyr Leu Gly Phe His Asp Asn Pro Leu
 390 395 400 405

gat tgg gac aac gcg cgc aag aaa ttc gat gcc ctt gtc aca cca ttc 1363
 Asp Trp Asp Asn Ala Arg Lys Lys Phe Asp Ala Leu Val Thr Pro Phe
 410 415 420

acc ggt gaa gaa cta cgt gaa gaa atc gcc acg atc att cac gag ctc 1411
 Thr Gly Glu Glu Leu Arg Glu Glu Ile Ala Thr Ile Ile His Glu Leu
 425 430 435

gat agc cga cag gtt tct gaa ctc aca gaa gcc ctg gcc aaa gtc tcc 1459
 Asp Ser Arg Gln Val Ser Glu Leu Thr Glu Ala Leu Ala Lys Val Ser
 440 445 450

acc acc cgc agc taaaactttt tgaaaggagc tca 1494
 Thr Thr Arg Ser
 455

<210> 612

<211> 457

<212> PRT

<213> Corynebacterium glutamicum

<400> 612

Met Thr Glu Ser Gln Asp Leu Ala Ala Phe Val Glu Ala Ala Lys Leu
 1 5 10 15

Asn Asp Ala Ser Pro Glu Ala Val Glu Gln Leu Lys Ile Arg Val Leu
 20 25 30

Asp Thr Val Gly Val Ala Ile Gly Ala Leu Asp Ala Glu Pro Ile Val
 35 40 45

Ala Ile Arg Gly Leu Leu Glu Asp Leu Gly Gly Thr Glu Gln Ser Thr
 50 55 60

Leu Ile Gly Gly Gly Lys Thr Ser Pro Glu Arg Ala Ala Phe Phe Asn
 65 70 75 80

Ser Ala Leu Ser Arg Tyr Leu Asp Phe Met Asp Ala Tyr Leu Ala Lys
 85 90 95

Gly Glu Thr Asn His Pro Ser Asp Asn Phe Gly Ala Val Leu Ala Ala
 100 105 110
 Ala Glu Ser Val Gly Ala Ser Gly Lys Asp Leu Leu Thr Ala Phe Ala
 115 120 125
 Val Ala Tyr Gln Val His Thr Arg Leu Ser Asp Val Ala Pro Val Arg
 130 135 140
 Ala Lys Gly Phe Asp His Thr Thr Gln Gly Ala Phe Ala Ala Gly Ala
 145 150 155 160
 Ser Ala Ala Lys Ala Leu Gly Leu Pro Ala Asp Gln Ile Ala Asn Ala
 165 170 175
 Leu Ala Ile Ala Gly Thr Ala Asn Val Ala Leu Arg Val Thr Arg Thr
 180 185 190
 Gly Asn Leu Ser His Trp Lys Gly Leu Ala Tyr Pro His Val Ser Lys
 195 200 205
 Glu Gly Thr Trp Ala Ala Leu Leu Ala Ser Arg Gly Ile Thr Gly Pro
 210 215 220
 Glu Glu Val Phe Glu Gly Asn Lys Gly Phe Lys Glu Ser Val Ser Gly
 225 230 235 240
 Pro Phe Glu Ile Asp Trp Ser Lys Glu Asp Leu Glu Ser Val Lys Arg
 245 250 255
 Thr Ile Ile Lys Lys His Asn Ala Glu Ile His Ser Gln Ser Ala Leu
 260 265 270
 Asp Ala Ala Gln Glu Ile Arg Ala Gln Glu Gly Phe Asn Val Asp Asn
 275 280 285
 Ile Glu Lys Ile His Leu Thr Thr Phe Asp Val Ala Tyr Ser Ile Ile
 290 295 300
 Gly Gly Gly Glu Glu Gly Asp Lys Gln Leu Ile Arg Thr Lys Glu Glu
 305 310 315 320
 Ala Asp His Ser Leu Pro Trp Met Leu Ala Val Val Leu Leu Asp Gly
 325 330 335
 Gln Leu Asn Pro Glu Gln Tyr Glu Pro Ser Arg Ile Val Ala Asp Asp
 340 345 350
 Val Gln Thr Leu Met Lys Lys Ile Glu Ile Thr Pro Ser Asp Glu Phe
 355 360 365
 Ser Asp Arg Phe Pro Asp His Met Pro Ala Asp Leu Glu Val Thr Leu
 370 375 380
 Asn Asp Gly Ser Val Phe Lys Ala Ser Gln Asp Ser Tyr Leu Gly Phe
 385 390 395 400
 His Asp Asn Pro Leu Asp Trp Asp Asn Ala Arg Lys Lys Phe Asp Ala
 405 410 415
 Leu Val Thr Pro Phe Thr Gly Glu Glu Leu Arg Glu Glu Ile Ala Thr

Ile Ile His Glu Leu Asp Ser Arg Gln Val Ser Glu Leu Thr Glu Ala
435 440 445

Leu Ala Lys Val Ser Thr Thr Arg Ser
450 455

```
<210> 613
<211> 923
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (1)..(900)  
<223> RXN03144
```

<400> 613																
acc	acg	acg	gct	acc	agg	cag	tcg	cga	aaa	ggt	gag	att	tcc	agc	tgg	48
Thr	Thr	Thr	Ala	Thr	Arg	Gln	Ser	Arg	Lys	Gly	Glu	Ile	Ser	Ser	Trp	
1				5				10				15				
aag	gcg	ttc	gcg	cca	gcg	ttt	gcg	gga	aag	atg	gcc	att	gag	gcg	atg	96
Lys	Ala	Phe	Ala	Pro	Ala	Phe	Ala	Gly	Lys	Met	Ala	Ile	Glu	Ala	Met	
20				25				30								
gat	cgt	gcg	atg	cgt	ggg	gag	ggt	tcg	ccc	gca	ccg	att	tgg	gag	ggc	144
Asp	Arg	Ala	Met	Arg	Gly	Glu	Gly	Ser	Pro	Ala	Pro	Ile	Trp	Glu	Gly	
35				40				45								
gaa	gac	ggg	gtc	atc	gcg	tgg	ctg	tta	tcg	ggc	aaa	gat	cat	gtt	tat	192
Glu	Asp	Gly	Val	Ile	Ala	Trp	Leu	Leu	Ser	Gly	Lys	Asp	His	Val	Tyr	
50				55				60								
cat	gtg	cca	ttg	ccg	gaa	cac	ggc	gag	ccc	aag	ctg	ggg	att	cta	gag	240
His	Val	Pro	Leu	Pro	Glu	His	Gly	Glu	Pro	Lys	Leu	Gly	Ile	Leu	Glu	
65				70				75				80				
act	tac	aca	aag	gaa	cat	tca	gcg	gaa	tat	caa	tcg	cag	gca	ccg	att	288
Thr	Tyr	Thr	Lys	Glu	His	Ser	Ala	Glu	Tyr	Gln	Ser	Gln	Ala	Pro	Ile	
85				90				95								
gat	ctg	gcg	cgc	agg	atg	aag	cca	ctg	gtt	gac	gcg	gct	ggc	gga	acg	336
Asp	Leu	Ala	Arg	Arg	Met	Lys	Pro	Leu	Val	Asp	Ala	Ala	Gly	Gly	Thr	
100				105				110								
gaa	cac	att	gca	gag	att	gtg	ctg	cgc	acc	agt	cac	cac	acg	cat	tat	384
Glu	His	Ile	Ala	Glu	Ile	Val	Leu	Arg	Thr	Ser	His	His	Thr	His	Tyr	
115				120				125								
gtg	att	ggc	act	ggg	gcg	aac	gat	ccg	cag	aag	atg	gat	ccg	cag	gcc	432
Val	Ile	Gly	Thr	Gly	Ala	Asn	Asp	Pro	Gln	Lys	Met	Asp	Pro	Gln	Ala	
130				135				140								
tcg	cgt	gaa	acc	ctg	gat	cat	tcc	atc	atg	tac	att	ttc	gcc	gtc	gcg	480
Ser	Arg	Glu	Thr	Leu	Asp	His	Ser	Ile	Met	Tyr	Ile	Phe	Ala	Val	Ala	
145				150				155				160				
ctt	caa	gat	ggc	gtg	tgg	cac	cac	gag	ttt	tcc	tac	acc	cgc	aag	cgt	528

Leu Gln Asp Gly Val Trp His His Glu Phe Ser Tyr Thr Arg Lys Arg
 165 170 175
 tcc acc cgc ccg gaa act gtg gag ctg tgg cac aag att cgc acc gtg 576
 Ser Thr Arg Pro Glu Thr Val Glu Leu Trp His Lys Ile Arg Thr Val
 180 185 190
 gag gat cct gaa tgg acg cgc cga tac cat tct gat gat cct gca aaa 624
 Glu Asp Pro Glu Trp Thr Arg Arg Tyr His Ser Asp Asp Pro Ala Lys
 195 200 205
 aag gcc ttt ggt gcg aaa gca gtg atc aca atg gct gat ggc acc gtg 672
 Lys Ala Phe Gly Ala Lys Ala Val Ile Thr Met Ala Asp Gly Thr Val
 210 215 220
 att gag gat gaa ttg gct gtc gcg gat gcc cac ccg ctg ggt gct cgg 720
 Ile Glu Asp Glu Leu Ala Val Ala Asp Ala His Pro Leu Gly Ala Arg
 225 230 235 240
 ccg ttt gcg cgg gag aat tac att gaa aaa ttc cgc aca ctc gcg cag 768
 Pro Phe Ala Arg Glu Asn Tyr Ile Glu Lys Phe Arg Thr Leu Ala Gln
 245 250 255
 ggg att gtc att gat tca gaa cag gaa cgc ttc ttg cat gcc gtg caa 816
 Gly Ile Val Ile Asp Ser Glu Gln Glu Arg Phe Leu His Ala Val Gln
 260 265 270
 agc ctg cct gac ctg gat gat ctt gat cag ctc aac atc gaa gtc gac 864
 Ser Leu Pro Asp Leu Asp Asp Leu Asp Gln Leu Asn Ile Glu Val Asp
 275 280 285
 ata agc aac cag gcc gcg acg aaa gcg ggg ctg tta tgaatctctt 910
 Ile Ser Asn Gln Ala Ala Thr Lys Ala Gly Leu Leu
 290 295 300
 ttcgaatggt gtt 923

<210> 614

<211> 300

<212> PRT

<213> Corynebacterium glutamicum

<400> 614

Thr Thr Thr Ala Thr Arg Gln Ser Arg Lys Gly Glu Ile Ser Ser Trp
 1 5 10 15
 Lys Ala Phe Ala Pro Ala Phe Ala Gly Lys Met Ala Ile Glu Ala Met
 20 25 30
 Asp Arg Ala Met Arg Gly Glu Gly Ser Pro Ala Pro Ile Trp Glu Gly
 35 40 45
 Glu Asp Gly Val Ile Ala Trp Leu Leu Ser Gly Lys Asp His Val Tyr
 50 55 60
 His Val Pro Leu Pro Glu His Gly Glu Pro Lys Leu Gly Ile Leu Glu
 65 70 75 80
 Thr Tyr Thr Lys Glu His Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile
 85 90 95

Asp Leu Ala Arg Arg Met Lys Pro Leu Val Asp Ala Ala Gly Gly Thr
 100 105 110
 Glu His Ile Ala Glu Ile Val Leu Arg Thr Ser His His Thr His Tyr
 115 120 125
 Val Ile Gly Thr Gly Ala Asn Asp Pro Gln Lys Met Asp Pro Gln Ala
 130 135 140
 Ser Arg Glu Thr Leu Asp His Ser Ile Met Tyr Ile Phe Ala Val Ala
 145 150 155 160
 Leu Gln Asp Gly Val Trp His His Glu Phe Ser Tyr Thr Arg Lys Arg
 165 170 175
 Ser Thr Arg Pro Glu Thr Val Glu Leu Trp His Lys Ile Arg Thr Val
 180 185 190
 Glu Asp Pro Glu Trp Thr Arg Arg Tyr His Ser Asp Asp Pro Ala Lys
 195 200 205
 Lys Ala Phe Gly Ala Lys Ala Val Ile Thr Met Ala Asp Gly Thr Val
 210 215 220
 Ile Glu Asp Glu Leu Ala Val Ala Asp Ala His Pro Leu Gly Ala Arg
 225 230 235 240
 Pro Phe Ala Arg Glu Asn Tyr Ile Glu Lys Phe Arg Thr Leu Ala Gln
 245 250 255
 Gly Ile Val Ile Asp Ser Glu Gln Glu Arg Phe Leu His Ala Val Gln
 260 265 270
 Ser Leu Pro Asp Leu Asp Asp Leu Asp Gln Leu Asn Ile Glu Val Asp
 275 280 285
 Ile Ser Asn Gln Ala Ala Thr Lys Ala Gly Leu Leu
 290 295 300

<210> 615
 <211> 511
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(511)
 <223> FRXA02322

<400> 615
 cgcgagagc taaactgcgt gaggttggtg cctgtcacac ataatcggcc taggggtggga 60

ctttaaggaa acagtgcaca aataaatctc aaggagcccc atg cgc atc cac gat 115
 Met Arg Ile His Asp
 1 5

gtt tat acc cac ctt tcg gcc gat aac ttt ccc aaa gca gag cac ctt 163
 Val Tyr Thr His Leu Ser Ala Asp Asn Phe Pro Lys Ala Glu His Leu
 10 15 20

gcg tgg aaa ttc tcc gag ctt gcc acc gac ccc gtg gag gtg aca ccg 211
 Ala Trp Lys Phe Ser Glu Leu Ala Thr Asp Pro Val Glu Val Thr Pro
 25 30 35

gat gtt tcg gag atg atc atc aac cgg atc atc gac aac gcg gcg gtg 259
 Asp Val Ser Glu Met Ile Ile Asn Arg Ile Ile Asp Asn Ala Ala Val
 40 45 50

tct gcc gcg tcg gtg ttg cgc cgg cct gtg act gtg gcc agg caa caa 307
 Ser Ala Ala Ser Val Leu Arg Arg Pro Val Thr Val Ala Arg Gln Gln
 55 60 65

gcg cag tcc cat ccg cgg gaa aag ggc gga aaa gtt ttt gga att tca 355
 Ala Gln Ser His Pro Arg Glu Lys Gly Gly Lys Val Phe Gly Ile Ser
 70 75 80 85

ggc agc tac tca cca gag tgg gct gcc ttt gct aat ggt gtg gcc gta 403
 Gly Ser Tyr Ser Pro Glu Trp Ala Ala Phe Ala Asn Gly Val Ala Val
 90 95 100

cgt gaa ttg gac ttc cac gat aca ttt tta gca gct gaa tac tcc cat 451
 Arg Glu Leu Asp Phe His Asp Thr Phe Leu Ala Ala Glu Tyr Ser His
 105 110 115

ccc ggc gac aat att cca cca ctt ctt gca gta gcg cag gct cag aga 499
 Pro Gly Asp Asn Ile Pro Pro Leu Leu Ala Val Ala Gln Ala Gln Arg
 120 125 130

agc agc ggc agg 511
 Ser Ser Gly Arg
 135

<210> 616

<211> 137

<212> PRT

<213> Corynebacterium glutamicum

<400> 616

Met Arg Ile His Asp Val Tyr Thr His Leu Ser Ala Asp Asn Phe Pro
 1 5 10 15

Lys Ala Glu His Leu Ala Trp Lys Phe Ser Glu Leu Ala Thr Asp Pro
 20 25 30

Val Glu Val Thr Pro Asp Val Ser Glu Met Ile Ile Asn Arg Ile Ile
 35 40 45

Asp Asn Ala Ala Val Ser Ala Ala Ser Val Leu Arg Arg Pro Val Thr
 50 55 60

Val Ala Arg Gln Gln Ala Gln Ser His Pro Arg Glu Lys Gly Gly Lys
 65 70 75 80

Val Phe Gly Ile Ser Gly Ser Tyr Ser Pro Glu Trp Ala Ala Phe Ala
 85 90 95

Asn Gly Val Ala Val Arg Glu Leu Asp Phe His Asp Thr Phe Leu Ala
 100 105 110

Ala Glu Tyr Ser His Pro Gly Asp Asn Ile Pro Pro Leu Leu Ala Val
 115 120 125

Ala Gln Ala Gln Arg Ser Ser Gly Arg
 130 135

<210> 617

<211> 603

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(603)

<223> RXA02329

<400> 617

acg gct acc agg cag tcg cga aaa ggt gag att tcc agc tgg aag gcg 48
 Thr Ala Thr Arg Gln Ser Arg Lys Gly Glu Ile Ser Ser Trp Lys Ala
 1 5 10 15

ttc gcg cca gcg ttt gcg gga aag atg gcc att gag gcg atg gat cgt 96
 Phe Ala Pro Ala Phe Ala Gly Lys Met Ala Ile Glu Ala Met Asp Arg
 20 25 30

gcg atg cgt ggg gag ggt tcg ccc gca ccg att tgg gag ggc gaa gac 144
 Ala Met Arg Gly Glu Gly Ser Pro Ala Pro Ile Trp Glu Gly Glu Asp
 35 40 45

ggg gtc atc gcg tgg ctg tta tcg ggc aaa gat cat gtt tat cat gtg 192
 Gly Val Ile Ala Trp Leu Leu Ser Gly Lys Asp His Val Tyr His Val
 50 55 60

cca ttg ccg gaa cac ggc gag ccc aag ctg ggg att cta gag act tac 240
 Pro Leu Pro Glu His Gly Glu Pro Lys Leu Gly Ile Leu Glu Thr Tyr
 65 70 75 80

aca aag gaa cat tca gcg gaa tat caa tcg cag gca ccg att gat ctg 288
 Thr Lys Glu His Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile Asp Leu
 85 90 95

gcg cgc agg atg aag cca ctg gtt gac gcg gct ggc gga acg gaa cac 336
 Ala Arg Arg Met Lys Pro Leu Val Asp Ala Ala Gly Gly Thr Glu His
 100 105 110

att gca gag att gtg ctg cgc acc agt cac cac acg cat tat gtg att 384
 Ile Ala Glu Ile Val Leu Arg Thr Ser His His Thr His Tyr Val Ile
 115 120 125

ggc act ggg gcg aac gat ccg cag aag atg gat ccg cag gcc tcg cgt 432
 Gly Thr Gly Ala Asn Asp Pro Gln Lys Met Asp Pro Gln Ala Ser Arg
 130 135 140

gaa acc ctg gat cat tcc atc atg tac att ttc gcc gtc gcg ctt caa 480
 Glu Thr Leu Asp His Ser Ile Met Tyr Ile Phe Ala Val Ala Leu Gln
 145 150 155 160

gat ggc gtg tgg cac cac gag ttt tcc tac acc cgc aag cgt tcc acc 528
 Asp Gly Val Trp His His Glu Phe Ser Tyr Thr Arg Lys Arg Ser Thr
 165 170 175

cgc ccg gaa act gtg gag ctg tgg cac aag att cgc acc gtg gag gat 576
 Arg Pro Glu Thr Val Glu Leu Trp His Lys Ile Arg Thr Val Glu Asp
 180 185 190

cct gaa tgg acg cgc cga tac cat tct 603
 Pro Glu Trp Thr Arg Arg Tyr His Ser
 195 200

<210> 618

<211> 201

<212> PRT

<213> Corynebacterium glutamicum

<400> 618

Thr Ala Thr Arg Gln Ser Arg Lys Gly Glu Ile Ser Ser Trp Lys Ala
 1 5 10 15

Phe Ala Pro Ala Phe Ala Gly Lys Met Ala Ile Glu Ala Met Asp Arg
 20 25 30

Ala Met Arg Gly Glu Gly Ser Pro Ala Pro Ile Trp Glu Gly Glu Asp
 35 40 45

Gly Val Ile Ala Trp Leu Leu Ser Gly Lys Asp His Val Tyr His Val
 50 55 60

Pro Leu Pro Glu His Gly Glu Pro Lys Leu Gly Ile Leu Glu Thr Tyr
 65 70 75 80

Thr Lys Glu His Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile Asp Leu
 85 90 95

Ala Arg Arg Met Lys Pro Leu Val Asp Ala Ala Gly Gly Thr Glu His
 100 105 110

Ile Ala Glu Ile Val Leu Arg Thr Ser His His Thr His Tyr Val Ile
 115 120 125

Gly Thr Gly Ala Asn Asp Pro Gln Lys Met Asp Pro Gln Ala Ser Arg
 130 135 140

Glu Thr Leu Asp His Ser Ile Met Tyr Ile Phe Ala Val Ala Leu Gln
 145 150 155 160

Asp Gly Val Trp His His Glu Phe Ser Tyr Thr Arg Lys Arg Ser Thr
 165 170 175

Arg Pro Glu Thr Val Glu Leu Trp His Lys Ile Arg Thr Val Glu Asp
 180 185 190

Pro Glu Trp Thr Arg Arg Tyr His Ser
 195 200

<210> 619

<211> 1266

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1243)

<223> RXA02332

<400> 619

gaccgcatgc aacaccgcag cagattatat gagctcctgc gatacgaaga ctacaacgtc 60

tttgaccagc acattttcac ctacagaaaa ggagaaaaaca atg agt gac agc caa 115
 Met Ser Asp Ser Gln
 1 5

gtc cgc aaa gga ctc aac ggc gtc atc tct gac tac aca agc att tcc 163
 Val Arg Lys Gly Leu Asn Gly Val Ile Ser Asp Tyr Thr Ser Ile Ser
 10 15 20

aaa gtg atg cca gag agc aac tcg ctg act tac cgt ggc tac gcc gtg 211
 Lys Val Met Pro Glu Ser Asn Ser Leu Thr Tyr Arg Gly Tyr Ala Val
 25 30 35

gag gat ttg gtg gaa aac tgc agc ttt gaa gaa gtg atc tac ctc ctg 259
 Glu Asp Leu Val Glu Asn Cys Ser Phe Glu Glu Val Ile Tyr Leu Leu
 40 45 50

tgg ttt ggg gag ctg ccc acc act gaa caa ctc cgg acc ttc aac acg 307
 Trp Phe Gly Glu Leu Pro Thr Thr Glu Gln Leu Arg Thr Phe Asn Thr
 55 60 65

aca ggt cga agc tac cgc tca ctc gac gcc gga ctg att tcc ctc atc 355
 Thr Gly Arg Ser Tyr Arg Ser Leu Asp Ala Gly Leu Ile Ser Leu Ile
 70 75 80 85

cac tcc tta ccc aac acc tgc cac ccc atg gac gtg ctg cgc acc gca 403
 His Ser Leu Pro Asn Thr Cys His Pro Met Asp Val Leu Arg Thr Ala
 90 95 100

gtg tcc tac atg ggt acc ttt gat ccc gat ccg ttt acc cgc gat gcc 451
 Val Ser Tyr Met Gly Thr Phe Asp Pro Asp Pro Phe Thr Arg Asp Ala
 105 110 115

gat cat atc cga agc att gga cac aac ctg ctt gcg cag ctt ccc atg 499
 Asp His Ile Arg Ser Ile Gly His Asn Leu Leu Ala Gln Leu Pro Met
 120 125 130

gtg gtt gcc atg gat atc cgc agg cga agt ggg gaa gag atc atc gca 547
 Val Val Ala Met Asp Ile Arg Arg Arg Ser Gly Glu Glu Ile Ile Ala
 135 140 145

cct gac cac aac aaa ggt atc gct tcg aat ttc tta tcc atg gtg ttt 595
 Pro Asp His Asn Lys Gly Ile Ala Ser Asn Phe Leu Ser Met Val Phe
 150 155 160 165

ggc aat gat gat ggt tct gta gcc aac tcc gca gat gac atc cgc gat 643
 Gly Asn Asp Asp Gly Ser Val Ala Asn Ser Ala Asp Asp Ile Arg Asp
 170 175 180

ttt gaa cgc tcc ctc atc ctc tac gcc gag cac tcc ttc aac gcc tcc 691
 Phe Glu Arg Ser Leu Ile Leu Tyr Ala Glu His Ser Phe Asn Ala Ser
 185 190 195

aca ttc tca gcc cgc gtg atc tca tca acg cga tcc gat acg tat tcg 739

Thr	Phe	Ser	Ala	Arg	Val	Ile	Ser	Ser	Thr	Arg	Ser	Asp	Thr	Tyr	Ser	
		200					205					210				
gcg	atc	aca	ggt	gcg	atc	ggt	gct	ctc	aaa	ggc	cca	ctg	cac	gga	ggt	787
Ala	Ile	Thr	Gly	Ala	Ile	Gly	Ala	Leu	Lys	Gly	Pro	Leu	His	Gly	Gly	
	215					220				225						
gcc	aat	gag	ttt	gtc	atg	cac	acc	atg	ctg	gat	atc	gac	gat	ccc	aac	835
Ala	Asn	Glu	Phe	Val	Met	His	Thr	Met	Leu	Asp	Ile	Asp	Asp	Pro	Asn	
230				235					240					245		
aat	gct	gcc	gac	tgg	atg	ggc	aag	gcg	ttg	gat	cgt	aaa	gaa	cgc	atc	883
Asn	Ala	Ala	Asp	Trp	Met	Gly	Lys	Ala	Leu	Asp	Arg	Lys	Glu	Arg	Ile	
			250					255					260			
atg	gga	ttc	ggg	cac	cgc	gtg	tac	aaa	aac	ggc	gac	tcc	agg	gtc	ccc	931
Met	Gly	Phe	Gly	His	Arg	Val	Tyr	Lys	Asn	Gly	Asp	Ser	Arg	Val	Pro	
	265					270						275				
tcc	atg	gag	aaa	tcc	atg	cgc	tcc	ctt	gct	gct	cgt	cac	cgt	ggt	caa	979
Ser	Met	Glu	Lys	Ser	Met	Arg	Ser	Leu	Ala	Ala	Arg	His	Arg	Gly	Gln	
	280					285						290				
aaa	tgg	gtg	cac	atg	tat	gag	tcg	atg	caa	gaa	gtc	atg	gag	gct	cgc	1027
Lys	Trp	Val	His	Met	Tyr	Glu	Ser	Met	Gln	Glu	Val	Met	Glu	Ala	Arg	
	295					300				305						
act	ggc	att	aaa	ccc	aac	ctc	gac	ttc	ccg	gcc	ggc	cct	gcc	tat	tac	1075
Thr	Gly	Ile	Lys	Pro	Asn	Leu	Asp	Phe	Pro	Ala	Gly	Pro	Ala	Tyr	Tyr	
310				315					320					325		
atg	ctg	gga	ttc	ccc	gtc	gac	ttc	ttc	aca	cca	ctg	ttt	gtg	ctg	gcc	1123
Met	Leu	Gly	Phe	Pro	Val	Asp	Phe	Phe	Thr	Pro	Leu	Phe	Val	Leu	Ala	
			330					335					340			
cga	gtg	tca	ggg	tgg	acg	gca	cac	atc	gtg	gag	caa	ttt	gaa	aac	aat	1171
Arg	Val	Ser	Gly	Trp	Thr	Ala	His	Ile	Val	Glu	Gln	Phe	Glu	Asn	Asn	
		345				350						355				
gcg	ctg	atc	cga	cca	ttg	tct	gcc	tac	aac	gga	gtg	gaa	gaa	agg	gag	1219
Ala	Leu	Ile	Arg	Pro	Leu	Ser	Ala	Tyr	Asn	Gly	Val	Glu	Glu	Arg	Glu	
	360					365				370						
gtg	gtg	ccc	att	tcg	gag	aga	acc	taatcagtga	ggctgatttc	taa						1266
Val	Val	Pro	Ile	Ser	Glu	Arg	Thr									
	375				380											

<210> 620
 <211> 381
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 620
 Met Ser Asp Ser Gln Val Arg Lys Gly Leu Asn Gly Val Ile Ser Asp
 1 5 10 15
 Tyr Thr Ser Ile Ser Lys Val Met Pro Glu Ser Asn Ser Leu Thr Tyr
 20 25 30
 Arg Gly Tyr Ala Val Glu Asp Leu Val Glu Asn Cys Ser Phe Glu Glu

35	40	45
Val Ile Tyr Leu Leu Trp Phe Gly Glu Leu Pro Thr Thr Glu Gln Leu 50 55 60		
Arg Thr Phe Asn Thr Thr Gly Arg Ser Tyr Arg Ser Leu Asp Ala Gly 65 70 75 80		
Leu Ile Ser Leu Ile His Ser Leu Pro Asn Thr Cys His Pro Met Asp 85 90 95		
Val Leu Arg Thr Ala Val Ser Tyr Met Gly Thr Phe Asp Pro Asp Pro 100 105 110		
Phe Thr Arg Asp Ala Asp His Ile Arg Ser Ile Gly His Asn Leu Leu 115 120 125		
Ala Gln Leu Pro Met Val Val Ala Met Asp Ile Arg Arg Arg Ser Gly 130 135 140		
Glu Glu Ile Ile Ala Pro Asp His Asn Lys Gly Ile Ala Ser Asn Phe 145 150 155 160		
Leu Ser Met Val Phe Gly Asn Asp Asp Gly Ser Val Ala Asn Ser Ala 165 170 175		
Asp Asp Ile Arg Asp Phe Glu Arg Ser Leu Ile Leu Tyr Ala Glu His 180 185 190		
Ser Phe Asn Ala Ser Thr Phe Ser Ala Arg Val Ile Ser Ser Thr Arg 195 200 205		
Ser Asp Thr Tyr Ser Ala Ile Thr Gly Ala Ile Gly Ala Leu Lys Gly 210 215 220		
Pro Leu His Gly Gly Ala Asn Glu Phe Val Met His Thr Met Leu Asp 225 230 235 240		
Ile Asp Asp Pro Asn Asn Ala Ala Asp Trp Met Gly Lys Ala Leu Asp 245 250 255		
Arg Lys Glu Arg Ile Met Gly Phe Gly His Arg Val Tyr Lys Asn Gly 260 265 270		
Asp Ser Arg Val Pro Ser Met Glu Lys Ser Met Arg Ser Leu Ala Ala 275 280 285		
Arg His Arg Gly Gln Lys Trp Val His Met Tyr Glu Ser Met Gln Glu 290 295 300		
Val Met Glu Ala Arg Thr Gly Ile Lys Pro Asn Leu Asp Phe Pro Ala 305 310 315 320		
Gly Pro Ala Tyr Tyr Met Leu Gly Phe Pro Val Asp Phe Phe Thr Pro 325 330 335		
Leu Phe Val Leu Ala Arg Val Ser Gly Trp Thr Ala His Ile Val Glu 340 345 350		
Gln Phe Glu Asn Asn Ala Leu Ile Arg Pro Leu Ser Ala Tyr Asn Gly 355 360 365		

Val Glu Glu Arg Glu Val Val Pro Ile Ser Glu Arg Thr
 370 375 380

<210> 621
 <211> 1038
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1015)
 <223> RXN02333

<400> 621
 tcttgcatgc cgtgcaaagc ctgcctgacc tggatgatct tgatcagctc aacatcgaag 60
 tcgacataag caaccaggcc gcgacgaaag cggggctgtt atg aat ctc ttt tcg 115
 Met Asn Leu Phe Ser
 1 5
 aat ggt gtt gat gtg ggg agg cgt cga caa gca ttt aaa gcg gca ctc 163
 Asn Gly Val Asp Val Gly Arg Arg Arg Gln Ala Phe Lys Ala Ala Leu
 10 15 20
 gcc gca ccc cac atc gcc cgg ctg ccc ggc gca ttc tcc cct ctg att 211
 Ala Ala Pro His Ile Ala Arg Leu Pro Gly Ala Phe Ser Pro Leu Ile
 25 30 35
 gcg cgc tcc atc gaa gaa gcc ggc ttc gaa ggc gtc tac gtt tcc ggc 259
 Ala Arg Ser Ile Glu Glu Ala Gly Phe Glu Gly Val Tyr Val Ser Gly
 40 45 50
 gcc gtc ata gct gct gac ctg gca cta ccc gat atc ggc ttg acg acg 307
 Ala Val Ile Ala Ala Asp Leu Ala Leu Pro Asp Ile Gly Leu Thr Thr
 55 60 65
 ctg acc gaa gtc gcc cac cgc gcg cgg caa att gcg cgc gtc aca gac 355
 Leu Thr Glu Val Ala His Arg Ala Arg Gln Ile Ala Arg Val Thr Asp
 70 75 80 85
 cta gga gtg ctt gtc gac gcc gac acc ggc ttt ggc gaa ccc atg tcg 403
 Leu Gly Val Leu Val Asp Ala Asp Thr Gly Phe Gly Glu Pro Met Ser
 90 95 100
 gcc gca cgc acc gtc gcc gaa ttg gag gac gcc ggt gtg gcc gga tgc 451
 Ala Ala Arg Thr Val Ala Glu Leu Glu Asp Ala Gly Val Ala Gly Cys
 105 110 115
 cac ctt gaa gac caa gtc aac ccc aaa cgt tgc ggc cac ttg gac ggc 499
 His Leu Glu Asp Gln Val Asn Pro Lys Arg Cys Gly His Leu Asp Gly
 120 125 130
 aaa gaa gtc gtg cgc aca gac gtg atg gtt cga cgc atc gca gcc gcc 547
 Lys Glu Val Val Arg Thr Asp Val Met Val Arg Arg Ile Ala Ala Ala
 135 140 145
 gtc tcg gcc cgg cgc gac ccg aac ttt gtc atc tgc gcc cgc acc gac 595
 Val Ser Ala Arg Arg Asp Pro Asn Phe Val Ile Cys Ala Arg Thr Asp
 150 155 160 165

gcc gct gga gtg gaa gga atc gac gcc gcc att gag cgc gcg aaa gcc 643
 Ala Ala Gly Val Glu Gly Ile Asp Ala Ala Ile Glu Arg Ala Lys Ala
 170 175 180
 tac tta gat gcg ggc gcc gac atg att ttc acc gaa gcc ctc cac agc 691
 Tyr Leu Asp Ala Gly Ala Asp Met Ile Phe Thr Glu Ala Leu His Ser
 185 190 195
 gaa gcc gac ttc cga tac ttc cgg cac gcc atc cct gat gcc ttg ttg 739
 Glu Ala Asp Phe Arg Tyr Phe Arg His Ala Ile Pro Asp Ala Leu Leu
 200 205 210
 ctg gcg aat atg acc gaa ttt ggc aaa acg acg ctg ctg tca gcc gac 787
 Leu Ala Asn Met Thr Glu Phe Gly Lys Thr Thr Leu Leu Ser Ala Asp
 215 220 225
 gtg ttg gaa gag att ggc tac aac gcc gtg atc tac ccc gtg acc acg 835
 Val Leu Glu Glu Ile Gly Tyr Asn Ala Val Ile Tyr Pro Val Thr Thr
 230 235 240 245
 ctg cgt att gcc atg gga caa gta gaa caa gca cta gcc gaa atc aaa 883
 Leu Arg Ile Ala Met Gly Gln Val Glu Gln Ala Leu Ala Glu Ile Lys
 250 255 260
 gaa cac ggt acc caa gaa gga tgg ctg gac cgc atg caa cac cgc agc 931
 Glu His Gly Thr Gln Glu Gly Trp Leu Asp Arg Met Gln His Arg Ser
 265 270 275
 aga tta tat gag ctc ctg cga tac gaa gac tac aac gtc ttt gac cag 979
 Arg Leu Tyr Glu Leu Leu Arg Tyr Glu Asp Tyr Asn Val Phe Asp Gln
 280 285 290
 cac att ttc acc tac aga aaa gga gaa aac aat gag tgacagccaa 1025
 His Ile Phe Thr Tyr Arg Lys Gly Glu Asn Asn Glu
 295 300 305
 gtccgcaaag gac 1038

<210> 622

<211> 305

<212> PRT

<213> Corynebacterium glutamicum

<400> 622

Met Asn Leu Phe Ser Asn Gly Val Asp Val Gly Arg Arg Arg Gln Ala
 1 5 10 15
 Phe Lys Ala Ala Leu Ala Ala Pro His Ile Ala Arg Leu Pro Gly Ala
 20 25 30
 Phe Ser Pro Leu Ile Ala Arg Ser Ile Glu Glu Ala Gly Phe Glu Gly
 35 40 45
 Val Tyr Val Ser Gly Ala Val Ile Ala Ala Asp Leu Ala Leu Pro Asp
 50 55 60
 Ile Gly Leu Thr Thr Leu Thr Glu Val Ala His Arg Ala Arg Gln Ile
 65 70 75 80

Ala Arg Val Thr Asp Leu Gly Val Leu Val Asp Ala Asp Thr Gly Phe
85 90 95

Gly Glu Pro Met Ser Ala Ala Arg Thr Val Ala Glu Leu Glu Asp Ala
100 105 110

Gly Val Ala Gly Cys His Leu Glu Asp Gln Val Asn Pro Lys Arg Cys
115 120 125

Gly His Leu Asp Gly Lys Glu Val Val Arg Thr Asp Val Met Val Arg
130 135 140

Arg Ile Ala Ala Ala Val Ser Ala Arg Arg Asp Pro Asn Phe Val Ile
145 150 155 160

Cys Ala Arg Thr Asp Ala Ala Gly Val Glu Gly Ile Asp Ala Ala Ile
165 170 175

Glu Arg Ala Lys Ala Tyr Leu Asp Ala Gly Ala Asp Met Ile Phe Thr
180 185 190

Glu Ala Leu His Ser Glu Ala Asp Phe Arg Tyr Phe Arg His Ala Ile
195 200 205

Pro Asp Ala Leu Leu Leu Ala Asn Met Thr Glu Phe Gly Lys Thr Thr
210 215 220

Leu Leu Ser Ala Asp Val Leu Glu Glu Ile Gly Tyr Asn Ala Val Ile
225 230 235 240

Tyr Pro Val Thr Thr Leu Arg Ile Ala Met Gly Gln Val Glu Gln Ala
245 250 255

Leu Ala Glu Ile Lys Glu His Gly Thr Gln Glu Gly Trp Leu Asp Arg
260 265 270

Met Gln His Arg Ser Arg Leu Tyr Glu Leu Leu Arg Tyr Glu Asp Tyr
275 280 285

Asn Val Phe Asp Gln His Ile Phe Thr Tyr Arg Lys Gly Glu Asn Asn
290 295 300

Glu
305

<210> 623

<211> 242

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(219)

<223> FRXA02333

<400> 623

gag att ggc tac aac gcc gtg atc tac ccc gtg acc acg ctg cgt att 48
Glu Ile Gly Tyr Asn Ala Val Ile Tyr Pro Val Thr Thr Leu Arg Ile
1 5 10 15

gcc atg gga caa gta gaa caa gca cta gcc gaa atc aaa gaa cac ggt 96
 Ala Met Gly Gln Val Glu Gln Ala Leu Ala Glu Ile Lys Glu His Gly
 20 25 30

acc caa gaa gga tgg ctg gac cgc atg caa cac cgc agc aga tta tat 144
 Thr Gln Glu Gly Trp Leu Asp Arg Met Gln His Arg Ser Arg Leu Tyr
 35 40 45

gag ctc ctg cga tac gaa gac tac aac gtc ttt gac cag cac att ttc 192
 Glu Leu Leu Arg Tyr Glu Asp Tyr Asn Val Phe Asp Gln His Ile Phe
 50 55 60

acc tac aga aaa gga gaa aac aat gag tgacagccaa gtccgcaaag 239
 Thr Tyr Arg Lys Gly Glu Asn Asn Glu
 65 70

gac 242

<210> 624

<211> 73

<212> PRT

<213> Corynebacterium glutamicum

<400> 624

Glu Ile Gly Tyr Asn Ala Val Ile Tyr Pro Val Thr Thr Leu Arg Ile
 1 5 10 15

Ala Met Gly Gln Val Glu Gln Ala Leu Ala Glu Ile Lys Glu His Gly
 20 25 30

Thr Gln Glu Gly Trp Leu Asp Arg Met Gln His Arg Ser Arg Leu Tyr
 35 40 45

Glu Leu Leu Arg Tyr Glu Asp Tyr Asn Val Phe Asp Gln His Ile Phe
 50 55 60

Thr Tyr Arg Lys Gly Glu Asn Asn Glu
 65 70

<210> 625

<211> 513

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(490)

<223> RXA00030

<400> 625

taaaaacgcc acttttggtgt cgataacacc gaacttccga acataaaaga tgcgttggtg 60

ctctctgcac aatgtttctt tcggaactat tctggcgacc atg cga att gaa atc 115
 Met Arg Ile Glu Ile
 1 5

aca agc gta ttt gtt gat gac cag gcc aaa gca ctc gat ttc tac acc 163
 Thr Ser Val Phe Val Asp Asp Gln Ala Lys Ala Leu Asp Phe Tyr Thr
 10 15 20

acg aag ctc gga ttt gag ctc aaa cac gat gta act gct ggt gac tac 211
 Thr Lys Leu Gly Phe Glu Leu Lys His Asp Val Thr Ala Gly Asp Tyr
 25 30 35

cgc tgg ttg act gtt gtt gat cca gaa aac cca gat ggt gtg cag ctt 259
 Arg Trp Leu Thr Val Val Asp Pro Glu Asn Pro Asp Gly Val Gln Leu
 40 45 50

ttg ttg gaa cca aac cag cac cca gat gca gcg act tac caa gct gga 307
 Leu Leu Glu Pro Asn Gln His Pro Asp Ala Ala Thr Tyr Gln Ala Gly
 55 60 65

att aaa cga gac ggt att ccc gct aca cag ttt tat gtt gat gat gtg 355
 Ile Lys Arg Asp Gly Ile Pro Ala Thr Gln Phe Tyr Val Asp Asp Val
 70 75 80 85

cag gaa gaa tat gac agc ctc aag gat aaa ggc gtg gat ttc atc atg 403
 Gln Glu Glu Tyr Asp Ser Leu Lys Asp Lys Gly Val Asp Phe Ile Met
 90 95 100

gaa cca acc gat gtg ggc cct tca gtg att gcc att ctc gat gac acc 451
 Glu Pro Thr Asp Val Gly Pro Ser Val Ile Ala Ile Leu Asp Asp Thr
 105 110 115

gta gga aac cta att cag att gtt caa ttg aag cag aac taaccccgtg 500
 Val Gly Asn Leu Ile Gln Ile Val Gln Leu Lys Gln Asn
 120 125 130

gaatgacaaa atc 513

<210> 626

<211> 130

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 626

Met Arg Ile Glu Ile Thr Ser Val Phe Val Asp Asp Gln Ala Lys Ala
 1 5 10 15

Leu Asp Phe Tyr Thr Thr Lys Leu Gly Phe Glu Leu Lys His Asp Val
 20 25 30

Thr Ala Gly Asp Tyr Arg Trp Leu Thr Val Val Asp Pro Glu Asn Pro
 35 40 45

Asp Gly Val Gln Leu Leu Leu Glu Pro Asn Gln His Pro Asp Ala Ala
 50 55 60

Thr Tyr Gln Ala Gly Ile Lys Arg Asp Gly Ile Pro Ala Thr Gln Phe
 65 70 75 80

Tyr Val Asp Asp Val Gln Glu Glu Tyr Asp Ser Leu Lys Asp Lys Gly
 85 90 95

Val Asp Phe Ile Met Glu Pro Thr Asp Val Gly Pro Ser Val Ile Ala
 100 105 110

Ile Leu Asp Asp Thr Val Gly Asn Leu Ile Gln Ile Val Gln Leu Lys
 115 120 125

Gln Asn
130

<210> 627
<211> 2334
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2311)
<223> RXN00148

<400> 627
ctttgagggc agcgcgcatg cgcccgatgg ttatttgaac atgacaattg atgccgcggc 60
gacgctggct gacctgctag atgctttggg agcttaaadc atg acg tcg atc cct 115
Met Thr Ser Ile Pro
1 5
aat ttt tca gac atc cca ttg act gct gag aca cgt gca tcg gag tca 163
Asn Phe Ser Asp Ile Pro Leu Thr Ala Glu Thr Arg Ala Ser Glu Ser
10 15 20
cac aac gtt gac gcc ggc aag gtg tgg aac act ccc gaa ggc att gat 211
His Asn Val Asp Ala Gly Lys Val Trp Asn Thr Pro Glu Gly Ile Asp
25 30 35
gtc aag cgc gta ttc acg cag gct gac cgc gac gag gcg caa gcg gcg 259
Val Lys Arg Val Phe Thr Gln Ala Asp Arg Asp Glu Ala Gln Ala Ala
40 45 50
gga cat ccg gtg gat tct ttg cca ggt caa aag cca ttt atg cgc ggg 307
Gly His Pro Val Asp Ser Leu Pro Gly Gln Lys Pro Phe Met Arg Gly
55 60 65
ccg tac cca act atg tac acc aat cag ccg tgg acg att cgc cag tac 355
Pro Tyr Pro Thr Met Tyr Thr Asn Gln Pro Trp Thr Ile Arg Gln Tyr
70 75 80 85
gca ggc ttt tca acc gcc gcg gaa tcc aat gcg ttt tat cgg agg aac 403
Ala Gly Phe Ser Thr Ala Ala Glu Ser Asn Ala Phe Tyr Arg Arg Asn
90 95 100
ctt gct gcg ggt caa aaa ggt ttg tcg gtt gcg ttc gat cta gcg acc 451
Leu Ala Ala Gly Gln Lys Gly Leu Ser Val Ala Phe Asp Leu Ala Thr
105 110 115
cac cgc ggt tat gac tcg gat aat gag cgc gtg gtc ggc gat gtg ggt 499
His Arg Gly Tyr Asp Ser Asp Asn Glu Arg Val Val Gly Asp Val Gly
120 125 130
atg gcc ggc gtg gcg att gat tcg att ttg gat atg cgt cag ctg ttt 547
Met Ala Gly Val Ala Ile Asp Ser Ile Leu Asp Met Arg Gln Leu Phe
135 140 145
gat ggc att gat ttg tcc agc gtg tcg gtg tcg atg acc atg aat ggc 595
Asp Gly Ile Asp Leu Ser Ser Val Ser Val Ser Met Thr Met Asn Gly
150 155 160 165

gct gtg ctg ccg att ctt gcg ttc tat atc gtg gcg gct gag gaa caa	643
Ala Val Leu Pro Ile Leu Ala Phe Tyr Ile Val Ala Ala Glu Glu Gln	
170 175 180	
ggt gtg ggt ccg gag cag ctt gcg ggc acg atc cag aat gac atc ttg	691
Gly Val Gly Pro Glu Gln Leu Ala Gly Thr Ile Gln Asn Asp Ile Leu	
185 190 195	
aaa gaa ttt atg gtg cgc aac acc tat att tat ccg ccg aag ccg tcg	739
Lys Glu Phe Met Val Arg Asn Thr Tyr Ile Tyr Pro Pro Lys Pro Ser	
200 205 210	
atg cgc atc att tcc aac atc ttt gag tac acc tcc ttg aag atg cca	787
Met Arg Ile Ile Ser Asn Ile Phe Glu Tyr Thr Ser Leu Lys Met Pro	
215 220 225	
cgt ttt aac tcc att tcg att tct ggc tat cac atc cag gaa gcg gga	835
Arg Phe Asn Ser Ile Ser Ile Ser Gly Tyr His Ile Gln Glu Ala Gly	
230 235 240 245	
gcg act gcc gat ttg gag ctg gcc tac act ctg gcg gat ggt att gaa	883
Ala Thr Ala Asp Leu Glu Leu Ala Tyr Thr Leu Ala Asp Gly Ile Glu	
250 255 260	
tac atc cgt gca ggt aaa gag gta ggc ctt gac gtg gat aag ttc gcg	931
Tyr Ile Arg Ala Gly Lys Glu Val Gly Leu Asp Val Asp Lys Phe Ala	
265 270 275	
cct cgt ctg tcc ttc ttc tgg ggt att tct atg tac acc ttc atg gag	979
Pro Arg Leu Ser Phe Phe Trp Gly Ile Ser Met Tyr Thr Phe Met Glu	
280 285 290	
atc gca aag ctg cgt gcg gga cga ctg ctg tgg agc gag ttg gtg gca	1027
Ile Ala Lys Leu Arg Ala Gly Arg Leu Leu Trp Ser Glu Leu Val Ala	
295 300 305	
aaa ttc gat ccg aaa aac gcc aag tcc cag tcg ctg cgc acg cac tcg	1075
Lys Phe Asp Pro Lys Asn Ala Lys Ser Gln Ser Leu Arg Thr His Ser	
310 315 320 325	
cag acc tct ggt tgg tcg ttg acc gcg cag gat gtg tac aac aac gtc	1123
Gln Thr Ser Gly Trp Ser Leu Thr Ala Gln Asp Val Tyr Asn Asn Val	
330 335 340	
gcc cgc acc gcg att gag gcg atg gct gca acc cag ggc cac acc cag	1171
Ala Arg Thr Ala Ile Glu Ala Met Ala Ala Thr Gln Gly His Thr Gln	
345 350 355	
tcg ctg cac acc aat gca ctt gat gag gcg ttg gcg ctg ccc acc gat	1219
Ser Leu His Thr Asn Ala Leu Asp Glu Ala Leu Ala Leu Pro Thr Asp	
360 365 370	
ttc tct gct cgt atc gcc cga aac acc cag ctg ttg ctg cag cag gaa	1267
Phe Ser Ala Arg Ile Ala Arg Asn Thr Gln Leu Leu Leu Gln Gln Glu	
375 380 385	
tct ggc acg gtg cgt cca gtt gat cca tgg gcg ggc tcc tat tac gtg	1315
Ser Gly Thr Val Arg Pro Val Asp Pro Trp Ala Gly Ser Tyr Tyr Val	
390 395 400 405	

gag	ttg	acc	aat	gag	ctg	gct	aac	cgc	gcg	cgc	aag	cac	atc	gat	1363	
Glu	Trp	Leu	Thr	Asn	Glu	Leu	Ala	Asn	Arg	Ala	Arg	Lys	His	Ile	Asp	
			410						415					420		
gag	gtg	gag	gaa	gcc	ggc	gga	atg	gcg	cag	gcc	acc	gcg	cag	gga	att	1411
Glu	Val	Glu	Glu	Ala	Gly	Gly	Met	Ala	Gln	Ala	Thr	Ala	Gln	Gly	Ile	
			425						430					435		
cct	aag	ctg	cgc	att	gag	gaa	tca	gcg	gca	cgc	acc	cag	gct	cgc	att	1459
Pro	Lys	Leu	Arg	Ile	Glu	Glu	Ser	Ala	Ala	Arg	Thr	Gln	Ala	Arg	Ile	
			440						445					450		
gat	tcc	ggc	cgc	cag	gcg	ctg	atc	ggc	gtg	aat	cgc	tac	gtg	gcg	gaa	1507
Asp	Ser	Gly	Arg	Gln	Ala	Leu	Ile	Gly	Val	Asn	Arg	Tyr	Val	Ala	Glu	
			455						460					465		
gaa	gat	gag	gaa	att	gaa	gtc	ctc	aag	gtt	gac	aac	acc	aag	gtt	cgc	1555
Glu	Asp	Glu	Glu	Ile	Glu	Val	Leu	Lys	Val	Asp	Asn	Thr	Lys	Val	Arg	
			470												485	
gca	gaa	cag	ttg	gct	aaa	ctc	gcg	caa	ctg	aaa	gca	gag	cgc	aac	gat	1603
Ala	Glu	Gln	Leu	Ala	Lys	Leu	Ala	Gln	Leu	Lys	Ala	Glu	Arg	Asn	Asp	
			490												500	
gcg	gaa	gtc	aag	gct	gcg	ctg	gat	gcg	ttg	aca	gct	gct	gcc	cgc	aac	1651
Ala	Glu	Val	Lys	Ala	Ala	Leu	Asp	Ala	Leu	Thr	Ala	Ala	Ala	Arg	Asn	
			505												515	
gag	cat	aaa	gag	cca	ggg	gat	ttg	gat	cag	aac	ctg	ctc	aaa	ctt	gcc	1699
Glu	His	Lys	Glu	Pro	Gly	Asp	Leu	Asp	Gln	Asn	Leu	Leu	Lys	Leu	Ala	
			520												530	
gtc	gat	gct	gcg	cgc	gca	aaa	gct	acc	att	gga	gag	atc	tcc	gat	gct	1747
Val	Asp	Ala	Ala	Arg	Ala	Lys	Ala	Thr	Ile	Gly	Glu	Ile	Ser	Asp	Ala	
			535												545	
ttg	gaa	gtt	gtc	ttt	ggc	cgc	cac	gaa	gca	gaa	atc	agg	acg	ctg	tct	1795
Leu	Glu	Val	Val	Phe	Gly	Arg	His	Glu	Ala	Glu	Ile	Arg	Thr	Leu	Ser	
			550												565	
ggc	gtg	tac	aag	gat	gag	gtt	gga	aag	gaa	ggc	aca	gtg	agc	aac	gtc	1843
Gly	Val	Tyr	Lys	Asp	Glu	Val	Gly	Lys	Glu	Gly	Thr	Val	Ser	Asn	Val	
				570											580	
gaa	cgc	gcg	atc	gcc	ctg	gct	gac	gcc	ttt	gag	gct	gag	gaa	ggc	cgc	1891
Glu	Arg	Ala	Ile	Ala	Leu	Ala	Asp	Ala	Phe	Glu	Ala	Glu	Glu	Gly	Arg	
			585												595	
cgc	cca	cgt	atc	ttt	att	gcc	aag	atg	ggc	cag	gat	gga	cat	gac	cgt	1939
Arg	Pro	Arg	Ile	Phe	Ile	Ala	Lys	Met	Gly	Gln	Asp	Gly	His	Asp	Arg	
			600												610	
gga	cag	aag	gtt	gtc	gcg	tct	gcc	tat	gct	gac	ctg	ggc	atg	gac	gtg	1987
Gly	Gln	Lys	Val	Val	Ala	Ser	Ala	Tyr	Ala	Asp	Leu	Gly	Met	Asp	Val	
			615												620	
gat	gtt	gga	ccg	ctg	ttt	caa	act	cca	gcc	gaa	gct	gcc	cgc	gcc	gcc	2035
Asp	Val	Gly	Pro	Leu	Phe	Gln	Thr	Pro	Ala	Glu	Ala	Ala	Arg	Ala	Ala	
															645	
gtg	gac	gcc	gat	gtt	cac	gtg	gtg	ggt	atg	tct	tcg	ctg	gca	gca	ggc	2083

Val Asp Ala Asp Val His Val Val Gly Met Ser Ser Leu Ala Ala Gly
650 655 660

cac ctc acc ttg ctg ccc gag ctg aag aaa gaa ctt gca gct ctt ggc 2131
His Leu Thr Leu Leu Pro Glu Leu Lys Lys Glu Leu Ala Ala Leu Gly
665 670 675

cgc gat gac att ctg gtc acc gtg ggc ggc gtc att ccg ccg ggc gat 2179
Arg Asp Asp Ile Leu Val Thr Val Gly Gly Val Ile Pro Pro Gly Asp
680 685 690

ttc cag gat ctc tac gat atg ggt gcc gcc gcg att tac cct tca gga 2227
Phe Gln Asp Leu Tyr Asp Met Gly Ala Ala Ala Ile Tyr Pro Ser Gly
695 700 705

acc gtc atc gcg gag tcg gcg atc gat ctg atc acc cga ctc gcc gca 2275
Thr Val Ile Ala Glu Ser Ala Ile Asp Leu Ile Thr Arg Leu Ala Ala
710 715 720 725

cac ctg ggc ttt gac ctg gat gtg gat gtg aat gaa tgatcacggt 2321
His Leu Gly Phe Asp Leu Asp Val Asp Val Asn Glu
730 735

ttcctagaag aca 2334

<210> 628
<211> 737
<212> PRT
<213> Corynebacterium glutamicum

<400> 628
Met Thr Ser Ile Pro Asn Phe Ser Asp Ile Pro Leu Thr Ala Glu Thr
1 5 10 15

Arg Ala Ser Glu Ser His Asn Val Asp Ala Gly Lys Val Trp Asn Thr
20 25 30

Pro Glu Gly Ile Asp Val Lys Arg Val Phe Thr Gln Ala Asp Arg Asp
35 40 45

Glu Ala Gln Ala Ala Gly His Pro Val Asp Ser Leu Pro Gly Gln Lys
50 55 60

Pro Phe Met Arg Gly Pro Tyr Pro Thr Met Tyr Thr Asn Gln Pro Trp
65 70 75 80

Thr Ile Arg Gln Tyr Ala Gly Phe Ser Thr Ala Ala Glu Ser Asn Ala
85 90 95

Phe Tyr Arg Arg Asn Leu Ala Ala Gly Gln Lys Gly Leu Ser Val Ala
100 105 110

Phe Asp Leu Ala Thr His Arg Gly Tyr Asp Ser Asp Asn Glu Arg Val
115 120 125

Val Gly Asp Val Gly Met Ala Gly Val Ala Ile Asp Ser Ile Leu Asp
130 135 140

Met Arg Gln Leu Phe Asp Gly Ile Asp Leu Ser Ser Val Ser Val Ser
145 150 155 160

Met Thr Met Asn Gly Ala Val Leu Pro Ile Leu Ala Phe Tyr Ile Val
 165 170 175
 Ala Ala Glu Glu Gln Gly Val Gly Pro Glu Gln Leu Ala Gly Thr Ile
 180 185 190
 Gln Asn Asp Ile Leu Lys Glu Phe Met Val Arg Asn Thr Tyr Ile Tyr
 195 200 205
 Pro Pro Lys Pro Ser Met Arg Ile Ile Ser Asn Ile Phe Glu Tyr Thr
 210 215 220
 Ser Leu Lys Met Pro Arg Phe Asn Ser Ile Ser Ile Ser Gly Tyr His
 225 230 235 240
 Ile Gln Glu Ala Gly Ala Thr Ala Asp Leu Glu Leu Ala Tyr Thr Leu
 245 250 255
 Ala Asp Gly Ile Glu Tyr Ile Arg Ala Gly Lys Glu Val Gly Leu Asp
 260 265 270
 Val Asp Lys Phe Ala Pro Arg Leu Ser Phe Phe Trp Gly Ile Ser Met
 275 280 285
 Tyr Thr Phe Met Glu Ile Ala Lys Leu Arg Ala Gly Arg Leu Leu Trp
 290 295 300
 Ser Glu Leu Val Ala Lys Phe Asp Pro Lys Asn Ala Lys Ser Gln Ser
 305 310 315 320
 Leu Arg Thr His Ser Gln Thr Ser Gly Trp Ser Leu Thr Ala Gln Asp
 325 330 335
 Val Tyr Asn Asn Val Ala Arg Thr Ala Ile Glu Ala Met Ala Ala Thr
 340 345 350
 Gln Gly His Thr Gln Ser Leu His Thr Asn Ala Leu Asp Glu Ala Leu
 355 360 365
 Ala Leu Pro Thr Asp Phe Ser Ala Arg Ile Ala Arg Asn Thr Gln Leu
 370 375 380
 Leu Leu Gln Gln Glu Ser Gly Thr Val Arg Pro Val Asp Pro Trp Ala
 385 390 395 400
 Gly Ser Tyr Tyr Val Glu Trp Leu Thr Asn Glu Leu Ala Asn Arg Ala
 405 410 415
 Arg Lys His Ile Asp Glu Val Glu Glu Ala Gly Gly Met Ala Gln Ala
 420 425 430
 Thr Ala Gln Gly Ile Pro Lys Leu Arg Ile Glu Glu Ser Ala Ala Arg
 435 440 445
 Thr Gln Ala Arg Ile Asp Ser Gly Arg Gln Ala Leu Ile Gly Val Asn
 450 455 460
 Arg Tyr Val Ala Glu Glu Asp Glu Glu Ile Glu Val Leu Lys Val Asp
 465 470 475 480

Asn Thr Lys Val Arg Ala Glu Gln Leu Ala Lys Leu Ala Gln Leu Lys
 485 490 495
 Ala Glu Arg Asn Asp Ala Glu Val Lys Ala Ala Leu Asp Ala Leu Thr
 500 505 510
 Ala Ala Ala Arg Asn Glu His Lys Glu Pro Gly Asp Leu Asp Gln Asn
 515 520 525
 Leu Leu Lys Leu Ala Val Asp Ala Ala Arg Ala Lys Ala Thr Ile Gly
 530 535 540
 Glu Ile Ser Asp Ala Leu Glu Val Val Phe Gly Arg His Glu Ala Glu
 545 550 555 560
 Ile Arg Thr Leu Ser Gly Val Tyr Lys Asp Glu Val Gly Lys Glu Gly
 565 570 575
 Thr Val Ser Asn Val Glu Arg Ala Ile Ala Leu Ala Asp Ala Phe Glu
 580 585 590
 Ala Glu Glu Gly Arg Arg Pro Arg Ile Phe Ile Ala Lys Met Gly Gln
 595 600 605
 Asp Gly His Asp Arg Gly Gln Lys Val Val Ala Ser Ala Tyr Ala Asp
 610 615 620
 Leu Gly Met Asp Val Asp Val Gly Pro Leu Phe Gln Thr Pro Ala Glu
 625 630 635 640
 Ala Ala Arg Ala Ala Val Asp Ala Asp Val His Val Val Gly Met Ser
 645 650 655
 Ser Leu Ala Ala Gly His Leu Thr Leu Leu Pro Glu Leu Lys Lys Glu
 660 665 670
 Leu Ala Ala Leu Gly Arg Asp Asp Ile Leu Val Thr Val Gly Gly Val
 675 680 685
 Ile Pro Pro Gly Asp Phe Gln Asp Leu Tyr Asp Met Gly Ala Ala Ala
 690 695 700
 Ile Tyr Pro Ser Gly Thr Val Ile Ala Glu Ser Ala Ile Asp Leu Ile
 705 710 715 720
 Thr Arg Leu Ala Ala His Leu Gly Phe Asp Leu Asp Val Asp Val Asn
 725 730 735

Glu

<210> 629

<211> 2098

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2098)

<223> FRXA00148

<400> 629

```

ctttgagggc agcgcgcatg cgcccgatgg ttatttgaac atgacaattg atgccgcggc 60
gacgctggct gacctgctag atgctttggg agcttaaata atg acg tcg atc cct 115
                                     Met Thr Ser Ile Pro
                                     1 5
aat ttt tca gac atc cca ttg act gct gag aca cgt gca tcg gag tca 163
Asn Phe Ser Asp Ile Pro Leu Thr Ala Glu Thr Arg Ala Ser Glu Ser
                10                15                20
cac aac gtt gac gcc ggc aag gtg tgg aac act ccc gaa ggc att gat 211
His Asn Val Asp Ala Gly Lys Val Trp Asn Thr Pro Glu Gly Ile Asp
                25                30                35
gtc aag cgc gta ttc acg cag gct gac cgc gac gag gcg caa gcg gcg 259
Val Lys Arg Val Phe Thr Gln Ala Asp Arg Asp Glu Ala Gln Ala Ala
                40                45                50
gga cat ccg gtg gat tct ttg cca ggt caa aag cca ttt atg cgc ggg 307
Gly His Pro Val Asp Ser Leu Pro Gly Gln Lys Pro Phe Met Arg Gly
                55                60                65
ccg tac cca act atg tac acc aat cag ccg tgg acg att cgc cag tac 355
Pro Tyr Pro Thr Met Tyr Thr Asn Gln Pro Trp Thr Ile Arg Gln Tyr
                70                75                80                85
gca ggc ttt tca acc gcc gcg gaa tcc aat gcg ttt tat cgg agg aac 403
Ala Gly Phe Ser Thr Ala Ala Glu Ser Asn Ala Phe Tyr Arg Arg Asn
                90                95                100
ctt gct gcg ggt caa aaa ggt ttg tcg gtt gcg ttc gat cta gcg acc 451
Leu Ala Ala Gly Gln Lys Gly Leu Ser Val Ala Phe Asp Leu Ala Thr
                105                110                115
cac cgc ggt tat gac tcg gat aat gag cgc gtg gtc ggc gat gtg ggt 499
His Arg Gly Tyr Asp Ser Asp Asn Glu Arg Val Val Gly Asp Val Gly
                120                125                130
atg gcc ggc gtg gcg att gat tcg att ttg gat atg cgt cag ctg ttt 547
Met Ala Gly Val Ala Ile Asp Ser Ile Leu Asp Met Arg Gln Leu Phe
                135                140                145
gat ggc att gat ttg tcc agc gtg tcg gtg tcg atg acc atg aat ggc 595
Asp Gly Ile Asp Leu Ser Ser Val Ser Val Ser Met Thr Met Asn Gly
                150                155                160                165
gct gtg ctg ccg att ctt gcg ttc tat atc gtg gcg gct gag gaa caa 643
Ala Val Leu Pro Ile Leu Ala Phe Tyr Ile Val Ala Ala Glu Glu Gln
                170                175                180
ggt gtg ggt ccg gag cag ctt gcg ggc acg atc cag aat gac atc ttg 691
Gly Val Gly Pro Glu Gln Leu Ala Gly Thr Ile Gln Asn Asp Ile Leu
                185                190                195
aaa gaa ttt atg gtg cgc aac acc tat att tat ccg ccg aag ccg tcg 739
Lys Glu Phe Met Val Arg Asn Thr Tyr Ile Tyr Pro Pro Lys Pro Ser
                200                205                210
atg cgc atc att tcc aac atc ttt gag tac acc tcc ttg aag atg cca 787

```

Met	Arg	Ile	Ile	Ser	Asn	Ile	Phe	Glu	Tyr	Thr	Ser	Leu	Lys	Met	Pro		
215						220					225						
cgt	ttt	aac	tcc	att	tcg	att	tct	ggc	tat	cac	atc	cag	gaa	gcg	gga	835	
Arg	Phe	Asn	Ser	Ile	Ser	Ile	Ser	Gly	Tyr	His	Ile	Gln	Glu	Ala	Gly		
230					235				240					245			
gcg	act	gcc	gat	ttg	gag	ctg	gcc	tac	act	ctg	gcg	gat	ggt	att	gaa	883	
Ala	Thr	Ala	Asp	Leu	Glu	Leu	Ala	Tyr	Thr	Leu	Ala	Asp	Gly	Ile	Glu		
				250					255					260			
tac	atc	cgt	gca	ggg	aaa	gag	gta	ggc	ctt	gac	gtg	gat	aag	ttc	gcg	931	
Tyr	Ile	Arg	Ala	Gly	Lys	Glu	Val	Gly	Leu	Asp	Val	Asp	Lys	Phe	Ala		
			265					270					275				
cct	cgt	ctg	tcc	ttc	ttc	tgg	ggg	att	tct	atg	tac	acc	ttc	atg	gag	979	
Pro	Arg	Leu	Ser	Phe	Phe	Trp	Gly	Ile	Ser	Met	Tyr	Thr	Phe	Met	Glu		
	280						285					290					
atc	gca	aag	ctg	cgt	gcg	gga	cga	ctg	ctg	tgg	agc	gag	ttg	gtg	gca	1027	
Ile	Ala	Lys	Leu	Arg	Ala	Gly	Arg	Leu	Leu	Trp	Ser	Glu	Leu	Val	Ala		
	295					300					305						
aaa	ttc	gat	ccg	aaa	aac	gcc	aag	tcc	cag	tcg	ctg	cgc	acg	cac	tcg	1075	
Lys	Phe	Asp	Pro	Lys	Asn	Ala	Lys	Ser	Gln	Ser	Leu	Arg	Thr	His	Ser		
310					315				320					325			
cag	acc	tct	ggg	tgg	tcg	ttg	acc	gcg	cag	gat	gtg	tac	aac	aac	gtc	1123	
Gln	Thr	Ser	Gly	Trp	Ser	Leu	Thr	Ala	Gln	Asp	Val	Tyr	Asn	Asn	Val		
				330					335					340			
gcc	cgc	acc	gcg	att	gag	gcg	atg	gct	gca	acc	cag	ggc	cac	acc	cag	1171	
Ala	Arg	Thr	Ala	Ile	Glu	Ala	Met	Ala	Ala	Thr	Gln	Gly	His	Thr	Gln		
			345					350					355				
tcg	ctg	cac	acc	aat	gca	ctt	gat	gag	gcg	ttg	gcg	ctg	ccc	acc	gat	1219	
Ser	Leu	His	Thr	Asn	Ala	Leu	Asp	Glu	Ala	Leu	Ala	Leu	Pro	Thr	Asp		
			360				365					370					
ttc	tct	gct	cgt	atc	gcc	cga	aac	acc	cag	ctg	ttg	ctg	cag	cag	gaa	1267	
Phe	Ser	Ala	Arg	Ile	Ala	Arg	Asn	Thr	Gln	Leu	Leu	Leu	Gln	Gln	Glu		
			375			380					385						
tct	ggc	acg	gtg	cgt	cca	gtt	gat	cca	tgg	gcg	ggc	tcc	tat	tac	gtg	1315	
Ser	Gly	Thr	Val	Arg	Pro	Val	Asp	Pro	Trp	Ala	Gly	Ser	Tyr	Tyr	Val		
390					395				400					405			
gag	tgg	ttg	acc	aat	gag	ctg	gct	aac	cgc	gcg	cgc	aag	cac	atc	gat	1363	
Glu	Trp	Leu	Thr	Asn	Glu	Leu	Ala	Asn	Arg	Ala	Arg	Lys	His	Ile	Asp		
				410					415					420			
gag	gtg	gag	gaa	gcc	ggc	gga	atg	gcg	cag	gcc	acc	gcg	cag	gga	att	1411	
Glu	Val	Glu	Glu	Ala	Gly	Gly	Met	Ala	Gln	Ala	Thr	Ala	Gln	Gly	Ile		
			425					430					435				
cct	aag	ctg	cgc	att	gag	gaa	tca	gcg	gca	cgc	acc	cag	gct	cgc	att	1459	
Pro	Lys	Leu	Arg	Ile	Glu	Glu	Ser	Ala	Ala	Arg	Thr	Gln	Ala	Arg	Ile		
			440				445					450					
gat	tcc	ggc	cgc	cag	gcg	ctg	atc	ggc	gtg	aat	cgc	tac	gtg	gcg	gaa	1507	
Asp	Ser	Gly	Arg	Gln	Ala	Leu	Ile	Gly	Val	Asn	Arg	Tyr	Val	Ala	Glu		

455	460	465	
gaa gat gag gaa att gaa gtc ctc aag gtt gac aac acc aag gtt cgc Glu Asp Glu Glu Ile Glu Val Leu Lys Val Asp Asn Thr Lys Val Arg 470 475 480 485			1555
gca gaa cag ttg gct aaa ctc gcg caa ctg aaa gca gag cgc aac gat Ala Glu Gln Leu Ala Lys Leu Ala Gln Leu Lys Ala Glu Arg Asn Asp 490 495 500			1603
gcg gaa gtc aag gct gcg ctg gat gcg ttg aca gct gct gcc cgc aac Ala Glu Val Lys Ala Ala Leu Asp Ala Leu Thr Ala Ala Arg Asn 505 510 515			1651
gag cat aaa gag cca ggg gat ttg gat cag aac ctg ctc aaa ctt gcc Glu His Lys Glu Pro Gly Asp Leu Asp Gln Asn Leu Leu Lys Leu Ala 520 525 530			1699
gtc gat gct gcg cgc gca aaa gct acc att gga gag atc tcc gat gct Val Asp Ala Ala Arg Ala Lys Ala Thr Ile Gly Glu Ile Ser Asp Ala 535 540 545			1747
ttg gaa gtt gtc ttt ggc cgc cac gaa gca gaa atc agg acg ctg tct Leu Glu Val Val Phe Gly Arg His Glu Ala Glu Ile Arg Thr Leu Ser 550 555 560 565			1795
ggc gtg tac aag gat gag gtt gga aag gaa ggc aca gtg agc aac gtc Gly Val Tyr Lys Asp Glu Val Gly Lys Glu Gly Thr Val Ser Asn Val 570 575 580			1843
gaa cgc gcg atc gcc ctg gct gac gcc ttt gag gct gag gaa ggc cgc Glu Arg Ala Ile Ala Leu Ala Asp Ala Phe Glu Ala Glu Glu Gly Arg 585 590 595			1891
cgc cca cgt atc ttt att gcc aag atg ggc cag gat gga cat gac cgt Arg Pro Arg Ile Phe Ile Ala Lys Met Gly Gln Asp Gly His Asp Arg 600 605 610			1939
gga cag aag gtt gtc gcg tct gcc tat gct gac ctg ggc atg gac gtg Gly Gln Lys Val Val Ala Ser Ala Tyr Ala Asp Leu Gly Met Asp Val 615 620 625			1987
gat gtt gga ccg ctg ttt caa act cca gcc gaa gct gcc cgc gcc gcc Asp Val Gly Pro Leu Phe Gln Thr Pro Ala Glu Ala Ala Arg Ala Ala 630 635 640 645			2035
gtg gac gcc gat gtt cac gtg gtg ggt atg tct tcg ctg gca gca ggc Val Asp Ala Asp Val His Val Val Gly Met Ser Ser Leu Ala Ala Gly 650 655 660			2083
cac ctc acc ttg ctg His Leu Thr Leu Leu 665			2098

<210> 630

<211> 666

<212> PRT

<213> Corynebacterium glutamicum

<400> 630

Met Thr Ser Ile Pro Asn Phe Ser Asp Ile Pro Leu Thr Ala Glu Thr
 1 5 10 15
 Arg Ala Ser Glu Ser His Asn Val Asp Ala Gly Lys Val Trp Asn Thr
 20 25 30
 Pro Glu Gly Ile Asp Val Lys Arg Val Phe Thr Gln Ala Asp Arg Asp
 35 40 45
 Glu Ala Gln Ala Ala Gly His Pro Val Asp Ser Leu Pro Gly Gln Lys
 50 55 60
 Pro Phe Met Arg Gly Pro Tyr Pro Thr Met Tyr Thr Asn Gln Pro Trp
 65 70 75 80
 Thr Ile Arg Gln Tyr Ala Gly Phe Ser Thr Ala Ala Glu Ser Asn Ala
 85 90 95
 Phe Tyr Arg Arg Asn Leu Ala Ala Gly Gln Lys Gly Leu Ser Val Ala
 100 105 110
 Phe Asp Leu Ala Thr His Arg Gly Tyr Asp Ser Asp Asn Glu Arg Val
 115 120 125
 Val Gly Asp Val Gly Met Ala Gly Val Ala Ile Asp Ser Ile Leu Asp
 130 135 140
 Met Arg Gln Leu Phe Asp Gly Ile Asp Leu Ser Ser Val Ser Val Ser
 145 150 155 160
 Met Thr Met Asn Gly Ala Val Leu Pro Ile Leu Ala Phe Tyr Ile Val
 165 170 175
 Ala Ala Glu Glu Gln Gly Val Gly Pro Glu Gln Leu Ala Gly Thr Ile
 180 185 190
 Gln Asn Asp Ile Leu Lys Glu Phe Met Val Arg Asn Thr Tyr Ile Tyr
 195 200 205
 Pro Pro Lys Pro Ser Met Arg Ile Ile Ser Asn Ile Phe Glu Tyr Thr
 210 215 220
 Ser Leu Lys Met Pro Arg Phe Asn Ser Ile Ser Ile Ser Gly Tyr His
 225 230 235 240
 Ile Gln Glu Ala Gly Ala Thr Ala Asp Leu Glu Leu Ala Tyr Thr Leu
 245 250 255
 Ala Asp Gly Ile Glu Tyr Ile Arg Ala Gly Lys Glu Val Gly Leu Asp
 260 265 270
 Val Asp Lys Phe Ala Pro Arg Leu Ser Phe Phe Trp Gly Ile Ser Met
 275 280 285
 Tyr Thr Phe Met Glu Ile Ala Lys Leu Arg Ala Gly Arg Leu Leu Trp
 290 295 300
 Ser Glu Leu Val Ala Lys Phe Asp Pro Lys Asn Ala Lys Ser Gln Ser
 305 310 315 320
 Leu Arg Thr His Ser Gln Thr Ser Gly Trp Ser Leu Thr Ala Gln Asp

325					330					335					
Val	Tyr	Asn	Asn	Val	Ala	Arg	Thr	Ala	Ile	Glu	Ala	Met	Ala	Ala	Thr
			340					345					350		
Gln	Gly	His	Thr	Gln	Ser	Leu	His	Thr	Asn	Ala	Leu	Asp	Glu	Ala	Leu
		355					360					365			
Ala	Leu	Pro	Thr	Asp	Phe	Ser	Ala	Arg	Ile	Ala	Arg	Asn	Thr	Gln	Leu
	370					375					380				
Leu	Leu	Gln	Gln	Glu	Ser	Gly	Thr	Val	Arg	Pro	Val	Asp	Pro	Trp	Ala
385					390					395					400
Gly	Ser	Tyr	Tyr	Val	Glu	Trp	Leu	Thr	Asn	Glu	Leu	Ala	Asn	Arg	Ala
				405					410					415	
Arg	Lys	His	Ile	Asp	Glu	Val	Glu	Glu	Ala	Gly	Gly	Met	Ala	Gln	Ala
			420					425					430		
Thr	Ala	Gln	Gly	Ile	Pro	Lys	Leu	Arg	Ile	Glu	Glu	Ser	Ala	Ala	Arg
	435						440					445			
Thr	Gln	Ala	Arg	Ile	Asp	Ser	Gly	Arg	Gln	Ala	Leu	Ile	Gly	Val	Asn
	450					455					460				
Arg	Tyr	Val	Ala	Glu	Glu	Asp	Glu	Glu	Ile	Glu	Val	Leu	Lys	Val	Asp
465					470					475					480
Asn	Thr	Lys	Val	Arg	Ala	Glu	Gln	Leu	Ala	Lys	Leu	Ala	Gln	Leu	Lys
			485					490					495		
Ala	Glu	Arg	Asn	Asp	Ala	Glu	Val	Lys	Ala	Ala	Leu	Asp	Ala	Leu	Thr
			500					505					510		
Ala	Ala	Ala	Arg	Asn	Glu	His	Lys	Glu	Pro	Gly	Asp	Leu	Asp	Gln	Asn
	515						520				525				
Leu	Leu	Lys	Leu	Ala	Val	Asp	Ala	Ala	Arg	Ala	Lys	Ala	Thr	Ile	Gly
	530					535					540				
Glu	Ile	Ser	Asp	Ala	Leu	Glu	Val	Val	Phe	Gly	Arg	His	Glu	Ala	Glu
545					550					555					560
Ile	Arg	Thr	Leu	Ser	Gly	Val	Tyr	Lys	Asp	Glu	Val	Gly	Lys	Glu	Gly
			565					570					575		
Thr	Val	Ser	Asn	Val	Glu	Arg	Ala	Ile	Ala	Leu	Ala	Asp	Ala	Phe	Glu
			580					585					590		
Ala	Glu	Glu	Gly	Arg	Arg	Pro	Arg	Ile	Phe	Ile	Ala	Lys	Met	Gly	Gln
	595						600					605			
Asp	Gly	His	Asp	Arg	Gly	Gln	Lys	Val	Val	Ala	Ser	Ala	Tyr	Ala	Asp
	610					615					620				
Leu	Gly	Met	Asp	Val	Asp	Val	Gly	Pro	Leu	Phe	Gln	Thr	Pro	Ala	Glu
625					630					635					640
Ala	Ala	Arg	Ala	Ala	Val	Asp	Ala	Asp	Val	His	Val	Val	Gly	Met	Ser
			645					650					655		

Ser Leu Ala Ala Gly His Leu Thr Leu Leu
660 665

<210> 631
<211> 1971
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1948)
<223> RXA00149

<400> 631
ttttcgtagg taaacacagg tgaaggcttt acaagcttgt gaactcccta cacaaaagca 60
atccaatagc tatccataag caagagaaag taagtctacg ttg act gat ctc aca 115
Leu Thr Asp Leu Thr
1 5
aag act gcg gtg ccc gag gaa ctt tca gag aac ctc gaa act tgg tac 163
Lys Thr Ala Val Pro Glu Glu Leu Ser Glu Asn Leu Glu Thr Trp Tyr
10 15 20
aag gct gtg gcc ggt gtt ttc gcg cgc aca cag aaa aaa gac atc ggc 211
Lys Ala Val Ala Gly Val Phe Ala Arg Thr Gln Lys Lys Asp Ile Gly
25 30 35
gac att gcc gta gat gtg tgg aag aaa ctc atc gtc act aca ccg gat 259
Asp Ile Ala Val Asp Val Trp Lys Lys Leu Ile Val Thr Thr Pro Asp
40 45 50
ggt gtt gat atc aat ccg ctg tac acc aga gca gat gag tcc cag agg 307
Gly Val Asp Ile Asn Pro Leu Tyr Thr Arg Ala Asp Glu Ser Gln Arg
55 60 65
aaa ttc act gag gtt cct ggt gag ttt ccc ttc act agg gga acc act 355
Lys Phe Thr Glu Val Pro Gly Glu Phe Pro Phe Thr Arg Gly Thr Thr
70 75 80 85
gtt gat ggt gaa cgc gtt ggt tgg ggt gtt act gag act ttc gga cat 403
Val Asp Gly Glu Arg Val Gly Trp Gly Val Thr Glu Thr Phe Gly His
90 95 100
gac agc ccg aag aat atc aac gct gcg gtg ctg aat gct ctg aat tct 451
Asp Ser Pro Lys Asn Ile Asn Ala Ala Val Leu Asn Ala Leu Asn Ser
105 110 115
ggc acc acc aca ttg ggt ttt gag ttc tct gag gaa ttc acg gca gct 499
Gly Thr Thr Thr Leu Gly Phe Glu Phe Ser Glu Glu Phe Thr Ala Ala
120 125 130
gat ctt aaa gtt gct ctc gaa ggc gtg tat ctc aac atg gct ccg ttg 547
Asp Leu Lys Val Ala Leu Glu Gly Val Tyr Leu Asn Met Ala Pro Leu
135 140 145
ctg att cat gcg ggt gga tcc acg tca gag gtt gca gcg gcg ttg tat 595
Leu Ile His Ala Gly Gly Ser Thr Ser Glu Val Ala Ala Ala Leu Tyr
150 155 160 165

acg ttg gcg gag gaa gcc gga acg ttt ttt gct gcg ttg acc ttg ggt	643
Thr Leu Ala Glu Glu Ala Gly Thr Phe Phe Ala Ala Leu Thr Leu Gly	
170 175 180	
tct cgt cct ttg acg gcg cag gtt gat ggt tcg cac agt gac acc att	691
Ser Arg Pro Leu Thr Ala Gln Val Asp Gly Ser His Ser Asp Thr Ile	
185 190 195	
gaa gaa gca gtt cag ttg gca gtg aat gct tcc aag cgt gcg aat gtg	739
Glu Glu Ala Val Gln Leu Ala Val Asn Ala Ser Lys Arg Ala Asn Val	
200 205 210	
cgc gct atc ttg gtg gat ggt tcc agt ttt tcc aac cag ggc gcg tcg	787
Arg Ala Ile Leu Val Asp Gly Ser Ser Phe Ser Asn Gln Gly Ala Ser	
215 220 225	
gat gct caa gaa att ggt cta agt atc gcc gcc ggt gtg gat tat gtc	835
Asp Ala Gln Glu Ile Gly Leu Ser Ile Ala Ala Gly Val Asp Tyr Val	
230 235 240 245	
cgt cgc ttg gtc gat gca ggc ctt tcc acg gaa gct gca ctt aag cag	883
Arg Arg Leu Val Asp Ala Gly Leu Ser Thr Glu Ala Ala Leu Lys Gln	
250 255 260	
gtg gcg ttc cgt ttt gcg gtc acc gat gag cag ttc gcg cag att tct	931
Val Ala Phe Arg Phe Ala Val Thr Asp Glu Gln Phe Ala Gln Ile Ser	
265 270 275	
aag ctg cgt gtg gct cga cgt ctg tgg gcc agg gtg tgt gag gtg ctt	979
Lys Leu Arg Val Ala Arg Arg Leu Trp Ala Arg Val Cys Glu Val Leu	
280 285 290	
ggt ttt cca gag ctg gcc gta gca cca cag cat gcg gtg act gca cga	1027
Gly Phe Pro Glu Leu Ala Val Ala Pro Gln His Ala Val Thr Ala Arg	
295 300 305	
gcg atg ttt agc cag cgt gat ccg tgg gtg aat atg ctg cgc agt act	1075
Ala Met Phe Ser Gln Arg Asp Pro Trp Val Asn Met Leu Arg Ser Thr	
310 315 320 325	
gtt gca gct ttc gct gca ggc gtc ggt gga gca acc gat gtg gag gtt	1123
Val Ala Ala Phe Ala Ala Gly Val Gly Gly Ala Thr Asp Val Glu Val	
330 335 340	
cgt act ttt gat gat gcg atc cca gat gga gtt cct gga gtg tcg agg	1171
Arg Thr Phe Asp Asp Ala Ile Pro Asp Gly Val Pro Gly Val Ser Arg	
345 350 355	
aat ttc gct cac cgc atc gcg cgc aat act aat ttg ttg ttg cta gaa	1219
Asn Phe Ala His Arg Ile Ala Arg Asn Thr Asn Leu Leu Leu Leu Glu	
360 365 370	
gag tca cat ctt ggt cac gtg gtt gat cct gct ggt gga tca tat ttc	1267
Glu Ser His Leu Gly His Val Val Asp Pro Ala Gly Gly Ser Tyr Phe	
375 380 385	
gtg gag agc ttc acc gat gat cta gcg gag aag gcg tgg gct gtg ttc	1315
Val Glu Ser Phe Thr Asp Asp Leu Ala Glu Lys Ala Trp Ala Val Phe	
390 395 400 405	

```

agt ggc atc gaa gct gag ggc gga tac agt gca gct tgt gca tcc ggc 1363
Ser Gly Ile Glu Ala Glu Gly Gly Tyr Ser Ala Ala Cys Ala Ser Gly
      410                      415                      420

acg gtg act gcc atg ctt gat cag acg tgg gag cag act cgc gct gat 1411
Thr Val Thr Ala Met Leu Asp Gln Thr Trp Glu Gln Thr Arg Ala Asp
      425                      430                      435

gtg gcg tcg aga aag aag aag ctc act gga att aat gag ttc ccg aac 1459
Val Ala Ser Arg Lys Lys Lys Leu Thr Gly Ile Asn Glu Phe Pro Asn
      440                      445                      450

ttg gcg gag tct ccg ctg cca gct gat cgt cgg gta gaa cct gca ggt 1507
Leu Ala Glu Ser Pro Leu Pro Ala Asp Arg Arg Val Glu Pro Ala Gly
      455                      460                      465

gtg cgt cga tgg gca gcg gat ttt gaa gcg ctg cgc aat cgt tcg gat 1555
Val Arg Arg Trp Ala Ala Asp Phe Glu Ala Leu Arg Asn Arg Ser Asp
      470                      475                      480                      485

gct ttc ttg gaa aag aac ggc gcg agg cca cag atc acg atg att cct 1603
Ala Phe Leu Glu Lys Asn Gly Ala Arg Pro Gln Ile Thr Met Ile Pro
      490                      495                      500

ctg gga ccg ttg tcc aag cac aat att cgc act ggt ttt act tcc aac 1651
Leu Gly Pro Leu Ser Lys His Asn Ile Arg Thr Gly Phe Thr Ser Asn
      505                      510                      515

ctg ttg gct tcc ggt ggc att gaa gca atc aac ccg ggt caa ctt gtt 1699
Leu Leu Ala Ser Gly Gly Ile Glu Ala Ile Asn Pro Gly Gln Leu Val
      520                      525                      530

ccc ggc act gac gct ttt gca gaa gct gca cag gcc gca ggc att gta 1747
Pro Gly Thr Asp Ala Phe Ala Glu Ala Ala Gln Ala Ala Gly Ile Val
      535                      540                      545

gtg gtg tgt gga acg gac caa gag tat gcc gaa acg ggg gag gga gcc 1795
Val Val Cys Gly Thr Asp Gln Glu Tyr Ala Glu Thr Gly Glu Gly Ala
      550                      555                      560                      565

gtc gaa aag ctc cgc gaa gcg ggc gtt gag cgc atc ctg ctt gct ggc 1843
Val Glu Lys Leu Arg Glu Ala Gly Val Glu Arg Ile Leu Leu Ala Gly
      570                      575                      580

gcg ccg aag agc ttt gag ggc agc gcg cat gcg ccc gat ggt tat ttg 1891
Ala Pro Lys Ser Phe Glu Gly Ser Ala His Ala Pro Asp Gly Tyr Leu
      585                      590                      595

aac atg aca att gat gcc gcg gcg acg ctg gct gac ctg cta gat gct 1939
Asn Met Thr Ile Asp Ala Ala Ala Thr Leu Ala Asp Leu Leu Asp Ala
      600                      605                      610

ttg gga gct taaatcatga cgtcgatccc taa 1971
Leu Gly Ala
      615

```

<210> 632

<211> 616

<212> PRT

<213> Corynebacterium glutamicum

<400> 632

Leu Thr Asp Leu Thr Lys Thr Ala Val Pro Glu Glu Leu Ser Glu Asn
 1 5 10 15
 Leu Glu Thr Trp Tyr Lys Ala Val Ala Gly Val Phe Ala Arg Thr Gln
 20 25 30
 Lys Lys Asp Ile Gly Asp Ile Ala Val Asp Val Trp Lys Lys Leu Ile
 35 40 45
 Val Thr Thr Pro Asp Gly Val Asp Ile Asn Pro Leu Tyr Thr Arg Ala
 50 55 60
 Asp Glu Ser Gln Arg Lys Phe Thr Glu Val Pro Gly Glu Phe Pro Phe
 65 70 75 80
 Thr Arg Gly Thr Thr Val Asp Gly Glu Arg Val Gly Trp Gly Val Thr
 85 90 95
 Glu Thr Phe Gly His Asp Ser Pro Lys Asn Ile Asn Ala Ala Val Leu
 100 105 110
 Asn Ala Leu Asn Ser Gly Thr Thr Thr Leu Gly Phe Glu Phe Ser Glu
 115 120 125
 Glu Phe Thr Ala Ala Asp Leu Lys Val Ala Leu Glu Gly Val Tyr Leu
 130 135 140
 Asn Met Ala Pro Leu Leu Ile His Ala Gly Gly Ser Thr Ser Glu Val
 145 150 155 160
 Ala Ala Ala Leu Tyr Thr Leu Ala Glu Glu Ala Gly Thr Phe Phe Ala
 165 170 175
 Ala Leu Thr Leu Gly Ser Arg Pro Leu Thr Ala Gln Val Asp Gly Ser
 180 185 190
 His Ser Asp Thr Ile Glu Glu Ala Val Gln Leu Ala Val Asn Ala Ser
 195 200 205
 Lys Arg Ala Asn Val Arg Ala Ile Leu Val Asp Gly Ser Ser Phe Ser
 210 215 220
 Asn Gln Gly Ala Ser Asp Ala Gln Glu Ile Gly Leu Ser Ile Ala Ala
 225 230 235 240
 Gly Val Asp Tyr Val Arg Arg Leu Val Asp Ala Gly Leu Ser Thr Glu
 245 250 255
 Ala Ala Leu Lys Gln Val Ala Phe Arg Phe Ala Val Thr Asp Glu Gln
 260 265 270
 Phe Ala Gln Ile Ser Lys Leu Arg Val Ala Arg Arg Leu Trp Ala Arg
 275 280 285
 Val Cys Glu Val Leu Gly Phe Pro Glu Leu Ala Val Ala Pro Gln His
 290 295 300
 Ala Val Thr Ala Arg Ala Met Phe Ser Gln Arg Asp Pro Trp Val Asn
 305 310 315 320

Met Leu Arg Ser Thr Val Ala Ala Phe Ala Ala Gly Val Gly Gly Ala
 325 330 335
 Thr Asp Val Glu Val Arg Thr Phe Asp Asp Ala Ile Pro Asp Gly Val
 340 345 350
 Pro Gly Val Ser Arg Asn Phe Ala His Arg Ile Ala Arg Asn Thr Asn
 355 360 365
 Leu Leu Leu Leu Glu Glu Ser His Leu Gly His Val Val Asp Pro Ala
 370 375 380
 Gly Gly Ser Tyr Phe Val Glu Ser Phe Thr Asp Asp Leu Ala Glu Lys
 385 390 395 400
 Ala Trp Ala Val Phe Ser Gly Ile Glu Ala Glu Gly Gly Tyr Ser Ala
 405 410 415
 Ala Cys Ala Ser Gly Thr Val Thr Ala Met Leu Asp Gln Thr Trp Glu
 420 425 430
 Gln Thr Arg Ala Asp Val Ala Ser Arg Lys Lys Lys Leu Thr Gly Ile
 435 440 445
 Asn Glu Phe Pro Asn Leu Ala Glu Ser Pro Leu Pro Ala Asp Arg Arg
 450 455 460
 Val Glu Pro Ala Gly Val Arg Arg Trp Ala Ala Asp Phe Glu Ala Leu
 465 470 475 480
 Arg Asn Arg Ser Asp Ala Phe Leu Glu Lys Asn Gly Ala Arg Pro Gln
 485 490 495
 Ile Thr Met Ile Pro Leu Gly Pro Leu Ser Lys His Asn Ile Arg Thr
 500 505 510
 Gly Phe Thr Ser Asn Leu Leu Ala Ser Gly Gly Ile Glu Ala Ile Asn
 515 520 525
 Pro Gly Gln Leu Val Pro Gly Thr Asp Ala Phe Ala Glu Ala Ala Gln
 530 535 540
 Ala Ala Gly Ile Val Val Val Cys Gly Thr Asp Gln Glu Tyr Ala Glu
 545 550 555 560
 Thr Gly Glu Gly Ala Val Glu Lys Leu Arg Glu Ala Gly Val Glu Arg
 565 570 575
 Ile Leu Leu Ala Gly Ala Pro Lys Ser Phe Glu Gly Ser Ala His Ala
 580 585 590
 Pro Asp Gly Tyr Leu Asn Met Thr Ile Asp Ala Ala Ala Thr Leu Ala
 595 600 605
 Asp Leu Leu Asp Ala Leu Gly Ala
 610 615

<210> 633

<211> 777

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(754)

<223> RXN00317

<400> 633

```

caacggttac atcactcacg cattaactcc cctggttggt accgcatggt cgtttcccaa 60
gtctagccaa gccttgaaaa attctggcaa ggttaatggt gtg act acg cct tct 115
                               Val Thr Thr Pro Ser
                               1                               5

aag aaa act ctg ctc ttt gat ctc gac gga acc ctc gtc gat tct ttc 163
Lys Lys Thr Leu Leu Phe Asp Leu Asp Gly Thr Leu Val Asp Ser Phe
                               10                               15                               20

ccc ggt atc cgc act tca ttc ctt cac acc ctg cac gaa aag aac tgg 211
Pro Gly Ile Arg Thr Ser Phe Leu His Thr Leu His Glu Lys Asn Trp
                               25                               30                               35

gaa atc ccc tct gag gaa cgc atc tcg caa gtt cca gga cct ccc atg 259
Glu Ile Pro Ser Glu Glu Arg Ile Ser Gln Val Pro Gly Pro Pro Met
                               40                               45                               50

gaa tgg acg ttc cag gat ttg ggc atg act cca gag cag gca caa gac 307
Glu Trp Thr Phe Gln Asp Leu Gly Met Thr Pro Glu Gln Ala Gln Asp
                               55                               60                               65

gct ctg cag acc tac ctt gag cat tac ggc cag gtg ggt tgg gat ctt 355
Ala Leu Gln Thr Tyr Leu Glu His Tyr Gly Gln Val Gly Trp Asp Leu
                               70                               75                               80                               85

tcc gaa gca ttc ccc ggc atg cga gat ttg ctg atc cgc ttg aaa tac 403
Ser Glu Ala Phe Pro Gly Met Arg Asp Leu Leu Ile Arg Leu Lys Tyr
                               90                               95                               100

gaa ggt ttc cgt ctg tgc acc gcc acc tcc aag ggc gag ttc ttt gcg 451
Glu Gly Phe Arg Leu Cys Thr Ala Thr Ser Lys Gly Glu Phe Phe Ala
                               105                               110                               115

gag aag gta ctt cgc aaa ttc gag atg ttc gat ctc ttc gaa ttc atg 499
Glu Lys Val Leu Arg Lys Phe Glu Met Phe Asp Leu Phe Glu Phe Met
                               120                               125                               130

ggt gcc gcc acc gac agc ggc aac cga cgc agc aaa tct gcc gtg atc 547
Gly Ala Ala Thr Asp Ser Gly Asn Arg Arg Ser Lys Ser Ala Val Ile
                               135                               140                               145

aaa cat gtc ctc gac agc gtt ggg ttg gac gaa cca aat gat att ttg 595
Lys His Val Leu Asp Ser Val Gly Leu Asp Glu Pro Asn Asp Ile Leu
                               150                               155                               160                               165

atg att ggt gat cga tca cac gat att gaa ggt tcg agt gaa ttc ggc 643
Met Ile Gly Asp Arg Ser His Asp Ile Glu Gly Ser Ser Glu Phe Gly
                               170                               175                               180

atc gat tgt gtt gcc gta acc tgg ggc tac ggc agc aaa act gaa tgg 691
Ile Asp Cys Val Ala Val Thr Trp Gly Tyr Gly Ser Lys Thr Glu Trp

```

185 190 195
gac gct gcc cgc tac acc gtg agc acc gca gaa gaa tta gaa agg atc 739
Asp Ala Ala Arg Tyr Thr Val Ser Thr Ala Glu Glu Leu Glu Arg Ile
200 205 210

atc cat gac tgg gcc taaaacttcg ctacctgtgg aaa 777
Ile His Asp Trp Ala
215

<210> 634

<211> 218

<212> PRT

<213> Corynebacterium glutamicum

<400> 634

Val Thr Thr Pro Ser Lys Lys Thr Leu Leu Phe Asp Leu Asp Gly Thr
1 5 10 15

Leu Val Asp Ser Phe Pro Gly Ile Arg Thr Ser Phe Leu His Thr Leu
20 25 30

His Glu Lys Asn Trp Glu Ile Pro Ser Glu Glu Arg Ile Ser Gln Val
35 40 45

Pro Gly Pro Pro Met Glu Trp Thr Phe Gln Asp Leu Gly Met Thr Pro
50 55 60

Glu Gln Ala Gln Asp Ala Leu Gln Thr Tyr Leu Glu His Tyr Gly Gln
65 70 75 80

Val Gly Trp Asp Leu Ser Glu Ala Phe Pro Gly Met Arg Asp Leu Leu
85 90 95

Ile Arg Leu Lys Tyr Glu Gly Phe Arg Leu Cys Thr Ala Thr Ser Lys
100 105 110

Gly Glu Phe Phe Ala Glu Lys Val Leu Arg Lys Phe Glu Met Phe Asp
115 120 125

Leu Phe Glu Phe Met Gly Ala Ala Thr Asp Ser Gly Asn Arg Arg Ser
130 135 140

Lys Ser Ala Val Ile Lys His Val Leu Asp Ser Val Gly Leu Asp Glu
145 150 155 160

Pro Asn Asp Ile Leu Met Ile Gly Asp Arg Ser His Asp Ile Glu Gly
165 170 175

Ser Ser Glu Phe Gly Ile Asp Cys Val Ala Val Thr Trp Gly Tyr Gly
180 185 190

Ser Lys Thr Glu Trp Asp Ala Ala Arg Tyr Thr Val Ser Thr Ala Glu
195 200 205

Glu Leu Glu Arg Ile Ile His Asp Trp Ala
210 215

<210> 635

<400> 636
Val Thr Thr Pro Ser Lys Lys Thr Leu Leu Phe Asp Leu Asp Gly Thr
1 5 10 15
Leu Val Asp Ser Phe Pro Gly Ile Arg Thr Ser Phe Leu His Thr Leu
20 25 30
His Glu Lys Asn Trp Glu Ile Pro Ser Glu Glu Arg Ile Ser Gln Val
35 40 45
Pro Gly Pro Pro Met Glu Trp Thr Phe Gln Asp Leu Gly Met Thr Pro

50					55					60					
Glu 65	Gln	Ala	Gln	Asp	Ala 70	Leu	Gln	Thr	Tyr	Leu 75	Glu	His	Tyr	Gly	Gln 80
Val	Gly	Trp	Asp	Leu 85	Ser	Glu	Ala	Phe	Pro 90	Gly	Met	Arg	Asp	Leu 95	Leu
Ile	Pro	Leu	Ile 100	Tyr	Glu	Gly	Phe	Arg 105	Leu	Cys	Thr	Ala	Thr 110	Phe	Gln
Gly															

```
<210> 637
<211> 816
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(793)
<223> RXA02196
```

<400> 637																						
tct	acc	accc	agagg	caaag	tactt	taacg	tcta	acac	ct	ttg	agag	gga	aaact	tttccc	60							
gcacattgca gatcgtgcc															ctttaactaa	ggttgacggc	atg	att	aag	gcg	att	115
																	Met	Ile	Lys	Ala	Ile	
																	1				5	
ttc	tgg	gac	atg	gac	ggc	acg	atg	gtg	gac	tct	gag	cca	cag	tgg	ggc	163						
Phe	Trp	Asp	Met	Asp	Gly	Thr	Met	Val	Asp	Ser	Glu	Pro	Gln	Trp	Gly							
															10		15				20	
att	gct	acc	tac	gag	ctc	agc	gaa	gcc	atg	ggc	cgc	cgc	ctc	acc	ccg	211						
Ile	Ala	Thr	Tyr	Glu	Leu	Ser	Glu	Ala	Met	Gly	Arg	Arg	Leu	Thr	Pro							
															25		30				35	
gag	ctc	cgg	gaa	ctc	acc	gtc	ggc	tcg	agc	ctg	ccg	cgc	acc	atg	cgc	259						
Glu	Leu	Arg	Glu	Leu	Thr	Val	Gly	Ser	Ser	Leu	Pro	Arg	Thr	Met	Arg							
															40		45				50	
tta	tgc	gca	gag	cac	gca	ggc	att	aca	ttg	agc	gac	gcg	gac	tac	gag	307						
Leu	Cys	Ala	Glu	His	Ala	Gly	Ile	Thr	Leu	Ser	Asp	Ala	Asp	Tyr	Glu							
															55		60				65	
cgc	tac	cgg	gct	ggc	atg	ttc	gcc	cgg	gtc	cat	gag	ctt	ttc	gac	gaa	355						
Arg	Tyr	Arg	Ala	Gly	Met	Phe	Ala	Arg	Val	His	Glu	Leu	Phe	Asp	Glu							
															70		75				85	
tcc	ctc	gtc	cca	aat	cca	ggc	gtc	acc	gaa	ctc	ctg	aca	gag	ttg	aag	403						
Ser	Leu	Val	Pro	Asn	Pro	Gly	Val	Thr	Glu	Leu	Leu	Thr	Glu	Leu	Lys							
															90		95				100	
gcc	ctc	gag	atc	ccc	atg	ttg	gtc	acc	acc	aac	aca	gag	cgc	gat	ctc	451						
Ala	Leu	Glu	Ile	Pro	Met	Leu	Val	Thr	Thr	Asn	Thr	Glu	Arg	Asp	Leu							
															105		110				115	
gcg	acc	cgt	tca	gtc	gca	gcc	gtg	gga	aat	gag	ttc	ttc	atc	ggt	tct	499						

Ala Thr Arg Ser Val Ala Ala Val Gly Asn Glu Phe Phe Ile Gly Ser
 120 125 130

atc gct ggt gat gaa gtc cca aca gca aag cca gcc ccc gac atg tac 547
 Ile Ala Gly Asp Glu Val Pro Thr Ala Lys Pro Ala Pro Asp Met Tyr
 135 140 145

ctc gaa gca gca cga cgt gtg ggc ttt gac cca tca gag tgc ctc gtg 595
 Leu Glu Ala Ala Arg Arg Val Gly Phe Asp Pro Ser Glu Cys Leu Val
 150 155 160 165

ttc gaa gat tcc tac aac ggc atg ctg ggc gct gtt act gca ggt tgc 643
 Phe Glu Asp Ser Tyr Asn Gly Met Leu Gly Ala Val Thr Ala Gly Cys
 170 175 180

cgc gtc att ggt ctg cac cca gaa gaa gtc caa gcg cca gaa ggt gta 691
 Arg Val Ile Gly Leu His Pro Glu Glu Val Gln Ala Pro Glu Gly Val
 185 190 195

gtg cct ttg cgt tcc ctc cac ggt aaa aac tct ttc gaa ggt gtc acc 739
 Val Pro Leu Arg Ser Leu His Gly Lys Asn Ser Phe Glu Gly Val Thr
 200 205 210

gct gag atg gtc act gcc tgg tac cac cag atc gag ccg gca ggt gtc 787
 Ala Glu Met Val Thr Ala Trp Tyr His Gln Ile Glu Pro Ala Gly Val
 215 220 225

gca aaa taaaaccagg tgggggagtg aaa 816
 Ala Lys
 230

<210> 638

<211> 231

<212> PRT

<213> Corynebacterium glutamicum

<400> 638

Met Ile Lys Ala Ile Phe Trp Asp Met Asp Gly Thr Met Val Asp Ser
 1 5 10 15

Glu Pro Gln Trp Gly Ile Ala Thr Tyr Glu Leu Ser Glu Ala Met Gly
 20 25 30

Arg Arg Leu Thr Pro Glu Leu Arg Glu Leu Thr Val Gly Ser Ser Leu
 35 40 45

Pro Arg Thr Met Arg Leu Cys Ala Glu His Ala Gly Ile Thr Leu Ser
 50 55 60

Asp Ala Asp Tyr Glu Arg Tyr Arg Ala Gly Met Phe Ala Arg Val His
 65 70 75 80

Glu Leu Phe Asp Glu Ser Leu Val Pro Asn Pro Gly Val Thr Glu Leu
 85 90 95

Leu Thr Glu Leu Lys Ala Leu Glu Ile Pro Met Leu Val Thr Thr Asn
 100 105 110

Thr Glu Arg Asp Leu Ala Thr Arg Ser Val Ala Ala Val Gly Asn Glu
 115 120 125

Phe Phe Ile Gly Ser Ile Ala Gly Asp Glu Val Pro Thr Ala Lys Pro
 130 135 140

Ala Pro Asp Met Tyr Leu Glu Ala Ala Arg Arg Val Gly Phe Asp Pro
 145 150 155 160

Ser Glu Cys Leu Val Phe Glu Asp Ser Tyr Asn Gly Met Leu Gly Ala
 165 170 175

Val Thr Ala Gly Cys Arg Val Ile Gly Leu His Pro Glu Glu Val Gln
 180 185 190

Ala Pro Glu Gly Val Val Pro Leu Arg Ser Leu His Gly Lys Asn Ser
 195 200 205

Phe Glu Gly Val Thr Ala Glu Met Val Thr Ala Trp Tyr His Gln Ile
 210 215 220

Glu Pro Ala Gly Val Ala Lys
 225 230

<210> 639

<211> 531

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(508)

<223> RXN02461

<400> 639

agaaaatctc aaggcaaaaa acaagccacc ccaatctgtg cgacaatcaa accacagact 60
 acgactatta tgtcacgaag aaaccaaaga aagggaata atg cgc gga cta att 115
 Met Arg Gly Leu Ile
 1 5
 gtt gac tac gct gga gta cta gac gga acc gat gag gac cag cgt cgc 163
 Val Asp Tyr Ala Gly Val Leu Asp Gly Thr Asp Glu Asp Gln Arg Arg
 10 15 20
 tgg cgc aac ctg ctc gcc gca gca aag aaa aat ggc gtc gga acc gtg 211
 Trp Arg Asn Leu Leu Ala Ala Ala Lys Lys Asn Gly Val Gly Thr Val
 25 30 35
 atc ctc agc aac gat cca ggt ggg ctc ggc gca gcg ccg atc cgg gaa 259
 Ile Leu Ser Asn Asp Pro Gly Gly Leu Gly Ala Ala Pro Ile Arg Glu
 40 45 50
 ctc gaa aca aac ggg gta gtc gat aag gtg ctg ctg tcg gga gaa ctt 307
 Leu Glu Thr Asn Gly Val Val Asp Lys Val Leu Leu Ser Gly Glu Leu
 55 60 65
 ggc gtc gaa aag cca gag gaa gca gct ttc cag gcc gcc gca gac gcc 355
 Gly Val Glu Lys Pro Glu Glu Ala Ala Phe Gln Ala Ala Ala Asp Ala
 70 75 80 85
 atc gac ctg ccc atg cgt gac tgc gtg ctt gtc gac gac tcg atc ctc 403

Ile Asp Leu Pro Met Arg Asp Cys Val Leu Val Asp Asp Ser Ile Leu
 90 95 100

aac gtg cgc ggc gcc gtc gaa gcc gga ctc gta ggc gtc tac tac cag 451
 Asn Val Arg Gly Ala Val Glu Ala Gly Leu Val Gly Val Tyr Tyr Gln
 105 110 115

caa ttt gac cgt gca gtc gtc gaa atc gtc gga ctg ttc ggg cta gaa 499
 Gln Phe Asp Arg Ala Val Val Glu Ile Val Gly Leu Phe Gly Leu Glu
 120 125 130

gga gaa ttc taatcttgcg cgtctacatc cca 531
 Gly Glu Phe
 135

<210> 640

<211> 136

<212> PRT

<213> Corynebacterium glutamicum

<400> 640

Met Arg Gly Leu Ile Val Asp Tyr Ala Gly Val Leu Asp Gly Thr Asp
 1 5 10 15

Glu Asp Gln Arg Arg Trp Arg Asn Leu Leu Ala Ala Ala Lys Lys Asn
 20 25 30

Gly Val Gly Thr Val Ile Leu Ser Asn Asp Pro Gly Gly Leu Gly Ala
 35 40 45

Ala Pro Ile Arg Glu Leu Glu Thr Asn Gly Val Val Asp Lys Val Leu
 50 55 60

Leu Ser Gly Glu Leu Gly Val Glu Lys Pro Glu Glu Ala Ala Phe Gln
 65 70 75 80

Ala Ala Ala Asp Ala Ile Asp Leu Pro Met Arg Asp Cys Val Leu Val
 85 90 95

Asp Asp Ser Ile Leu Asn Val Arg Gly Ala Val Glu Ala Gly Leu Val
 100 105 110

Gly Val Tyr Tyr Gln Gln Phe Asp Arg Ala Val Val Glu Ile Val Gly
 115 120 125

Leu Phe Gly Leu Glu Gly Glu Phe
 130 135

<210> 641

<211> 1662

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1639)

<223> RXN01744

<400> 641

```

tcttattggt tcttcgtttt gtatcgataa atacaatcgg tttcctggct taataaggct 60

gttcctgtca acctgcaatg gaagaggaag tgtacctagc gtg gat gtc gtc gac 115
                               Val Asp Val Val Asp
                               1      5

atc gca cgg tgg caa ttc gga att acc acc gtc tat cac ttc att ttt 163
Ile Ala Arg Trp Gln Phe Gly Ile Thr Thr Val Tyr His Phe Ile Phe
                               10      15      20

gtc cca ctg acc att ggc tta gcg ccg ctg gtc gca atc atg caa acg 211
Val Pro Leu Thr Ile Gly Leu Ala Pro Leu Val Ala Ile Met Gln Thr
                               25      30      35

ttt tgg caa gtt acc ggc aaa gag cac tgg tat cgg gcc aca aga ttt 259
Phe Trp Gln Val Thr Gly Lys Glu His Trp Tyr Arg Ala Thr Arg Phe
                               40      45      50

ttt ggc act gtg ctg ctc atc aac ttc gcg gtt ggt gta gca acg ggc 307
Phe Gly Thr Val Leu Leu Ile Asn Phe Ala Val Gly Val Ala Thr Gly
                               55      60      65

att gtg cag gag ttc cag ttc ggt atg aac tgg tcg gaa tat tcg cgt 355
Ile Val Gln Glu Phe Gln Phe Gly Met Asn Trp Ser Glu Tyr Ser Arg
                               70      75      80      85

ttc gtc ggt gat gtt ttc ggc gga ccg ctg gct ttg gag ggt ctt atc 403
Phe Val Gly Asp Val Phe Gly Gly Pro Leu Ala Leu Glu Gly Leu Ile
                               90      95      100

gcg ttc ttc ctt gag tct gta ttc ctg gga ctg tgg att ttc gga tgg 451
Ala Phe Phe Leu Glu Ser Val Phe Leu Gly Leu Trp Ile Phe Gly Trp
                               105      110      115

ggg aag att cct ggt tgg ttg cac act gca tcc att tgg atc gtt gct 499
Gly Lys Ile Pro Gly Trp Leu His Thr Ala Ser Ile Trp Ile Val Ala
                               120      125      130

att gcg acg aat att tct gcc tat ttc atc atc gtg gcc aac tcg ttt 547
Ile Ala Thr Asn Ile Ser Ala Tyr Phe Ile Ile Val Ala Asn Ser Phe
                               135      140      145

atg cag cat ccg gtg ggt gct gag tat aac cct gag act ggt cgt gcg 595
Met Gln His Pro Val Gly Ala Glu Tyr Asn Pro Glu Thr Gly Arg Ala
                               150      155      160      165

gag ctt act gat ttt tgg gct ctt ctc aca aac tcc acc gcg ctg gct 643
Glu Leu Thr Asp Phe Trp Ala Leu Leu Thr Asn Ser Thr Ala Leu Ala
                               170      175      180

gcg ttc ccg cat gct gtt gcc ggt ggt ttt tta aca gct gga act ttc 691
Ala Phe Pro His Ala Val Ala Gly Gly Phe Leu Thr Ala Gly Thr Phe
                               185      190      195

gtt ctc gga att tcg ggt tgg tgg att att cgt gcg cac cgt cag gcc 739
Val Leu Gly Ile Ser Gly Trp Trp Ile Ile Arg Ala His Arg Gln Ala
                               200      205      210

aag aag gct gag tcg gaa atc gag tcg aag cat tcg atg cac agg ccc 787
Lys Lys Ala Glu Ser Glu Ile Glu Ser Lys His Ser Met His Arg Pro
                               215      220      225

```


gcg ttg tgg gtt ggt tgg tgg acc aca gtt gtc tct tcc gtg gcg ctg	835
Ala Leu Trp Val Gly Trp Trp Thr Thr Val Val Ser Ser Val Ala Leu	
230 235 240 245	
ttc atc act ggc gat atc cag gcg aag ctc atg ttc gtg caa cag cca	883
Phe Ile Thr Gly Asp Ile Gln Ala Lys Leu Met Phe Val Gln Gln Pro	
250 255 260	
atg aag atg gcg tcg gcg gaa tcc ttg tgt gaa acc gcc aca gat cca	931
Met Lys Met Ala Ser Ala Glu Ser Leu Cys Glu Thr Ala Thr Asp Pro	
265 270 275	
aac ttc tcc att ctg aca att ggt acg cac aac aac tgc gat acg gta	979
Asn Phe Ser Ile Leu Thr Ile Gly Thr His Asn Asn Cys Asp Thr Val	
280 285 290	
acc cac ctg atc gat gtt ccg ttt gtg ctt cca ttc ttg gct gaa gga	1027
Thr His Leu Ile Asp Val Pro Phe Val Leu Pro Phe Leu Ala Glu Gly	
295 300 305	
aaa ttc acc ggt gtg act ttg cag ggt gta aac cag ctc caa gct gca	1075
Lys Phe Thr Gly Val Thr Leu Gln Gly Val Asn Gln Leu Gln Ala Ala	
310 315 320 325	
gcg gag caa gca tac ggt cct ggc aac tac tcc cct aac ttg ttt gtc	1123
Ala Glu Gln Ala Tyr Gly Pro Gly Asn Tyr Ser Pro Asn Leu Phe Val	
330 335 340	
acc tac tgg tca ttc cgc gca atg atc ggc ctg atg ctt ggt tct ttg	1171
Thr Tyr Trp Ser Phe Arg Ala Met Ile Gly Leu Met Leu Gly Ser Leu	
345 350 355	
gct atc gct gcg att gcg tgg ctg ttg ctg cgt aag aag cgc aca cca	1219
Ala Ile Ala Ala Ile Ala Trp Leu Leu Leu Arg Lys Lys Arg Thr Pro	
360 365 370	
act gga aag att gct cgt ctg ttc cag atc ggc agc ctc att gct atc	1267
Thr Gly Lys Ile Ala Arg Leu Phe Gln Ile Gly Ser Leu Ile Ala Ile	
375 380 385	
ccg ttc cca ttc ttg gcc aac tct gct ggt tgg atc ttc acc gag atg	1315
Pro Phe Pro Phe Leu Ala Asn Ser Ala Gly Trp Ile Phe Thr Glu Met	
390 395 400 405	
ggc cgc cag cct tgg gtg gtg cac ccg aac cct gaa tct gcc gcc gat	1363
Gly Arg Gln Pro Trp Val Val His Pro Asn Pro Glu Ser Ala Gly Asp	
410 415 420	
gcc cga aca gag atg atc cgg atg act gtt gat atg ggt gta tct gat	1411
Ala Arg Thr Glu Met Ile Arg Met Thr Val Asp Met Gly Val Ser Asp	
425 430 435	
cat gcg cca tgg caa gtc tgg ctg act ctc att ggc ttc acg att ctc	1459
His Ala Pro Trp Gln Val Trp Leu Thr Leu Ile Gly Phe Thr Ile Leu	
440 445 450	
tat ctc att ttg ttc gtg gtg tgg gtg tgg ctg att cgc cgc gca gtt	1507
Tyr Leu Ile Leu Phe Val Trp Val Trp Leu Ile Arg Arg Ala Val	
455 460 465	

ctg atc gga cca cca gag gaa ggc gct cca tcc gtg gag gca aag act 1555
 Leu Ile Gly Pro Pro Glu Glu Gly Ala Pro Ser Val Glu Ala Lys Thr
 470 475 480 485

gga ccg gca acc ccg att ggt tca gat atg ccc atg aca ccg ctg caa 1603
 Gly Pro Ala Thr Pro Ile Gly Ser Asp Met Pro Met Thr Pro Leu Gln
 490 495 500

ttt act gcc gct gcc cca acc aca ggt gaa aag gaa taaccatgga 1649
 Phe Thr Ala Ala Ala Pro Thr Thr Gly Glu Lys Glu
 505 510

tctcaatacc ttt 1662

<210> 642

<211> 513

<212> PRT

<213> Corynebacterium glutamicum

<400> 642

Val Asp Val Val Asp Ile Ala Arg Trp Gln Phe Gly Ile Thr Thr Val
 1 5 10 15

Tyr His Phe Ile Phe Val Pro Leu Thr Ile Gly Leu Ala Pro Leu Val
 20 25 30

Ala Ile Met Gln Thr Phe Trp Gln Val Thr Gly Lys Glu His Trp Tyr
 35 40 45

Arg Ala Thr Arg Phe Phe Gly Thr Val Leu Leu Ile Asn Phe Ala Val
 50 55 60

Gly Val Ala Thr Gly Ile Val Gln Glu Phe Gln Phe Gly Met Asn Trp
 65 70 75 80

Ser Glu Tyr Ser Arg Phe Val Gly Asp Val Phe Gly Gly Pro Leu Ala
 85 90 95

Leu Glu Gly Leu Ile Ala Phe Phe Leu Glu Ser Val Phe Leu Gly Leu
 100 105 110

Trp Ile Phe Gly Trp Gly Lys Ile Pro Gly Trp Leu His Thr Ala Ser
 115 120 125

Ile Trp Ile Val Ala Ile Ala Thr Asn Ile Ser Ala Tyr Phe Ile Ile
 130 135 140

Val Ala Asn Ser Phe Met Gln His Pro Val Gly Ala Glu Tyr Asn Pro
 145 150 155 160

Glu Thr Gly Arg Ala Glu Leu Thr Asp Phe Trp Ala Leu Leu Thr Asn
 165 170 175

Ser Thr Ala Leu Ala Ala Phe Pro His Ala Val Ala Gly Gly Phe Leu
 180 185 190

Thr Ala Gly Thr Phe Val Leu Gly Ile Ser Gly Trp Trp Ile Ile Arg
 195 200 205

Ala His Arg Gln Ala Lys Lys Ala Glu Ser Glu Ile Glu Ser Lys His

210	215	220
Ser Met His Arg Pro Ala Leu Trp Val Gly Trp Trp Thr Thr Val Val 225 230 235 240		
Ser Ser Val Ala Leu Phe Ile Thr Gly Asp Ile Gln Ala Lys Leu Met 245 250 255		
Phe Val Gln Gln Pro Met Lys Met Ala Ser Ala Glu Ser Leu Cys Glu 260 265 270		
Thr Ala Thr Asp Pro Asn Phe Ser Ile Leu Thr Ile Gly Thr His Asn 275 280 285		
Asn Cys Asp Thr Val Thr His Leu Ile Asp Val Pro Phe Val Leu Pro 290 295 300		
Phe Leu Ala Glu Gly Lys Phe Thr Gly Val Thr Leu Gln Gly Val Asn 305 310 315 320		
Gln Leu Gln Ala Ala Ala Glu Gln Ala Tyr Gly Pro Gly Asn Tyr Ser 325 330 335		
Pro Asn Leu Phe Val Thr Tyr Trp Ser Phe Arg Ala Met Ile Gly Leu 340 345 350		
Met Leu Gly Ser Leu Ala Ile Ala Ala Ile Ala Trp Leu Leu Leu Arg 355 360 365		
Lys Lys Arg Thr Pro Thr Gly Lys Ile Ala Arg Leu Phe Gln Ile Gly 370 375 380		
Ser Leu Ile Ala Ile Pro Phe Pro Phe Leu Ala Asn Ser Ala Gly Trp 385 390 395 400		
Ile Phe Thr Glu Met Gly Arg Gln Pro Trp Val Val His Pro Asn Pro 405 410 415		
Glu Ser Ala Gly Asp Ala Arg Thr Glu Met Ile Arg Met Thr Val Asp 420 425 430		
Met Gly Val Ser Asp His Ala Pro Trp Gln Val Trp Leu Thr Leu Ile 435 440 445		
Gly Phe Thr Ile Leu Tyr Leu Ile Leu Phe Val Val Trp Val Trp Leu 450 455 460		
Ile Arg Arg Ala Val Leu Ile Gly Pro Pro Glu Glu Gly Ala Pro Ser 465 470 475 480		
Val Glu Ala Lys Thr Gly Pro Ala Thr Pro Ile Gly Ser Asp Met Pro 485 490 495		
Met Thr Pro Leu Gln Phe Thr Ala Ala Ala Pro Thr Thr Gly Glu Lys 500 505 510		

Glu

<210> 643

```
<211> 238
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(238)  
<223> FRXA00055
```

<400> 643
tcttattgggt tcttcgtttt gtatcgataa atacaatcgg tttcctggct taataaggct 60

gttctgtca acctgcaatg gaagaggaag tgtacctagc gtg gat gtc gtc gac 115
Val Asp Val Val Asp
1 5

atc gca cgg tgg caa ttc gga att acc acc gtc tat cac ttc att ttt 163
Ile Ala Arg Trp Gln Phe Gly Ile Thr Thr Val Tyr His Phe Ile Phe
10 15 20

gtc cca ctg acc att ggc tta gca ccg ctg gtc gcg atc atg caa acg 211
Val Pro Leu Thr Ile Gly Leu Ala Pro Leu Val Ala Ile Met Gln Thr
25 30 35

ttt tgg caa gtt acc ggc aaa gag cac 238
Phe Trp Gln Val Thr Gly Lys Glu His
40 45

```
<210> 644
<211> 46
<212> PRT
<213> Corynebacterium glutamicum
```

```
<400> 644
Val Asp Val Val Asp Ile Ala Arg Trp Gln Phe Gly Ile Thr Thr Val
  1             5             10             15
```

Tyr His Phe Ile Phe Val Pro Leu Thr Ile Gly Leu Ala Pro Leu Val
20 25 30

Ala Ile Met Gln Thr Phe Trp Gln Val Thr Gly Lys Glu His
35 40 45

```
<210> 645
<211> 1325
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (1)..(1302)
<223> FRXA01744
```

<400> 645
tgg tcg gaa tat tcg cgt ttc gtc ggt gat gtt ttc ggc gga ccg ctg 48
Trp Ser Glu Tyr Ser Arg Phe Val Gly Asp Val Phe Gly Gly Pro Leu
1 5 10 15

gct ttg gag ggt ctt atc gcg ttc ttc ctt gag tct gta ttc ctg gga 96

Ala	Leu	Glu	Gly	Leu	Ile	Ala	Phe	Phe	Leu	Glu	Ser	Val	Phe	Leu	Gly	
			20						25						30	
ctg	tgg	att	ttc	gga	tgg	ggg	aag	att	cct	ggt	tgg	ttg	cac	act	gca	144
Leu	Trp	Ile	Phe	Gly	Trp	Gly	Lys	Ile	Pro	Gly	Trp	Leu	His	Thr	Ala	
			35				40					45				
tcc	att	tgg	atc	gtt	gct	att	gcg	acg	aat	att	tct	gcc	tat	ttc	atc	192
Ser	Ile	Trp	Ile	Val	Ala	Ile	Ala	Thr	Asn	Ile	Ser	Ala	Tyr	Phe	Ile	
			50				55				60					
atc	gtg	gcc	aac	tcg	ttt	atg	cag	cat	ccg	gtg	ggt	gct	gag	tat	aac	240
Ile	Val	Ala	Asn	Ser	Phe	Met	Gln	His	Pro	Val	Gly	Ala	Glu	Tyr	Asn	
			65			70				75					80	
cct	gag	act	ggt	cgt	gcg	gag	ctt	act	gat	ttt	tgg	gct	ctt	ctc	aca	288
Pro	Glu	Thr	Gly	Arg	Ala	Glu	Leu	Thr	Asp	Phe	Trp	Ala	Leu	Leu	Thr	
				85					90					95		
aac	tcc	acc	gcg	ctg	gct	gcg	ttc	ccg	cat	gct	gtt	gcc	ggt	ggt	ttt	336
Asn	Ser	Thr	Ala	Leu	Ala	Ala	Phe	Pro	His	Ala	Val	Ala	Gly	Gly	Phe	
			100					105					110			
tta	aca	gct	gga	act	ttc	gtt	ctc	gga	att	tcg	ggt	tgg	tgg	att	att	384
Leu	Thr	Ala	Gly	Thr	Phe	Val	Leu	Gly	Ile	Ser	Gly	Trp	Trp	Ile	Ile	
			115				120					125				
cgt	gcg	cac	cgt	cag	gcc	aag	aag	gct	gag	tcg	gaa	atc	gag	tcg	aag	432
Arg	Ala	His	Arg	Gln	Ala	Lys	Lys	Ala	Glu	Ser	Glu	Ile	Glu	Ser	Lys	
			130			135					140					
cat	tcg	atg	cac	agg	ccc	gcg	ttg	tgg	gtt	ggt	tgg	tgg	acc	aca	gtt	480
His	Ser	Met	His	Arg	Pro	Ala	Leu	Trp	Val	Gly	Trp	Trp	Thr	Thr	Val	
					150				155						160	
gtc	tct	tcc	gtg	gcg	ctg	ttc	atc	act	ggc	gat	atc	cag	gcg	aag	ctc	528
Val	Ser	Ser	Val	Ala	Leu	Phe	Ile	Thr	Gly	Asp	Ile	Gln	Ala	Lys	Leu	
				165					170					175		
atg	ttc	gtg	caa	cag	cca	atg	aag	atg	gcg	tcg	gcg	gaa	tcc	ttg	tgt	576
Met	Phe	Val	Gln	Gln	Pro	Met	Lys	Met	Ala	Ser	Ala	Glu	Ser	Leu	Cys	
			180				185						190			
gaa	acc	gcc	aca	gat	cca	aac	ttc	tcc	att	ctg	aca	att	ggt	acg	cac	624
Glu	Thr	Ala	Thr	Asp	Pro	Asn	Phe	Ser	Ile	Leu	Thr	Ile	Gly	Thr	His	
			195				200					205				
aac	aac	tgc	gat	acg	gta	acc	cac	ctg	atc	gat	gtt	ccg	ttt	gtg	ctt	672
Asn	Asn	Cys	Asp	Thr	Val	Thr	His	Leu	Ile	Asp	Val	Pro	Phe	Val	Leu	
			210				215				220					
cca	ttc	ttg	gct	gaa	gga	aaa	ttc	acc	ggt	gtg	act	ttg	cag	ggt	gta	720
Pro	Phe	Leu	Ala	Glu	Gly	Lys	Phe	Thr	Gly	Val	Thr	Leu	Gln	Gly	Val	
			225			230				235					240	
aac	cag	ctc	caa	gct	gca	gcg	gag	caa	gca	tac	ggt	cct	ggc	aac	tac	768
Asn	Gln	Leu	Gln	Ala	Ala	Ala	Glu	Gln	Ala	Tyr	Gly	Pro	Gly	Asn	Tyr	
				245					250					255		
tcc	cct	aac	ttg	ttt	gtc	acc	tac	tgg	tca	ttc	cgc	gca	atg	atc	ggc	816
Ser	Pro	Asn	Leu	Phe	Val	Thr	Tyr	Trp	Ser	Phe	Arg	Ala	Met	Ile	Gly	

260	265	270	
ctg atg ctt ggt tct ttg gct atc gct gcg att gcg tgg ctg ttg ctg Leu Met Leu Gly Ser Leu Ala Ile Ala Ala Ile Ala Trp Leu Leu Leu 275 280 285			864
cgt aag aag cgc aca cca act gga aag att gct cgt ctg ttc cag atc Arg Lys Lys Arg Thr Pro Thr Gly Lys Ile Ala Arg Leu Phe Gln Ile 290 295 300			912
ggc agc ctc att gct atc ccg ttc cca ttc ttg gcc aac tct gct ggt Gly Ser Leu Ile Ala Ile Pro Phe Pro Phe Leu Ala Asn Ser Ala Gly 305 310 315 320			960
tgg atc ttc acc gag atg ggc cgc cag cct tgg gtg gtg cac ccg aac Trp Ile Phe Thr Glu Met Gly Arg Gln Pro Trp Val Val His Pro Asn 325 330 335			1008
cct gaa tct gcc ggc gat gcc cga aca gag atg atc cgg atg act gtt Pro Glu Ser Ala Gly Asp Ala Arg Thr Glu Met Ile Arg Met Thr Val 340 345 350			1056
gat atg ggt gta tct gat cat gcg cca tgg caa gtc tgg ctg act ctc Asp Met Gly Val Ser Asp His Ala Pro Trp Gln Val Trp Leu Thr Leu 355 360 365			1104
att ggc ttc acg att ctc tat ctc att ttg ttc gtg gtg tgg gtg tgg Ile Gly Phe Thr Ile Leu Tyr Leu Ile Leu Phe Val Val Trp Val Trp 370 375 380			1152
ctg att cgc cgc gca gtt ctg atc gga cca cca gag gaa ggc gct cca Leu Ile Arg Arg Ala Val Leu Ile Gly Pro Pro Glu Glu Gly Ala Pro 385 390 395 400			1200
tcc gtg gag gca aag act gga ccg gca acc ccg att ggt tca gat atg Ser Val Glu Ala Lys Thr Gly Pro Ala Thr Pro Ile Gly Ser Asp Met 405 410 415			1248
ccc atg aca ccg ctg caa ttt act gcc gct gcc cca acc aca ggt gaa Pro Met Thr Pro Leu Gln Phe Thr Ala Ala Pro Thr Thr Gly Glu 420 425 430			1296
aag gaa taaccatgga tctcaataacc ttt Lys Glu			1325

<210> 646

<211> 434

<212> PRT

<213> Corynebacterium glutamicum

<400> 646

Trp	Ser	Glu	Tyr	Ser	Arg	Phe	Val	Gly	Asp	Val	Phe	Gly	Gly	Pro	Leu
1				5				10						15	

Ala	Leu	Glu	Gly	Leu	Ile	Ala	Phe	Phe	Leu	Glu	Ser	Val	Phe	Leu	Gly
		20						25					30		

Leu	Trp	Ile	Phe	Gly	Trp	Gly	Lys	Ile	Pro	Gly	Trp	Leu	His	Thr	Ala
		35					40					45			

Ser Ile Trp Ile Val Ala Ile Ala Thr Asn Ile Ser Ala Tyr Phe Ile
 50 55 60
 Ile Val Ala Asn Ser Phe Met Gln His Pro Val Gly Ala Glu Tyr Asn
 65 70 75 80
 Pro Glu Thr Gly Arg Ala Glu Leu Thr Asp Phe Trp Ala Leu Leu Thr
 85 90 95
 Asn Ser Thr Ala Leu Ala Ala Phe Pro His Ala Val Ala Gly Gly Phe
 100 105 110
 Leu Thr Ala Gly Thr Phe Val Leu Gly Ile Ser Gly Trp Trp Ile Ile
 115 120 125
 Arg Ala His Arg Gln Ala Lys Lys Ala Glu Ser Glu Ile Glu Ser Lys
 130 135 140
 His Ser Met His Arg Pro Ala Leu Trp Val Gly Trp Trp Thr Thr Val
 145 150 155 160
 Val Ser Ser Val Ala Leu Phe Ile Thr Gly Asp Ile Gln Ala Lys Leu
 165 170 175
 Met Phe Val Gln Gln Pro Met Lys Met Ala Ser Ala Glu Ser Leu Cys
 180 185 190
 Glu Thr Ala Thr Asp Pro Asn Phe Ser Ile Leu Thr Ile Gly Thr His
 195 200 205
 Asn Asn Cys Asp Thr Val Thr His Leu Ile Asp Val Pro Phe Val Leu
 210 215 220
 Pro Phe Leu Ala Glu Gly Lys Phe Thr Gly Val Thr Leu Gln Gly Val
 225 230 235 240
 Asn Gln Leu Gln Ala Ala Ala Glu Gln Ala Tyr Gly Pro Gly Asn Tyr
 245 250 255
 Ser Pro Asn Leu Phe Val Thr Tyr Trp Ser Phe Arg Ala Met Ile Gly
 260 265 270
 Leu Met Leu Gly Ser Leu Ala Ile Ala Ala Ile Ala Trp Leu Leu Leu
 275 280 285
 Arg Lys Lys Arg Thr Pro Thr Gly Lys Ile Ala Arg Leu Phe Gln Ile
 290 295 300
 Gly Ser Leu Ile Ala Ile Pro Phe Pro Phe Leu Ala Asn Ser Ala Gly
 305 310 315 320
 Trp Ile Phe Thr Glu Met Gly Arg Gln Pro Trp Val Val His Pro Asn
 325 330 335
 Pro Glu Ser Ala Gly Asp Ala Arg Thr Glu Met Ile Arg Met Thr Val
 340 345 350
 Asp Met Gly Val Ser Asp His Ala Pro Trp Gln Val Trp Leu Thr Leu
 355 360 365

Ile Gly Phe Thr Ile Leu Tyr Leu Ile Leu Phe Val Val Trp Val Trp
 370 375 380

Leu Ile Arg Arg Ala Val Leu Ile Gly Pro Pro Glu Glu Gly Ala Pro
 385 390 395 400

Ser Val Glu Ala Lys Thr Gly Pro Ala Thr Pro Ile Gly Ser Asp Met
 405 410 415

Pro Met Thr Pro Leu Gln Phe Thr Ala Ala Ala Pro Thr Thr Gly Glu
 420 425 430

Lys Glu

<210> 647
 <211> 307
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(307)
 <223> RXA00379

<400> 647
 cgtgctggat aaacagcacc gccccgcagc agtggttcttg cgcgaaagtca cctccaaaga 60

tgtgttggat gttgcgttgc cattggtaga tgaggcctaa atg tct gag att gtg 115
 Met Ser Glu Ile Val
 1 5

gta gcc caa agc atc ggc cag cag ttt gct gac gtc gca gct tcc ggg 163
 Val Ala Gln Ser Ile Gly Gln Gln Phe Ala Asp Val Ala Ala Ser Gly
 10 15 20

cca ctg ttc ctt ggc atc ctt gcc gca gcg ctc gca ggt ctg gtg tct 211
 Pro Leu Phe Leu Gly Ile Leu Ala Ala Ala Leu Ala Gly Leu Val Ser
 25 30 35

ttt gcc agc ccg tgt gtt gtg ccg ttg gtg cca gga tat att tcc tac 259
 Phe Ala Ser Pro Cys Val Val Pro Leu Val Pro Gly Tyr Ile Ser Tyr
 40 45 50

ctc gcc ggc gtg gtc ggt ggg gaa gtg gaa tac agc gct cat gcc acc 307
 Leu Ala Gly Val Val Gly Gly Glu Val Glu Tyr Ser Ala His Ala Thr
 55 60 65

<210> 648
 <211> 69
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 648
 Met Ser Glu Ile Val Val Ala Gln Ser Ile Gly Gln Gln Phe Ala Asp
 1 5 10 15

Val Ala Ala Ser Gly Pro Leu Phe Leu Gly Ile Leu Ala Ala Ala Leu
 20 25 30

Ala Gly Leu Val Ser Phe Ala Ser Pro Cys Val Val Pro Leu Val Pro
 35 40 45

Gly Tyr Ile Ser Tyr Leu Ala Gly Val Val Gly Gly Glu Val Glu Tyr
 50 55 60

Ser Ala His Ala Thr
 65

<210> 649
 <211> 362
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(339)
 <223> RXA00385

<400> 649

ctt ggc gga gtg ttc gct ctc ggt tgg acc cct tgt ttg ggc ccc acc	48
Leu Gly Gly Val Phe Ala Leu Gly Trp Thr Pro Cys Leu Gly Pro Thr	
1 5 10 15	
ctg gct gcg atc atc tcc att tct gca ggt act gaa ggc atg acc gct	96
Leu Ala Ala Ile Ile Ser Ile Ser Ala Gly Thr Glu Gly Met Thr Ala	
20 25 30	
gcg cgt ggc gtg atc tta att gtg ggt tac tgc ctc gga ctg ggg ctg	144
Ala Arg Gly Val Ile Leu Ile Val Gly Tyr Cys Leu Gly Leu Gly Leu	
35 40 45	
ccg ttc ctg ctg atc gcg ttg ggc tcc agc aag gca ctc acc gga gtc	192
Pro Phe Leu Leu Ile Ala Leu Gly Ser Ser Lys Ala Leu Thr Gly Val	
50 55 60	
gag tgg ttg cgc aag cat tcc cgc acc ctg caa att atc ggc ggt gtg	240
Glu Trp Leu Arg Lys His Ser Arg Thr Leu Gln Ile Ile Gly Gly Val	
65 70 75 80	
ttt ttg atc ttg gtc gga gta gcg ttg ctc tct ggc tca tgg gca att	288
Phe Leu Ile Leu Val Gly Val Ala Leu Leu Ser Gly Ser Trp Ala Ile	
85 90 95	
ttt atc aac tgg gtc cgt cag tgg acc gtt gaa tac ggc gca aca ctg	336
Phe Ile Asn Trp Val Arg Gln Trp Thr Val Glu Tyr Gly Ala Thr Leu	
100 105 110	
ctc tagaaaaaga cttttagtag gaa	362
Leu	

<210> 650
 <211> 113
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 650

Leu Gly Gly Val Phe Ala Leu Gly Trp Thr Pro Cys Leu Gly Pro Thr
 1 5 10 15
 Leu Ala Ala Ile Ile Ser Ile Ser Ala Gly Thr Glu Gly Met Thr Ala
 20 25 30
 Ala Arg Gly Val Ile Leu Ile Val Gly Tyr Cys Leu Gly Leu Gly Leu
 35 40 45
 Pro Phe Leu Leu Ile Ala Leu Gly Ser Ser Lys Ala Leu Thr Gly Val
 50 55 60
 Glu Trp Leu Arg Lys His Ser Arg Thr Leu Gln Ile Ile Gly Gly Val
 65 70 75 80
 Phe Leu Ile Leu Val Gly Val Ala Leu Leu Ser Gly Ser Trp Ala Ile
 85 90 95
 Phe Ile Asn Trp Val Arg Gln Trp Thr Val Glu Tyr Gly Ala Thr Leu
 100 105 110

Leu

<210> 651

<211> 901

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(901)

<223> RXA01743

<400> 651

aggcaaagac tggaccggca accccgattg gttcagatat gcccatgaca ccgctgcaat 60
 ttactgccgc tgccccaacc acaggtgaaa aggaataacc atg gat ctc aat acc 115
 Met Asp Leu Asn Thr 5
 1
 ttt tgg ttt att ctc atc gca ttt ttg ttt gcg gga tac ttt ctc ctc 163
 Phe Trp Phe Ile Leu Ile Ala Phe Leu Phe Ala Gly Tyr Phe Leu Leu 20
 10 15
 gaa gga ttc gac ttc ggc gtc gga att ttg gca ccc atc atc ggt aaa 211
 Glu Gly Phe Asp Phe Gly Val Gly Ile Leu Ala Pro Ile Ile Gly Lys 35
 25 30
 gat tca gcg gct agg aac aca gtg atc cgt acg att ggc cct gtc tgg 259
 Asp Ser Ala Ala Arg Asn Thr Val Ile Arg Thr Ile Gly Pro Val Trp 50
 40 45
 gac gga aat gaa gtg tgg ctg atc gtg gca ggt ggc gct ttg ttt gct 307
 Asp Gly Asn Glu Val Trp Leu Ile Val Ala Gly Gly Ala Leu Phe Ala 65
 55 60
 gcc ttc cct gag tgg tac gca acg atg ttc tcc gga atg tat ctg ccg 355
 Ala Phe Pro Glu Trp Tyr Ala Thr Met Phe Ser Gly Met Tyr Leu Pro 85
 70 75 80

ctg ttc ctc gtg ctt gtg tcg ttg atc atg cgc gtg gtg ggc ctt gaa 403
 Leu Phe Leu Val Leu Val Ser Leu Ile Met Arg Val Val Gly Leu Glu
 90 95 100

tgg cgc aag aaa gtc gat gat cct cgt tgg caa aag tgg tct gac cgg 451
 Trp Arg Lys Lys Val Asp Asp Pro Arg Trp Gln Lys Trp Ser Asp Arg
 105 110 115

gcc atc ttt att ggt tct tgg act cca ccg ctg atg tgg gga ttc atc 499
 Ala Ile Phe Ile Gly Ser Trp Thr Pro Pro Leu Met Trp Gly Phe Ile
 120 125 130

ttc gcc aat att ttg cgt ggc atg ccc ctc aag gcg gat cac acc atc 547
 Phe Ala Asn Ile Leu Arg Gly Met Pro Leu Lys Ala Asp His Thr Ile
 135 140 145

gat gct gcg gca gcc ctt cct ggc atg gtc aac gtc ttc gcc att ctg 595
 Asp Ala Ala Ala Ala Leu Pro Gly Met Val Asn Val Phe Ala Ile Leu
 150 155 160 165

ggt gca ctt gcg ttc acc gca ctg ttc gcc ctt cat ggt ctc gca ttc 643
 Gly Ala Leu Ala Phe Thr Ala Leu Phe Ala Leu His Gly Leu Ala Phe
 170 175 180

atc cgc ctg aaa act gct ggt cgg gtg cgc acc gat gcg gcg aag gca 691
 Ile Arg Leu Lys Thr Ala Gly Arg Val Arg Thr Asp Ala Ala Lys Ala
 185 190 195

gct cca gta gtc gca ctt ctt gct gcg gtg act ggt gga cct ttc gtg 739
 Ala Pro Val Val Ala Leu Leu Ala Ala Val Thr Gly Gly Pro Phe Val
 200 205 210

ttg tgg gct gcc atc gca tac ggc cgt tcc tgg tcc tgg atc ctc gca 787
 Leu Trp Ala Ala Ile Ala Tyr Gly Arg Ser Trp Ser Trp Ile Leu Ala
 215 220 225

gtg ctg atc atc gca gcg gtt ctc ggt gga gct ttc gca ctg atc aaa 835
 Val Leu Ile Ile Ala Ala Val Leu Gly Gly Ala Phe Ala Leu Ile Lys
 230 235 240 245

gac cgc gat gga tta agc ttc ctg tcc act tcc gtc gct gtc atc ggt 883
 Asp Arg Asp Gly Leu Ser Phe Leu Ser Thr Ser Val Ala Val Ile Gly
 250 255 260

gtc gtt gca ctg ctg ttt 901
 Val Val Ala Leu Leu Phe
 265

<210> 652

<211> 267

<212> PRT

<213> Corynebacterium glutamicum

<400> 652

Met Asp Leu Asn Thr Phe Trp Phe Ile Leu Ile Ala Phe Leu Phe Ala
 1 5 10 15

Gly Tyr Phe Leu Leu Glu Gly Phe Asp Phe Gly Val Gly Ile Leu Ala
 20 25 30

Pro Ile Ile Gly Lys Asp Ser Ala Ala Arg Asn Thr Val Ile Arg Thr
 35 40 45
 Ile Gly Pro Val Trp Asp Gly Asn Glu Val Trp Leu Ile Val Ala Gly
 50 55 60
 Gly Ala Leu Phe Ala Ala Phe Pro Glu Trp Tyr Ala Thr Met Phe Ser
 65 70 75 80
 Gly Met Tyr Leu Pro Leu Phe Leu Val Leu Val Ser Leu Ile Met Arg
 85 90 95
 Val Val Gly Leu Glu Trp Arg Lys Lys Val Asp Asp Pro Arg Trp Gln
 100 105 110
 Lys Trp Ser Asp Arg Ala Ile Phe Ile Gly Ser Trp Thr Pro Pro Leu
 115 120 125
 Met Trp Gly Phe Ile Phe Ala Asn Ile Leu Arg Gly Met Pro Leu Lys
 130 135 140
 Ala Asp His Thr Ile Asp Ala Ala Ala Ala Leu Pro Gly Met Val Asn
 145 150 155 160
 Val Phe Ala Ile Leu Gly Ala Leu Ala Phe Thr Ala Leu Phe Ala Leu
 165 170 175
 His Gly Leu Ala Phe Ile Arg Leu Lys Thr Ala Gly Arg Val Arg Thr
 180 185 190
 Asp Ala Ala Lys Ala Ala Pro Val Val Ala Leu Leu Ala Ala Val Thr
 195 200 205
 Gly Gly Pro Phe Val Leu Trp Ala Ala Ile Ala Tyr Gly Arg Ser Trp
 210 215 220
 Ser Trp Ile Leu Ala Val Leu Ile Ile Ala Ala Val Leu Gly Gly Ala
 225 230 235 240
 Phe Ala Leu Ile Lys Asp Arg Asp Gly Leu Ser Phe Leu Ser Thr Ser
 245 250 255
 Val Ala Val Ile Gly Val Val Ala Leu Leu Phe
 260 265

<210> 653

<211> 1779

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1756)

<223> RXN02480

<400> 653

acctatgacc gctgtggcgc ctagggtcga cgggcacgtc gcccctcaga ggccccgagcc 60

gacaggccat gcacgcaagg gcagcaaagc atggttaatg atg acc acc acc gac 115

															Met Thr Thr Thr Asp 1 5									
cac aag cag ctg ggc att atg tac atc att atg tcc ttc agc ttc ttc																163								
His Lys Gln Leu Gly Ile Met Tyr Ile Ile Met Ser Phe Ser Phe Phe																								
				10					15					20										
ttc ctc ggt ggc ttg atg gcc ctg ctt atc cga gcg gag ctt ttc acc																211								
Phe Leu Gly Gly Leu Met Ala Leu Leu Ile Arg Ala Glu Leu Phe Thr																								
				25					30					35										
cct ggt ctg cag ttc ctg tct aat gag cag ttc aac cag ctg ttc acc																259								
Pro Gly Leu Gln Phe Leu Ser Asn Glu Gln Phe Asn Gln Leu Phe Thr																								
				40					45					50										
atg cac gga act gtc atg ctg ctg ctg tac gga act cca att gtt tgg																307								
Met His Gly Thr Val Met Leu Leu Leu Tyr Gly Thr Pro Ile Val Trp																								
				55					60					65										
ggt ttt gct aac tac gtc ctg cca ctt cag atc ggt gcg cct gac gta																355								
Gly Phe Ala Asn Tyr Val Leu Pro Leu Gln Ile Gly Ala Pro Asp Val																								
				70					75					80										
gct ttc cca cgt ttg aat gct ttc ggc ttc tgg atc acc acc gtc ggt																403								
Ala Phe Pro Arg Leu Asn Ala Phe Gly Phe Trp Ile Thr Thr Val Gly																								
				90					95					100										
ggt gtc gcg atg ctg acc ggc ttc ctg acc ccg ggt ggt gct gcc gac																451								
Gly Val Ala Met Leu Thr Gly Phe Leu Thr Pro Gly Gly Ala Ala Asp																								
				105					110					115										
ttc ggt tgg acc atg tac tcc cca ctg tct gac gca att cac tcc cca																499								
Phe Gly Trp Thr Met Tyr Ser Pro Leu Ser Asp Ala Ile His Ser Pro																								
				120					125					130										
ggc ctt ggc tct gac atg tgg att gtc ggt gtc ggt gca act ggt att																547								
Gly Leu Gly Ser Asp Met Trp Ile Val Gly Val Gly Ala Thr Gly Ile																								
				135					140					145										
ggc tcc gtt gct tcc gca att aac atg ctc acc acc atc ctc tgc ctc																595								
Gly Ser Val Ala Ser Ala Ile Asn Met Leu Thr Thr Ile Leu Cys Leu																								
				150					155					160										
cgc gca cct ggt atg acc atg ttc cgt atg cct att ttc acc tgg aat																643								
Arg Ala Pro Gly Met Thr Met Phe Arg Met Pro Ile Phe Thr Trp Asn																								
				170					175					180										
atc ttc gtt gtt tcc gtt ctt gct ctg ctg atc ttc cca ctg ctg ctc																691								
Ile Phe Val Val Ser Val Leu Ala Leu Leu Ile Phe Pro Leu Leu Leu																								
				185					190					195										
gct gct gca ctg ggt gtt ctg tat gac cgc aag ctt ggt gga cac ctg																739								
Ala Ala Ala Leu Gly Val Leu Tyr Asp Arg Lys Leu Gly Gly His Leu																								
				200					205					210										
tac gat cca gct aac ggc ggc tcc ctc ctg tgg cag cac ctg ttc tgg																787								
Tyr Asp Pro Ala Asn Gly Gly Ser Leu Leu Trp Gln His Leu Phe Trp																								
				215					220					225										
ttc ttc gga cac cct gag gtt tac gtt ctg gcg ctg ccg ttc ttc ggc																835								
Phe Phe Gly His Pro Glu Val Tyr Val Leu Ala Leu Pro Phe Phe Gly																								

230	235	240	245	
att gtt tct gag atc att cct gtg ttc tcc cgt aag cca atg ttc ggt Ile Val Ser Glu Ile Ile Pro Val Phe Ser Arg Lys Pro Met Phe Gly 250 255 260	883			
tac gtc ggc ctg atc ttc gca acc ttg tcc att ggt gca ctg tcc atg Tyr Val Gly Leu Ile Phe Ala Thr Leu Ser Ile Gly Ala Leu Ser Met 265 270 275	931			
gct gtg tgg gct cac cac atg ttc gtt act ggc gca gtt ttg ctt ccg Ala Val Trp Ala His His Met Phe Val Thr Gly Ala Val Leu Leu Pro 280 285 290	979			
ttc ttc tcc ttc atg acg ttc ctg att tcg gtt cct acc ggc gtt aag Phe Phe Ser Phe Met Thr Phe Leu Ile Ser Val Pro Thr Gly Val Lys 295 300 305	1027			
ttc ttc aac tgg gtt gga acc atg tgg aag ggt cac atc act tgg gaa Phe Phe Asn Trp Val Gly Thr Met Trp Lys Gly His Ile Thr Trp Glu 310 315 320 325	1075			
acc cca atg atc tgg tct gtt ggc ttc atg gct acc ttc ctc ttc ggt Thr Pro Met Ile Trp Ser Val Gly Phe Met Ala Thr Phe Leu Phe Gly 330 335 340	1123			
ggt ctg acc ggc att atg ctg gcg tcc cca cca ctg gac ttc cac ttg Gly Leu Thr Gly Ile Met Leu Ala Ser Pro Pro Leu Asp Phe His Leu 345 350 355	1171			
gct gac tcc tac ttc ctg atc gcg cac ttc cac tac acc ctc ttc ggt Ala Asp Ser Tyr Phe Leu Ile Ala His Phe His Tyr Thr Leu Phe Gly 360 365 370	1219			
acc gtg gtg ttc gca tcg tgt gca ggc gtt tac ttc tgg ttc ccg aag Thr Val Val Phe Ala Ser Cys Ala Gly Val Tyr Phe Trp Phe Pro Lys 375 380 385	1267			
atg act ggc cgc atg atg gac gag cgt ctt ggc aag atc cac ttc tgg Met Thr Gly Arg Met Met Asp Glu Arg Leu Gly Lys Ile His Phe Trp 390 395 400 405	1315			
ttg acc ttc gtc ggt ttc cac gga acc ttc ctc atc cag cac tgg gtg Leu Thr Phe Val Gly Phe His Gly Thr Phe Leu Ile Gln His Trp Val 410 415 420	1363			
ggc aac atg ggt atg cca cgt cgt tac gct gac tac ctg gat tct gat Gly Asn Met Gly Met Pro Arg Arg Tyr Ala Asp Tyr Leu Asp Ser Asp 425 430 435	1411			
ggt ttc acc atc tac aac cag atc tcc acc gtg ttc tac ttc ctg ctt Gly Phe Thr Ile Tyr Asn Gln Ile Ser Thr Val Phe Tyr Phe Leu Leu 440 445 450	1459			
ggc ctg tct gtc att cca ttc atc tgg aac gtc ttc aag tcc tgg cgc Gly Leu Ser Val Ile Pro Phe Ile Trp Asn Val Phe Lys Ser Trp Arg 455 460 465	1507			
tac ggt gag ctc gtt acc gtt gat gat cct tgg ggt tac ggc aac tcc Tyr Gly Glu Leu Val Thr Val Asp Asp Pro Trp Gly Tyr Gly Asn Ser 470 475 480 485	1555			

ctg gag tgg gca acc tcc tgc cct cct cct cgc cac aac ttc gca tcc 1603
Leu Glu Trp Ala Thr Ser Cys Pro Pro Pro Arg His Asn Phe Ala Ser
490 495 500

ttg cct cgt atc cgc tcc gag cgc cct gcg ttc gag ctg cac tac ccg 1651
Leu Pro Arg Ile Arg Ser Glu Arg Pro Ala Phe Glu Leu His Tyr Pro
505 510 515

cac atg att gaa cgc atg cgc gca gag gca cac act gga cat cac gat 1699
 His Met Ile Glu Arg Met Arg Ala Glu Ala His Thr Gly His His Asp
 520 525 530

gat att aat gct cca gaa ttg ggt acc gcc cca gcc ctt gca tct gac 1747
Asp Ile Asn Ala Pro Glu Leu Gly Thr Ala Pro Ala Leu Ala Ser Asp
535 540 545

tcc agc cgc taaaagcgtc tgatttaagt cgg 1779
Ser Ser Arg
550

<210> 654

<211> 552

<212> PRT

<213> Corynebacterium glutamicum

<400> 654

Met Thr Thr Thr Asp His Lys Gln Leu Gly Ile Met Tyr Ile Ile Met
1 5 10 15

Ser Phe Ser Phe Phe Phe Leu Gly Gly Leu Met Ala Leu Leu Ile Arg
20 25 30

Ala Glu Leu Phe Thr Pro Gly Leu Gln Phe Leu Ser Asn Glu Gln Phe
35 40 45

Asn Gln Leu Phe Thr Met His Gly Thr Val Met Leu Leu Leu Tyr Gly
50 55 60

Thr Pro Ile Val Trp Gly Phe Ala Asn Tyr Val Leu Pro Leu Gln Ile
65 70 75 80

Gly Ala Pro Asp Val Ala Phe Pro Arg Leu Asn Ala Phe Gly Phe Trp
85 90 95

Ile Thr Thr Val Gly Gly Val Ala Met Leu Thr Gly Phe Leu Thr Pro
100 105 110

Gly Gly Ala Ala Asp Phe Gly Trp Thr Met Tyr Ser Pro Leu Ser Asp
115 120 125

Ala Ile His Ser Pro Gly Leu Gly Ser Asp Met Trp Ile Val Gly Val
130 135 140

Gly Ala Thr Gly Ile Gly Ser Val Ala Ser Ala Ile Asn Met Leu Thr
145 150 155 160

Thr Ile Leu Cys Leu Arg Ala Pro Gly Met Thr Met Phe Arg Met Pro
165 170 175

Ile Phe Thr Trp Asn Ile Phe Val Val Ser Val Leu Ala Leu Leu Ile
 180 185 190
 Phe Pro Leu Leu Leu Ala Ala Ala Leu Gly Val Leu Tyr Asp Arg Lys
 195 200 205
 Leu Gly Gly His Leu Tyr Asp Pro Ala Asn Gly Gly Ser Leu Leu Trp
 210 215 220
 Gln His Leu Phe Trp Phe Phe Gly His Pro Glu Val Tyr Val Leu Ala
 225 230 235 240
 Leu Pro Phe Phe Gly Ile Val Ser Glu Ile Ile Pro Val Phe Ser Arg
 245 250 255
 Lys Pro Met Phe Gly Tyr Val Gly Leu Ile Phe Ala Thr Leu Ser Ile
 260 265 270
 Gly Ala Leu Ser Met Ala Val Trp Ala His His Met Phe Val Thr Gly
 275 280 285
 Ala Val Leu Leu Pro Phe Phe Ser Phe Met Thr Phe Leu Ile Ser Val
 290 295 300
 Pro Thr Gly Val Lys Phe Phe Asn Trp Val Gly Thr Met Trp Lys Gly
 305 310 315 320
 His Ile Thr Trp Glu Thr Pro Met Ile Trp Ser Val Gly Phe Met Ala
 325 330 335
 Thr Phe Leu Phe Gly Gly Leu Thr Gly Ile Met Leu Ala Ser Pro Pro
 340 345 350
 Leu Asp Phe His Leu Ala Asp Ser Tyr Phe Leu Ile Ala His Phe His
 355 360 365
 Tyr Thr Leu Phe Gly Thr Val Val Phe Ala Ser Cys Ala Gly Val Tyr
 370 375 380
 Phe Trp Phe Pro Lys Met Thr Gly Arg Met Met Asp Glu Arg Leu Gly
 385 390 395 400
 Lys Ile His Phe Trp Leu Thr Phe Val Gly Phe His Gly Thr Phe Leu
 405 410 415
 Ile Gln His Trp Val Gly Asn Met Gly Met Pro Arg Arg Tyr Ala Asp
 420 425 430
 Tyr Leu Asp Ser Asp Gly Phe Thr Ile Tyr Asn Gln Ile Ser Thr Val
 435 440 445
 Phe Tyr Phe Leu Leu Gly Leu Ser Val Ile Pro Phe Ile Trp Asn Val
 450 455 460
 Phe Lys Ser Trp Arg Tyr Gly Glu Leu Val Thr Val Asp Asp Pro Trp
 465 470 475 480
 Gly Tyr Gly Asn Ser Leu Glu Trp Ala Thr Ser Cys Pro Pro Pro Arg
 485 490 495
 His Asn Phe Ala Ser Leu Pro Arg Ile Arg Ser Glu Arg Pro Ala Phe

500 505 510
 Glu Leu His Tyr Pro His Met Ile Glu Arg Met Arg Ala Glu Ala His
 515 520 525
 Thr Gly His His Asp Asp Ile Asn Ala Pro Glu Leu Gly Thr Ala Pro
 530 535 540
 Ala Leu Ala Ser Asp Ser Ser Arg
 545 550

 <210> 655
 <211> 385
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
 <221> CDS
 <222> (101)..(385)
 <223> FRXA01919

 <400> 655
 acctatgacc gctgtggcgc ctagggtcga cgggcacgtc gcccctcaga ggcccagacc 60
 gacaggccat gcacgcaagg gcagcaaagc atgggtaatg atg acc acc acc gac 115
 Met Thr Thr Thr Asp
 1 5
 cac aag cag ctg ggc att atg tac atc att atg tcc ttc agc ttc ttt 163
 His Lys Gln Leu Gly Ile Met Tyr Ile Ile Met Ser Phe Ser Phe Phe
 10 15 20
 ttc ctc ggt ggc ttg atg gcc ctg ctt atc cga gcg gag ctt ttc acc 211
 Phe Leu Gly Gly Leu Met Ala Leu Leu Ile Arg Ala Glu Leu Phe Thr
 25 30 35
 cct ggt ctg cag ttc ctg tct aat gag cag ttc aac cag ctg ttc acc 259
 Pro Gly Leu Gln Phe Leu Ser Asn Glu Gln Phe Asn Gln Leu Phe Thr
 40 45 50
 atg cac gga act gtc atg ctg ctg ctg tac gga act cca att gtt tgg 307
 Met His Gly Thr Val Met Leu Leu Leu Tyr Gly Thr Pro Ile Val Trp
 55 60 65
 ggt ttt gct aac tac gtc ctg cca ctt cca acc acc ang caa gcc ttc 355
 Gly Phe Ala Asn Tyr Val Leu Pro Leu Pro Thr Thr Xaa Gln Ala Phe
 70 75 80 85
 tct aaa acc cgg gtg aac tct ccc agg gag 385
 Ser Lys Thr Arg Val Asn Ser Pro Arg Glu
 90 95

<210> 656
 <211> 95
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 656
 Met Thr Thr Thr Asp His Lys Gln Leu Gly Ile Met Tyr Ile Ile Met

1	5	10	15
Ser Phe Ser Phe Phe Phe Leu Gly Gly Leu Met Ala Leu Leu Ile Arg			
	20	25	30
Ala Glu Leu Phe Thr Pro Gly Leu Gln Phe Leu Ser Asn Glu Gln Phe			
	35	40	45
Asn Gln Leu Phe Thr Met His Gly Thr Val Met Leu Leu Leu Tyr Gly			
	50	55	60
Thr Pro Ile Val Trp Gly Phe Ala Asn Tyr Val Leu Pro Leu Pro Thr			
	65	70	75
			80
Thr Xaa Gln Ala Phe Ser Lys Thr Arg Val Asn Ser Pro Arg Glu			
	85	90	95

<210> 657

<211> 972

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(949)

<223> FRXA02480

<400> 657

```

tacgttctg cgctgccgtt cttcggcatt gtttctgaga tcattcctgt gttctcccgt 60
aagccaatgt tcgggttacg tcggcctgat cttcgcaacc ttg tcc att ggt gca 115
                                Leu Ser Ile Gly Ala
                                1 5
ctg tcc atg gct gtg tgg gct cac cac atg ttc gtt act ggc gca gtt 163
Leu Ser Met Ala Val Trp Ala His His Met Phe Val Thr Gly Ala Val
                                10 15 20
ttg ctt ccg ttc ttc tcc ttc atg acg ttc ctg att tcg gtt cct acc 211
Leu Leu Pro Phe Phe Ser Phe Met Thr Phe Leu Ile Ser Val Pro Thr
                                25 30 35
ggc gtt aag ttc ttc aac tgg gtt gga acc atg tgg aag ggt cac atc 259
Gly Val Lys Phe Phe Asn Trp Val Gly Thr Met Trp Lys Gly His Ile
                                40 45 50
act tgg gaa acc cca atg atc tgg tct gtt ggc ttc atg gct acc ttc 307
Thr Trp Glu Thr Pro Met Ile Trp Ser Val Gly Phe Met Ala Thr Phe
                                55 60 65
ctc ttc ggt ggt ctg acc ggc att atg ctg gcg tcc cca cca ctg gac 355
Leu Phe Gly Gly Leu Thr Gly Ile Met Leu Ala Ser Pro Pro Leu Asp
                                70 75 80 85
ttc cac ttg gct gac tcc tac ttc ctg atc gcg cac ttc cac tac acc 403
Phe His Leu Ala Asp Ser Tyr Phe Leu Ile Ala His Phe His Tyr Thr
                                90 95 100
ctc ttc ggt acc gtg gtg ttc gca tcg tgt gca ggc gtt tac ttc tgg 451
Leu Phe Gly Thr Val Val Phe Ala Ser Cys Ala Gly Val Tyr Phe Trp

```

105	110	115	
ttc ccg aag atg act ggc cgc atg atg gac gag cgt ctt ggc aag atc			499
Phe Pro Lys Met Thr Gly Arg Met Met Asp Glu Arg Leu Gly Lys Ile			
120	125	130	
cac ttc tgg ttg acc ttc gtc ggt ttc cac gga acc ttc ctc atc cag			547
His Phe Trp Leu Thr Phe Val Gly Phe His Gly Thr Phe Leu Ile Gln			
135	140	145	
cac tgg gtg ggc aac atg ggt atg cca cgt cgt tac gct gac tac ctg			595
His Trp Val Gly Asn Met Gly Met Pro Arg Arg Tyr Ala Asp Tyr Leu			
150	155	160	165
gat tct gat ggt ttc acc atc tac aac cag atc tcc acc gtg ttc tac			643
Asp Ser Asp Gly Phe Thr Ile Tyr Asn Gln Ile Ser Thr Val Phe Tyr			
170	175	180	
ttc ctg ctt ggc ctg tct gtc att cca ttc atc tgg aac gtc ttc aag			691
Phe Leu Leu Gly Leu Ser Val Ile Pro Phe Ile Trp Asn Val Phe Lys			
185	190	195	
tcc tgg cgc tac ggt gag ctc gtt acc gtt gat gat cct tgg ggt tac			739
Ser Trp Arg Tyr Gly Glu Leu Val Thr Val Asp Asp Pro Trp Gly Tyr			
200	205	210	
ggc aac tcc ctg gag tgg gca acc tcc tgc cct cct cct cgc cac aac			787
Gly Asn Ser Leu Glu Trp Ala Thr Ser Cys Pro Pro Pro Arg His Asn			
215	220	225	
ttc gca tcc ttg cct cgt atc cgc tcc gag cgc cct gcg ttc gag ctg			835
Phe Ala Ser Leu Pro Arg Ile Arg Ser Glu Arg Pro Ala Phe Glu Leu			
230	235	240	245
cac tac ccg cac atg att gaa cgc atg cgc gca gag gca cac act gga			883
His Tyr Pro His Met Ile Glu Arg Met Arg Ala Glu Ala His Thr Gly			
250	255	260	
cat cac gat gat att aat gct cca gaa ttg ggt acc gcc cca gcc ctt			931
His His Asp Asp Ile Asn Ala Pro Glu Leu Gly Thr Ala Pro Ala Leu			
265	270	275	
gca tct gac tcc agc cgc taaaagcgtc tgatttaagt cgg			972
Ala Ser Asp Ser Ser Arg			
280			

<210> 658

<211> 283

<212> PRT

<213> Corynebacterium glutamicum

<400> 658

Leu Ser Ile Gly Ala Leu Ser Met Ala Val Trp Ala His His Met Phe
 1 5 10 15

Val Thr Gly Ala Val Leu Leu Pro Phe Phe Ser Phe Met Thr Phe Leu
 20 25 30

Ile Ser Val Pro Thr Gly Val Lys Phe Phe Asn Trp Val Gly Thr Met
 35 40 45

Trp Lys Gly His Ile Thr Trp Glu Thr Pro Met Ile Trp Ser Val Gly
 50 55 60
 Phe Met Ala Thr Phe Leu Phe Gly Gly Leu Thr Gly Ile Met Leu Ala
 65 70 75 80
 Ser Pro Pro Leu Asp Phe His Leu Ala Asp Ser Tyr Phe Leu Ile Ala
 85 90 95
 His Phe His Tyr Thr Leu Phe Gly Thr Val Val Phe Ala Ser Cys Ala
 100 105 110
 Gly Val Tyr Phe Trp Phe Pro Lys Met Thr Gly Arg Met Met Asp Glu
 115 120 125
 Arg Leu Gly Lys Ile His Phe Trp Leu Thr Phe Val Gly Phe His Gly
 130 135 140
 Thr Phe Leu Ile Gln His Trp Val Gly Asn Met Gly Met Pro Arg Arg
 145 150 155 160
 Tyr Ala Asp Tyr Leu Asp Ser Asp Gly Phe Thr Ile Tyr Asn Gln Ile
 165 170 175
 Ser Thr Val Phe Tyr Phe Leu Leu Gly Leu Ser Val Ile Pro Phe Ile
 180 185 190
 Trp Asn Val Phe Lys Ser Trp Arg Tyr Gly Glu Leu Val Thr Val Asp
 195 200 205
 Asp Pro Trp Gly Tyr Gly Asn Ser Leu Glu Trp Ala Thr Ser Cys Pro
 210 215 220
 Pro Pro Arg His Asn Phe Ala Ser Leu Pro Arg Ile Arg Ser Glu Arg
 225 230 235 240
 Pro Ala Phe Glu Leu His Tyr Pro His Met Ile Glu Arg Met Arg Ala
 245 250 255
 Glu Ala His Thr Gly His His Asp Asp Ile Asn Ala Pro Glu Leu Gly
 260 265 270
 Thr Ala Pro Ala Leu Ala Ser Asp Ser Ser Arg
 275 280

<210> 659

<211> 735

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(712)

<223> FRXA02481

<400> 659

tgctaactac gtcctgccac ttcagatcgg tgcgcctgac gtagctttcc cacgttgaaa 60

tgctttcggc ttctgaatca ccaccgtcgg tgggtgcgcg atg ctg acc ggc ttc 115

	Met	Leu	Thr	Gly	Phe	
	1				5	
cta acc ccg ggt ggt gct gcc gac ttg ggt gga cca tgt act ccc cac						163
Leu Thr Pro Gly Gly Ala Ala Asp Leu Gly Gly Pro Cys Thr Pro His						
				10		20
tgt ctg acg caa ttc act ccc cag gcc ttg gtt cta aca tgt gga ttg						211
Cys Leu Thr Gln Phe Thr Pro Gln Ala Leu Val Leu Thr Cys Gly Leu						
				25		35
tcg ggt gtc ggt gca act ggt att ggc tcc gtt gct tcc gca att aac						259
Ser Gly Val Gly Ala Thr Gly Ile Gly Ser Val Ala Ser Ala Ile Asn						
				40		50
atg ctc acc acc atc ctc tgc ctc cgc gca cct ggt atg acc atg ttc						307
Met Leu Thr Thr Ile Leu Cys Leu Arg Ala Pro Gly Met Thr Met Phe						
				55		65
cgt atg cct att ttc acc tgg aat atc ttc gtt gtt tcc gtt ctt gct						355
Arg Met Pro Ile Phe Thr Trp Asn Ile Phe Val Val Ser Val Leu Ala						
				70		85
ctg ctg atc ttc cca ctg ctg ctc gct gct gca ctg ggt gtt ctg tat						403
Leu Leu Ile Phe Pro Leu Leu Leu Ala Ala Leu Gly Val Leu Tyr						
				90		100
gac cgc aag ctt ggt gga cac ctg tac gat cca gct aac ggc ggc tcc						451
Asp Arg Lys Leu Gly Gly His Leu Tyr Asp Pro Ala Asn Gly Gly Ser						
				105		115
ctc ctg tgg cag cac ctg ttc tgg ttc ttc gga cac cct gag gtt tac						499
Leu Leu Trp Gln His Leu Phe Trp Phe Phe Gly His Pro Glu Val Tyr						
				120		130
gtt ctg gcg ctg ccg ttc ttc ggc att gtt tct gag atc att cct gtg						547
Val Leu Ala Leu Pro Phe Phe Gly Ile Val Ser Glu Ile Ile Pro Val						
				135		145
ttc tcc cgt aag cca atg ttc ggg tta cgt cgg cct gat ctt cgc aac						595
Phe Ser Arg Lys Pro Met Phe Gly Leu Arg Arg Pro Asp Leu Arg Asn						
				150		165
ctt gtc cat tgg tgc act gtc cat ggc tgt gtg ggc tca cca cat gtt						643
Leu Val His Trp Cys Thr Val His Gly Cys Val Gly Ser Pro His Val						
				170		180
cgt tac tgg cgc agt ttt gct tcc gtt ctt ctc ctt cat gac gtt cct						691
Arg Tyr Trp Arg Ser Phe Ala Ser Val Leu Leu Leu His Asp Val Pro						
				185		195
gat ttc ggt tcc tac cgg cgt taagttcttc aactgggttg gaa						735
Asp Phe Gly Ser Tyr Arg Arg						
				200		

<210> 660

<211> 204

<212> PRT

<213> Corynebacterium glutamicum

<400> 660

Met Leu Thr Gly Phe Leu Thr Pro Gly Gly Ala Ala Asp Leu Gly Gly
 1 5 10 15

Pro Cys Thr Pro His Cys Leu Thr Gln Phe Thr Pro Gln Ala Leu Val
 20 25 30

Leu Thr Cys Gly Leu Ser Gly Val Gly Ala Thr Gly Ile Gly Ser Val
 35 40 45

Ala Ser Ala Ile Asn Met Leu Thr Thr Ile Leu Cys Leu Arg Ala Pro
 50 55 60

Gly Met Thr Met Phe Arg Met Pro Ile Phe Thr Trp Asn Ile Phe Val
 65 70 75 80

Val Ser Val Leu Ala Leu Leu Ile Phe Pro Leu Leu Leu Ala Ala Ala
 85 90 95

Leu Gly Val Leu Tyr Asp Arg Lys Leu Gly Gly His Leu Tyr Asp Pro
 100 105 110

Ala Asn Gly Gly Ser Leu Leu Trp Gln His Leu Phe Trp Phe Phe Gly
 115 120 125

His Pro Glu Val Tyr Val Leu Ala Leu Pro Phe Phe Gly Ile Val Ser
 130 135 140

Glu Ile Ile Pro Val Phe Ser Arg Lys Pro Met Phe Gly Leu Arg Arg.
 145 150 155 160

Pro Asp Leu Arg Asn Leu Val His Trp Cys Thr Val His Gly Cys Val
 165 170 175

Gly Ser Pro His Val Arg Tyr Trp Arg Ser Phe Ala Ser Val Leu Leu
 180 185 190

Leu His Asp Val Pro Asp Phe Gly Ser Tyr Arg Arg
 195 200

<210> 661

<211> 1200

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1177)

<223> RXA02140

<400> 661

aacacaagat atggaatcgg ctggcaaata ggctattctg cgaagataga aatgaccgta 60

aggtctctggt tttttgtgtg gacaggaagg cagaacacac gtg gaa cag caa aat 115
 Val Glu Gln Gln Asn
 1 5

aag cgt ggt tta aag cgc aag gcc ctg ctt ggc ggt gtc ttg ggc tta 163
 Lys Arg Gly Leu Lys Arg Lys Ala Leu Leu Gly Gly Val Leu Gly Leu
 10 15 20

ggt ggc ctc gcc atg gca ggc tgt gaa gtc gcc cct cct ggc ggt gtg	211
Gly Gly Leu Ala Met Ala Gly Cys Glu Val Ala Pro Pro Gly Gly Val	
25 30 35	
ctt gga gat ttc cta cgt atg ggt tgg cct gat ggc att acc cct gaa	259
Leu Gly Asp Phe Leu Arg Met Gly Trp Pro Asp Gly Ile Thr Pro Glu	
40 45 50	
gca gtg gcc atg ggt aac ttc tgg tca tgg gtc tgg gtt gct gcc tgg	307
Ala Val Ala Met Gly Asn Phe Trp Ser Trp Val Trp Val Ala Ala Trp	
55 60 65	
atc atc ggc atc atc atg tgg ggt cta ttc ctc acc gcc atc ttt gcc	355
Ile Ile Gly Ile Ile Met Trp Gly Leu Phe Leu Thr Ala Ile Phe Ala	
70 75 80 85	
tgg ggc gca aag agg gct gaa aag cgc ggc gag ggt gaa ttc cct aag	403
Trp Gly Ala Lys Arg Ala Glu Lys Arg Gly Glu Gly Glu Phe Pro Lys	
90 95 100	
cag ctc cag tac aac gtt cca ctt gag ctc gtt ctg acg atc gtt ccg	451
Gln Leu Gln Tyr Asn Val Pro Leu Glu Leu Val Leu Thr Ile Val Pro	
105 110 115	
atc atc att gtt atg gtg ctg ttc ttc ttc acc gtt caa act cag gac	499
Ile Ile Ile Val Met Val Leu Phe Phe Phe Thr Val Gln Thr Gln Asp	
120 125 130	
aag gtc acc gct ctg gat aag aac cca gag gtt acc gtg gac gtc acc	547
Lys Val Thr Ala Leu Asp Lys Asn Pro Glu Val Thr Val Asp Val Thr	
135 140 145	
gct tac cag tgg aac tgg aag ttc gga tac tcc gaa att gat ggc tca	595
Ala Tyr Gln Trp Asn Trp Lys Phe Gly Tyr Ser Glu Ile Asp Gly Ser	
150 155 160 165	
ctg gca cct ggt gga cag gat tac caa gga agc gac ccg gag cgt cag	643
Leu Ala Pro Gly Gly Gln Asp Tyr Gln Gly Ser Asp Pro Glu Arg Gln	
170 175 180	
gca gct gcc gag gct tcc aag aag gat cct tct gga gat aac cca att	691
Ala Ala Ala Glu Ala Ser Lys Lys Asp Pro Ser Gly Asp Asn Pro Ile	
185 190 195	
cac ggc aac tca aag tct gac gtt tct tac ctt gag ttc aac cga att	739
His Gly Asn Ser Lys Ser Asp Val Ser Tyr Leu Glu Phe Asn Arg Ile	
200 205 210	
gaa acc ctc gga acc act gat gaa atc cca gtg atg gtt ctt cct gtg	787
Glu Thr Leu Gly Thr Thr Asp Glu Ile Pro Val Met Val Leu Pro Val	
215 220 225	
aac acc cca atc gag ttc aac ctc gca tct gct gac gtt gca cac tcc	835
Asn Thr Pro Ile Glu Phe Asn Leu Ala Ser Ala Asp Val Ala His Ser	
230 235 240 245	
ttc tgg gtt cca gag ttc ctc ttc aag cga gat gct tac gca cac cct	883
Phe Trp Val Pro Glu Phe Leu Phe Lys Arg Asp Ala Tyr Ala His Pro	
250 255 260	

gag gca aac aag tcc cag cgt gtc ttc cag att gaa gag atc act gag 931
 Glu Ala Asn Lys Ser Gln Arg Val Phe Gln Ile Glu Glu Ile Thr Glu
 265 270 275
 gaa ggc gca ttc gtt ggt cgc tgt gca gaa atg tgc ggt act tac cac 979
 Glu Gly Ala Phe Val Gly Arg Cys Ala Glu Met Cys Gly Thr Tyr His
 280 285 290
 gca atg atg aac ttc gag ctt cgt gtc gtc gat cgc gat tcc ttc gct 1027
 Ala Met Met Asn Phe Glu Leu Arg Val Val Asp Arg Asp Ser Phe Ala
 295 300 305
 gag tac atc agc ttc cgt gac tcc aac cca gac gca acc aac gct cag 1075
 Glu Tyr Ile Ser Phe Arg Asp Ser Asn Pro Asp Ala Thr Asn Ala Gln
 310 315 320 325
 gca ctt gag cac att ggt caa gct cct tac gct act tcc act agc cca 1123
 Ala Leu Glu His Ile Gly Gln Ala Pro Tyr Ala Thr Ser Thr Ser Pro
 330 335 340
 ttc gtt tcc gat cgc acc gca acc cgc gac ggc gaa aac act cag agc 1171
 Phe Val Ser Asp Arg Thr Ala Thr Arg Asp Gly Glu Asn Thr Gln Ser
 345 350 355
 aac gct taagaaggag tggcgaaaaa atg 1200
 Asn Ala

<210> 662

<211> 359

<212> PRT

<213> Corynebacterium glutamicum

<400> 662

Val Glu Gln Gln Asn Lys Arg Gly Leu Lys Arg Lys Ala Leu Leu Gly
 1 5 10 15
 Gly Val Leu Gly Leu Gly Gly Leu Ala Met Ala Gly Cys Glu Val Ala
 20 25 30
 Pro Pro Gly Gly Val Leu Gly Asp Phe Leu Arg Met Gly Trp Pro Asp
 35 40 45
 Gly Ile Thr Pro Glu Ala Val Ala Met Gly Asn Phe Trp Ser Trp Val
 50 55 60
 Trp Val Ala Ala Trp Ile Ile Gly Ile Ile Met Trp Gly Leu Phe Leu
 65 70 75 80
 Thr Ala Ile Phe Ala Trp Gly Ala Lys Arg Ala Glu Lys Arg Gly Glu
 85 90 95
 Gly Glu Phe Pro Lys Gln Leu Gln Tyr Asn Val Pro Leu Glu Leu Val
 100 105 110
 Leu Thr Ile Val Pro Ile Ile Ile Val Met Val Leu Phe Phe Phe Thr
 115 120 125
 Val Gln Thr Gln Asp Lys Val Thr Ala Leu Asp Lys Asn Pro Glu Val
 130 135 140

Thr Val Asp Val Thr Ala Tyr Gln Trp Asn Trp Lys Phe Gly Tyr Ser
 145 150 155 160
 Glu Ile Asp Gly Ser Leu Ala Pro Gly Gly Gln Asp Tyr Gln Gly Ser
 165 170 175
 Asp Pro Glu Arg Gln Ala Ala Ala Glu Ala Ser Lys Lys Asp Pro Ser
 180 185 190
 Gly Asp Asn Pro Ile His Gly Asn Ser Lys Ser Asp Val Ser Tyr Leu
 195 200 205
 Glu Phe Asn Arg Ile Glu Thr Leu Gly Thr Thr Asp Glu Ile Pro Val
 210 215 220
 Met Val Leu Pro Val Asn Thr Pro Ile Glu Phe Asn Leu Ala Ser Ala
 225 230 235 240
 Asp Val Ala His Ser Phe Trp Val Pro Glu Phe Leu Phe Lys Arg Asp
 245 250 255
 Ala Tyr Ala His Pro Glu Ala Asn Lys Ser Gln Arg Val Phe Gln Ile
 260 265 270
 Glu Glu Ile Thr Glu Glu Gly Ala Phe Val Gly Arg Cys Ala Glu Met
 275 280 285
 Cys Gly Thr Tyr His Ala Met Met Asn Phe Glu Leu Arg Val Val Asp
 290 295 300
 Arg Asp Ser Phe Ala Glu Tyr Ile Ser Phe Arg Asp Ser Asn Pro Asp
 305 310 315 320
 Ala Thr Asn Ala Gln Ala Leu Glu His Ile Gly Gln Ala Pro Tyr Ala
 325 330 335
 Thr Ser Thr Ser Pro Phe Val Ser Asp Arg Thr Ala Thr Arg Asp Gly
 340 345 350
 Glu Asn Thr Gln Ser Asn Ala
 355

<210> 663

<211> 774

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(751)

<223> RXA02142

<400> 663

acgaaaagtt cccggaaggt cgattgaaaa gtttgccaat tgggggaaaa ttcgcatcaa 60

aagccgagtt caaactttca attgaaacgg ggggcttgaa gtg act ttg gcc aac 115

Val Thr Leu Ala Asn

1

5

caa aca gcc ata cta gat agc gtg acg agc gca gtt gga aat aca ggt	163
Gln Thr Ala Ile Leu Asp Ser Val Thr Ser Ala Val Gly Asn Thr Gly	
10 15 20	
atg gca gca cca caa cgt gtt gcg gca ctg aac cgt ccg aat atg gtc	211
Met Ala Ala Pro Gln Arg Val Ala Ala Leu Asn Arg Pro Asn Met Val	
25 30 35	
agt gtc ggc acc att gtg ttc ctg tct cag gaa tta atg ttc ttc gcc	259
Ser Val Gly Thr Ile Val Phe Leu Ser Gln Glu Leu Met Phe Phe Ala	
40 45 50	
ggg cta ttc gcg atg tac ttc gtg tcc cgt gcg aac gga ctg gca aat	307
Gly Leu Phe Ala Met Tyr Phe Val Ser Arg Ala Asn Gly Leu Ala Asn	
55 60 65	
gga tca tgg gga gag cag aca gat cac ctc aac gtg ccc tac gca ctg	355
Gly Ser Trp Gly Glu Gln Thr Asp His Leu Asn Val Pro Tyr Ala Leu	
70 75 80 85	
ttg att acg gtc att ctg gtg tct tcc tca gtg act tgc cag ttc gga	403
Leu Ile Thr Val Ile Leu Val Ser Ser Ser Val Thr Cys Gln Phe Gly	
90 95 100	
gtt ttt gcg gct gaa agg ggt gac gtt tac ggc ctc cgc aag tgg ttc	451
Val Phe Ala Glu Arg Gly Asp Val Tyr Gly Leu Arg Lys Trp Phe	
105 110 115	
ttg gtc acg att atc ctc gga tca atc ttc gtg atc gga'cag ggc tac	499
Leu Val Thr Ile Ile Leu Gly Ser Ile Phe Val Ile Gly Gln Gly Tyr	
120 125 130	
gag tac atc act ctc gta ggt cac gga ctt aca atc cag agc agt gtc	547
Glu Tyr Ile Thr Leu Val Gly His Gly Leu Thr Ile Gln Ser Ser Val	
135 140 145	
tac gga tcg gca ttc ttt att aca acc ggt ttc cac gca ctg cac gtg	595
Tyr Gly Ser Ala Phe Phe Ile Thr Thr Gly Phe His Ala Leu His Val	
150 155 160 165	
atc gcg ggt gtt atg gcc ttc gtt gtg gtt ctt atg aga atc cat aag	643
Ile Ala Gly Val Met Ala Phe Val Val Val Leu Met Arg Ile His Lys	
170 175 180	
tcg aag ttc act ccg gca cag gca acc gca gca atg gtt gtg tct tat	691
Ser Lys Phe Thr Pro Ala Gln Ala Thr Ala Ala Met Val Val Ser Tyr	
185 190 195	
tac tgg cac ttc gtt gac gtg gtc tgg atc ggc ctc ttc atc act att	739
Tyr Trp His Phe Val Asp Val Val Trp Ile Gly Leu Phe Ile Thr Ile	
200 205 210	
tac ttc att cag taggcagtaa ggaatcctca acg	774
Tyr Phe Ile Gln	
215	

<210> 664

<211> 217

<212> PRT

<213> Corynebacterium glutamicum

<400> 664

Val Thr Leu Ala Asn Gln Thr Ala Ile Leu Asp Ser Val Thr Ser Ala
 1 5 10 15

Val Gly Asn Thr Gly Met Ala Ala Pro Gln Arg Val Ala Ala Leu Asn
 20 25 30

Arg Pro Asn Met Val Ser Val Gly Thr Ile Val Phe Leu Ser Gln Glu
 35 40 45

Leu Met Phe Phe Ala Gly Leu Phe Ala Met Tyr Phe Val Ser Arg Ala
 50 55 60

Asn Gly Leu Ala Asn Gly Ser Trp Gly Glu Gln Thr Asp His Leu Asn
 65 70 75 80

Val Pro Tyr Ala Leu Leu Ile Thr Val Ile Leu Val Ser Ser Ser Val
 85 90 95

Thr Cys Gln Phe Gly Val Phe Ala Ala Glu Arg Gly Asp Val Tyr Gly
 100 105 110

Leu Arg Lys Trp Phe Leu Val Thr Ile Ile Leu Gly Ser Ile Phe Val
 115 120 125

Ile Gly Gln Gly Tyr Glu Tyr Ile Thr Leu Val Gly His Gly Leu Thr
 130 135 140

Ile Gln Ser Ser Val Tyr Gly Ser Ala Phe Phe Ile Thr Thr Gly Phe
 145 150 155 160

His Ala Leu His Val Ile Ala Gly Val Met Ala Phe Val Val Val Leu
 165 170 175

Met Arg Ile His Lys Ser Lys Phe Thr Pro Ala Gln Ala Thr Ala Ala
 180 185 190

Met Val Val Ser Tyr Tyr Trp His Phe Val Asp Val Val Trp Ile Gly
 195 200 205

Leu Phe Ile Thr Ile Tyr Phe Ile Gln
 210 215

<210> 665

<211> 1347

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1324)

<223> RXA02144

<400> 665

actcactcgg tagcttgggc ccagtggctg agggctctgtt catgtgggta ttcggcatct 60

tggtcctcgt ggccgccgct atgtggattg gatcacgttc atg agt aac aac aac 115

Met Ser Asn Asn Asn
 1 5

gac aaa cag tac aca acc caa gaa ctc aac gcg atg agc aat gag gat	163
Asp Lys Gln Tyr Thr Thr Gln Glu Leu Asn Ala Met Ser Asn Glu Asp	
10 15 20	
ctt gca cga ctt ggt aca gag ctg gac gac gtt acc att gca tac cgc	211
Leu Ala Arg Leu Gly Thr Glu Leu Asp Asp Val Thr Ile Ala Tyr Arg	
25 30 35	
aag gaa cgt ttc cca atc gct aat gac cca gct gag aag cgc gct gca	259
Lys Glu Arg Phe Pro Ile Ala Asn Asp Pro Ala Glu Lys Arg Ala Ala	
40 45 50	
cgt gca gtt act ttc tgg cta gtc ctc ggc atc att ggt gga ctt ggg	307
Arg Ala Val Thr Phe Trp Leu Val Leu Gly Ile Ile Gly Gly Leu Gly	
55 60 65	
ttc ctg gct acc tac att ttc tgg cct tgg gag tac aag gca cac gga	355
Phe Leu Ala Thr Tyr Ile Phe Trp Pro Trp Glu Tyr Lys Ala His Gly	
70 75 80 85	
gat gaa ggt ctc ctg gcg tac acc ttg tac acc cca atg ctg ggt att	403
Asp Glu Gly Leu Leu Ala Tyr Thr Leu Tyr Thr Pro Met Leu Gly Ile	
90 95 100	
act tcc ggt ctt tgc atc ctg tcc ctg gga ttt gca gtt gtc ctt tat	451
Thr Ser Gly Leu Cys Ile Leu Ser Leu Gly Phe Ala Val Val Leu Tyr	
105 110 115	
gtc aag aag ttc att cca gag gaa atc gca gta cag cgt cgc cac gac	499
Val Lys Lys Phe Ile Pro Glu Glu Ile Ala Val Gln Arg Arg His Asp	
120 125 130	
ggt cct tct gaa gaa gtt gac cgc cgc acc atc gtt gca ctt ctc aat	547
Gly Pro Ser Glu Glu Val Asp Arg Arg Thr Ile Val Ala Leu Leu Asn	
135 140 145	
gac tct tgg cag acc tct act ctt ggt cgt cgc aag ctg atc atg gga	595
Asp Ser Trp Gln Thr Ser Thr Leu Gly Arg Arg Lys Leu Ile Met Gly	
150 155 160 165	
ctt gca ggt ggc gga gca gta ctg gcc ggc ctg acc atc atc gct cca	643
Leu Ala Gly Gly Gly Ala Val Leu Ala Gly Leu Thr Ile Ile Ala Pro	
170 175 180	
atg ggc ggt atg atc aag aac cct tgg aat cct aag gaa ggc cca atg	691
Met Gly Gly Met Ile Lys Asn Pro Trp Asn Pro Lys Glu Gly Pro Met	
185 190 195	
gac gtt cag ggt gac ggc acc ctg tgg act tcc ggt tgg act ctc gtt	739
Asp Val Gln Gly Asp Gly Thr Leu Trp Thr Ser Gly Trp Thr Leu Val	
200 205 210	
gag aac gac gtc aag gtt tac ctc ggc cgc gac act gca gca att gcg	787
Glu Asn Asp Val Lys Val Tyr Leu Gly Arg Asp Thr Ala Ala Ile Ala	
215 220 225	
gag tcc cac acc gat gca acc ggt gag cac tgg tca acc act ggt gtt	835
Glu Ser His Thr Asp Ala Thr Gly Glu His Trp Ser Thr Thr Gly Val	
230 235 240 245	

tcc cgc ctg gtt cgt atg cgc cca gaa gat ctg gca gca gca tcc atg 883
 Ser Arg Leu Val Arg Met Arg Pro Glu Asp Leu Ala Ala Ala Ser Met
 250 255 260

gaa act gtc ttc cca ctt cca gct gaa atg gtg aac gac ggt gct gaa 931
 Glu Thr Val Phe Pro Leu Pro Ala Glu Met Val Asn Asp Gly Ala Glu
 265 270 275

tac gat cct gcg aag gac gtc tac gag cac caa atg cac tcg gtg cac 979
 Tyr Asp Pro Ala Lys Asp Val Tyr Glu His Gln Met His Ser Val His
 280 285 290

ggc cca cgc aac gca gtt atg ttg atc cgt ctc cgt acc gct gac gct 1027
 Gly Pro Arg Asn Ala Val Met Leu Ile Arg Leu Arg Thr Ala Asp Ala
 295 300 305

gaa aag gtt atc gaa cgc gaa ggc cag gag tcc ttc cac tac ggt gac 1075
 Glu Lys Val Ile Glu Arg Glu Gly Gln Glu Ser Phe His Tyr Gly Asp
 310 315 320 325

tac tac gct tac tcc aag att tgt aca cac att ggt tgc cca acc tca 1123
 Tyr Tyr Ala Tyr Ser Lys Ile Cys Thr His Ile Gly Cys Pro Thr Ser
 330 335 340

ctg tac gag gct cag acc aat cgt att ctg tgc cca tgt cac cag tcg 1171
 Leu Tyr Glu Ala Gln Thr Asn Arg Ile Leu Cys Pro Cys His Gln Ser
 345 350 355

cag ttt gac gca ttg cac tac gga aag cca gtc ttt gga cct gct gcc 1219
 Gln Phe Asp Ala Leu His Tyr Gly Lys Pro Val Phe Gly Pro Ala Ala
 360 365 370

cgt gca ctg cca cag ctg cca att acc gtt gat gaa gag ggc tac ctc 1267
 Arg Ala Leu Pro Gln Leu Pro Ile Thr Val Asp Glu Glu Gly Tyr Leu
 375 380 385

atc gcc gct ggt aac ttc att gag cca ctc ggc cct gca ttc tgg gag 1315
 Ile Ala Ala Gly Asn Phe Ile Glu Pro Leu Gly Pro Ala Phe Trp Glu
 390 395 400 405

cgt aag tca tgagtctagc taccgtggga aac 1347
 Arg Lys Ser

<210> 666

<211> 408

<212> PRT

<213> Corynebacterium glutamicum

<400> 666

Met Ser Asn Asn Asn Asp Lys Gln Tyr Thr Thr Gln Glu Leu Asn Ala
 1 5 10 15

Met Ser Asn Glu Asp Leu Ala Arg Leu Gly Thr Glu Leu Asp Asp Val
 20 25 30

Thr Ile Ala Tyr Arg Lys Glu Arg Phe Pro Ile Ala Asn Asp Pro Ala
 35 40 45

Glu Lys Arg Ala Ala Arg Ala Val Thr Phe Trp Leu Val Leu Gly Ile

50	55	60
Ile Gly Gly Leu Gly Phe Leu Ala Thr Tyr Ile Phe Trp Pro Trp Glu 65 70 75 80		
Tyr Lys Ala His Gly Asp Glu Gly Leu Leu Ala Tyr Thr Leu Tyr Thr 85 90 95		
Pro Met Leu Gly Ile Thr Ser Gly Leu Cys Ile Leu Ser Leu Gly Phe 100 105 110		
Ala Val Val Leu Tyr Val Lys Lys Phe Ile Pro Glu Glu Ile Ala Val 115 120 125		
Gln Arg Arg His Asp Gly Pro Ser Glu Glu Val Asp Arg Arg Thr Ile 130 135 140		
Val Ala Leu Leu Asn Asp Ser Trp Gln Thr Ser Thr Leu Gly Arg Arg 145 150 155 160		
Lys Leu Ile Met Gly Leu Ala Gly Gly Gly Ala Val Leu Ala Gly Leu 165 170 175		
Thr Ile Ile Ala Pro Met Gly Gly Met Ile Lys Asn Pro Trp Asn Pro 180 185 190		
Lys Glu Gly Pro Met Asp Val Gln Gly Asp Gly Thr Leu Trp Thr Ser 195 200 205		
Gly Trp Thr Leu Val Glu Asn Asp Val Lys Val Tyr Leu Gly Arg Asp 210 215 220		
Thr Ala Ala Ile Ala Glu Ser His Thr Asp Ala Thr Gly Glu His Trp 225 230 235 240		
Ser Thr Thr Gly Val Ser Arg Leu Val Arg Met Arg Pro Glu Asp Leu 245 250 255		
Ala Ala Ala Ser Met Glu Thr Val Phe Pro Leu Pro Ala Glu Met Val 260 265 270		
Asn Asp Gly Ala Glu Tyr Asp Pro Ala Lys Asp Val Tyr Glu His Gln 275 280 285		
Met His Ser Val His Gly Pro Arg Asn Ala Val Met Leu Ile Arg Leu 290 295 300		
Arg Thr Ala Asp Ala Glu Lys Val Ile Glu Arg Glu Gly Gln Glu Ser 305 310 315 320		
Phe His Tyr Gly Asp Tyr Tyr Ala Tyr Ser Lys Ile Cys Thr His Ile 325 330 335		
Gly Cys Pro Thr Ser Leu Tyr Glu Ala Gln Thr Asn Arg Ile Leu Cys 340 345 350		
Pro Cys His Gln Ser Gln Phe Asp Ala Leu His Tyr Gly Lys Pro Val 355 360 365		
Phe Gly Pro Ala Ala Arg Ala Leu Pro Gln Leu Pro Ile Thr Val Asp 370 375 380		

Glu Glu Gly Tyr Leu Ile Ala Ala Gly Asn Phe Ile Glu Pro Leu Gly
 385 390 395 400

Pro Ala Phe Trp Glu Arg Lys Ser
 405

<210> 667
 <211> 1053
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1030)
 <223> RXA02740

<400> 667
 aacgcaaggt gcacactcac cgcagggata tttaaataat aaggactcac aacttaaata 60
 tatgagtgat ttgaaaatgc aacgttctgg aggagaaccc ttg gac acg atc aag 115
 Leu Asp Thr Ile Lys
 1 5
 gcc tat att gcg cta acg aag ccc agg gtt att gaa ctc ctc ctt gtc 163
 Ala Tyr Ile Ala Leu Thr Lys Pro Arg Val Ile Glu Leu Leu Leu Val
 10 15 20
 gcc aca atc ccc aca atg ctt cag gct gaa cgc ggt gag aac aac att 211
 Ala Thr Ile Pro Thr Met Leu Gln Ala Glu Arg Gly Glu Asn Asn Ile
 25 30 35
 gtg ctc atc ttg ctg act gtg ttc ggt ggc tgg atg ggt gcg gcc gcc 259
 Val Leu Ile Leu Leu Thr Val Phe Gly Gly Trp Met Gly Ala Ala Ala
 40 45 50
 gcc aac acc ttc aac atg gtg gca gac tcc gat att gat cag cgc atg 307
 Ala Asn Thr Phe Asn Met Val Ala Asp Ser Asp Ile Asp Gln Arg Met
 55 60 65
 gga cgc act agg gct cgc cct ttg gtg cgc cac acc gtg agt aat cgc 355
 Gly Arg Thr Arg Ala Arg Pro Leu Val Arg His Thr Val Ser Asn Arg
 70 75 80 85
 gac gcc tcc att ttt gcg tgg gtc ctg aca gtg gcc agc ttc ttg tgg 403
 Asp Ala Ser Ile Phe Ala Trp Val Leu Thr Val Ala Ser Phe Leu Trp
 90 95 100
 ctg tgg ctg ctg tgc gat tgc atg ctc gcc ggc atc ttc gtg ttg atc 451
 Leu Trp Leu Leu Cys Asp Ser Met Leu Ala Gly Ile Phe Val Leu Ile
 105 110 115
 acg att ttc ttc tac att ttt gtc tac acc aag tgg ctg aag cgc cgc 499
 Thr Ile Phe Phe Tyr Ile Phe Val Tyr Thr Lys Trp Leu Lys Arg Arg
 120 125 130
 acg cac atg aat atc gtg tgg ggc gga gcc gca ggt tgt atg cca gtg 547
 Thr His Met Asn Ile Val Trp Gly Gly Ala Ala Gly Cys Met Pro Val
 135 140 145

ctc gtc ggc tgg gca gtg atc gtt gat cag ttt gag cca ggc gtt cca 595
 Leu Val Gly Trp Ala Val Ile Val Asp Gln Phe Glu Pro Gly Val Pro
 150 155 160 165

cag cag tgg tgg cag gca att gtc ctg ttc atg gtg att ttc ttc tgg 643
 Gln Gln Trp Trp Gln Ala Ile Val Leu Phe Met Val Ile Phe Phe Trp
 170 175 180

acc cca cct cac acc tgg gct ctg gcc atg aag tac cgc gaa gac tac 691
 Thr Pro Pro His Thr Trp Ala Leu Ala Met Lys Tyr Arg Glu Asp Tyr
 185 190 195

aag gcg gct ggc gtc cca atg ctt cct gtc gtg cgc acc cca gtc cag 739
 Lys Ala Ala Gly Val Pro Met Leu Pro Val Val Arg Thr Pro Val Gln
 200 205 210

gtc acc gca caa atc gtg tgg tac tcc gtg gca act gtg ctg acc acc 787
 Val Thr Ala Gln Ile Val Trp Tyr Ser Val Ala Thr Val Leu Thr Thr
 215 220 225

ttc ttg ctc atc cca gca act ggt tgg atc tac gca gcg atc gcc gtc 835
 Phe Leu Leu Ile Pro Ala Thr Gly Trp Ile Tyr Ala Ala Ile Ala Val
 230 235 240 245

att tcc ggc gtc acc ttc ttg ttc atg gcc atc aag ctg cac ctc ggc 883
 Ile Ser Gly Val Thr Phe Leu Phe Met Ala Ile Lys Leu His Leu Gly
 250 255 260

atc aaa aac ggt ggc aag gtc aag cct ctg aag ctg ttt att ttg tcc 931
 Ile Lys Asn Gly Gly Lys Val Lys Pro Leu Lys Leu Phe Ile Leu Ser
 265 270 275

aac aac tac ttg gca gtc ctc ttc gtg gca ttg tcc gtc gac gcg gtc 979
 Asn Asn Tyr Leu Ala Val Leu Phe Val Ala Leu Ser Val Asp Ala Val
 280 285 290

ctc ggc ctt gag acc atc ggc gag atg ctc ggc tgg acc acc acc ttc 1027
 Leu Gly Leu Glu Thr Ile Gly Glu Met Leu Gly Trp Thr Thr Thr Phe
 295 300 305

ttc taaaagcttg cttttcgacg aaa 1053
 Phe
 310

<210> 668

<211> 310

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 668

Leu Asp Thr Ile Lys Ala Tyr Ile Ala Leu Thr Lys Pro Arg Val Ile
 1 5 10 15

Glu Leu Leu Leu Val Ala Thr Ile Pro Thr Met Leu Gln Ala Glu Arg
 20 25 30

Gly Glu Asn Asn Ile Val Leu Ile Leu Leu Thr Val Phe Gly Gly Trp
 35 40 45

Met Gly Ala Ala Ala Ala Asn Thr Phe Asn Met Val Ala Asp Ser Asp

50	55	60
Ile Asp Gln Arg Met Gly Arg Thr Arg Ala Arg Pro Leu Val Arg His 65 70 75 80		
Thr Val Ser Asn Arg Asp Ala Ser Ile Phe Ala Trp Val Leu Thr Val 85 90 95		
Ala Ser Phe Leu Trp Leu Trp Leu Leu Cys Asp Ser Met Leu Ala Gly 100 105 110		
Ile Phe Val Leu Ile Thr Ile Phe Phe Tyr Ile Phe Val Tyr Thr Lys 115 120 125		
Trp Leu Lys Arg Arg Thr His Met Asn Ile Val Trp Gly Gly Ala Ala 130 135 140		
Gly Cys Met Pro Val Leu Val Gly Trp Ala Val Ile Val Asp Gln Phe 145 150 155 160		
Glu Pro Gly Val Pro Gln Gln Trp Trp Gln Ala Ile Val Leu Phe Met 165 170 175		
Val Ile Phe Phe Trp Thr Pro Pro His Thr Trp Ala Leu Ala Met Lys 180 185 190		
Tyr Arg Glu Asp Tyr Lys Ala Ala Gly Val Pro Met Leu Pro Val Val 195 200 205		
Arg Thr Pro Val Gln Val Thr Ala Gln Ile Val Trp Tyr Ser Val Ala 210 215 220		
Thr Val Leu Thr Thr Phe Leu Leu Ile Pro Ala Thr Gly Trp Ile Tyr 225 230 235 240		
Ala Ala Ile Ala Val Ile Ser Gly Val Thr Phe Leu Phe Met Ala Ile 245 250 255		
Lys Leu His Leu Gly Ile Lys Asn Gly Gly Lys Val Lys Pro Leu Lys 260 265 270		
Leu Phe Ile Leu Ser Asn Asn Tyr Leu Ala Val Leu Phe Val Ala Leu 275 280 285		
Ser Val Asp Ala Val Leu Gly Leu Glu Thr Ile Gly Glu Met Leu Gly 290 295 300		
Trp Thr Thr Thr Phe Phe 305 310		

<210> 669

<211> 1161

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1138)

<223> RXA02743

atataccttaa aagttcccgg gagtttcagt ggcaaataacc accacttcca taccgggaac															60
aattgtataa aactagccat gacctgctag gatcagcgac															115
Val Ser Thr Ser Asp															1
gct ccc tca aat aat cca gtt gag ttg aag ccc att act ttc tgg gca															163
Ala Pro Ser Asn Asn Pro Val Glu Leu Lys Pro Ile Thr Phe Trp Ala															10
ccg acc atc aaa gtg cag cgc att ctc gcg ctc cta ctg ttg att ttc															211
Pro Thr Ile Lys Val Gln Arg Ile Leu Ala Leu Leu Leu Ile Phe															25
cag gga ggc atc acc gtt acg ggc tct atc gtc cgt gtc aca ggc tcc															259
Gln Gly Gly Ile Thr Val Thr Gly Ser Ile Val Arg Val Thr Gly Ser															40
ggc ctc ggt tgt gat acc tgg cca cta tgc cac gaa ggt tca cta gtc															307
Gly Leu Gly Cys Asp Thr Trp Pro Leu Cys His Glu Gly Ser Leu Val															55
cca gtc gca ggc gca gca cca tgg atc cac cag gca gtg gaa ttt ggt															355
Pro Val Ala Gly Ala Ala Pro Trp Ile His Gln Ala Val Glu Phe Gly															70
aac cgc atg ctc act ttc gtg ctt gct gcc gca gcg ctt gcg ttg ttc															403
Asn Arg Met Leu Thr Phe Val Leu Ala Ala Ala Leu Ala Leu Phe															90
att gca gtt ctt ggc gca aaa cgc cgc cgc gag atc ctg gtc cat tcc															451
Ile Ala Val Leu Gly Ala Lys Arg Arg Arg Glu Ile Leu Val His Ser															105
ttc atc cag ggt ttg ggc atc atc ttg cag gct gtc atc ggt ggc atc															499
Phe Ile Gln Gly Leu Gly Ile Ile Leu Gln Ala Val Ile Gly Gly Ile															120
acc gtg ctg gtt gat ttg cac tgg tac gcc gtt gct ttg cac ttc ctg															547
Thr Val Leu Val Asp Leu His Trp Tyr Ala Val Ala Leu His Phe Leu															135
cca tcc atg atc ctt gtt ttc atg gcc gcg att ttg tac acc cgc atc															595
Pro Ser Met Ile Leu Val Phe Met Ala Ala Ile Leu Tyr Thr Arg Ile															150
ggc gag ccc gat gac ggc gag att acc acc aca ttc ccc acg tgg atc															643
Gly Glu Pro Asp Asp Gly Glu Ile Thr Thr Thr Phe Pro Thr Trp Ile															170
cgc aat gta gct gtc att ggt gca gta gcg ctc tcc gta gta ctg atc															691
Arg Asn Val Ala Val Ile Gly Ala Val Ala Leu Ser Val Val Leu Ile															185
acc ggc acc atg acc acc ggc gct ggc gtt cac tct ggc gat gca tca															739
Thr Gly Thr Met Thr Thr Gly Ala Gly Val His Ser Gly Asp Ala Ser															200
atc acc atg gat gat cgc ctc gat gtc agc atc gac ttg atg gcc cac															787
Ile Thr Met Asp Asp Arg Leu Asp Val Ser Ile Asp Leu Met Ala His															

215	220	225	
atc cac ggc tac agc atg tac atc tac ctc ttc ttc acc ctc atc gtg			835
Ile His Gly Tyr Ser Met Tyr Ile Tyr Leu Phe Phe Thr Leu Ile Val			
230	235	240	245
gtc gcc ggt ctg tac aag gca aaa acc acc aag cac aac aag cag ctt			883
Val Ala Gly Leu Tyr Lys Ala Lys Thr Thr Lys His Asn Lys Gln Leu			
	250	255	260
ggc ctc atg ctg att ctg ttc att ctg att cag gca ggt atc ggc atc			931
Gly Leu Met Leu Ile Leu Phe Ile Leu Ile Gln Ala Gly Ile Gly Ile			
	265	270	275
ttg cag tac cgc atg ggt gtg cca cgc tgg agc atc cca ttc cac atc			979
Leu Gln Tyr Arg Met Gly Val Pro Arg Trp Ser Ile Pro Phe His Ile			
	280	285	290
gca atg tct tct gtc gtt gtt gcc ttc act tcc ctt ctg tgg gcg cag			1027
Ala Met Ser Ser Val Val Val Ala Phe Thr Ser Leu Leu Trp Ala Gln			
	295	300	305
ggt cgt ata cgc gtc ggc ggt aaa gcc acc gtt act ggt tct gtt gat			1075
Gly Arg Ile Arg Val Gly Gly Lys Ala Thr Val Thr Gly Ser Val Asp			
	310	315	320
ggc gat att aag aac gag atc att acg aac ccc ttt gag aag aaa tca			1123
Gly Asp Ile Lys Asn Glu Ile Ile Thr Asn Pro Phe Glu Lys Lys Ser			
	330	335	340
aag cag cct gtt aaa taacacgcaa ctgtatcggt aaa			1161
Lys Gln Pro Val Lys			
	345		
<210> 670			
<211> 346			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 670			
Val Ser Thr Ser Asp Ala Pro Ser Asn Asn Pro Val Glu Leu Lys Pro			
1	5	10	15
Ile Thr Phe Trp Ala Pro Thr Ile Lys Val Gln Arg Ile Leu Ala Leu			
	20	25	30
Leu Leu Leu Ile Phe Gln Gly Gly Ile Thr Val Thr Gly Ser Ile Val			
	35	40	45
Arg Val Thr Gly Ser Gly Leu Gly Cys Asp Thr Trp Pro Leu Cys His			
	50	55	60
Glu Gly Ser Leu Val Pro Val Ala Gly Ala Ala Pro Trp Ile His Gln			
	65	70	75
Ala Val Glu Phe Gly Asn Arg Met Leu Thr Phe Val Leu Ala Ala Ala			
	85	90	95
Ala Leu Ala Leu Phe Ile Ala Val Leu Gly Ala Lys Arg Arg Arg Glu			
	100	105	110

Ile Leu Val His Ser Phe Ile Gln Gly Leu Gly Ile Ile Leu Gln Ala
 115 120 125
 Val Ile Gly Gly Ile Thr Val Leu Val Asp Leu His Trp Tyr Ala Val
 130 135 140
 Ala Leu His Phe Leu Pro Ser Met Ile Leu Val Phe Met Ala Ala Ile
 145 150 155 160
 Leu Tyr Thr Arg Ile Gly Glu Pro Asp Asp Gly Glu Ile Thr Thr Thr
 165 170 175
 Phe Pro Thr Trp Ile Arg Asn Val Ala Val Ile Gly Ala Val Ala Leu
 180 185 190
 Ser Val Val Leu Ile Thr Gly Thr Met Thr Thr Gly Ala Gly Val His
 195 200 205
 Ser Gly Asp Ala Ser Ile Thr Met Asp Asp Arg Leu Asp Val Ser Ile
 210 215 220
 Asp Leu Met Ala His Ile His Gly Tyr Ser Met Tyr Ile Tyr Leu Phe
 225 230 235 240
 Phe Thr Leu Ile Val Val Ala Gly Leu Tyr Lys Ala Lys Thr Thr Lys
 245 250 255
 His Asn Lys Gln Leu Gly Leu Met Leu Ile Leu Phe Ile Leu Ile Gln
 260 265 270
 Ala Gly Ile Gly Ile Leu Gln Tyr Arg Met Gly Val Pro Arg Trp Ser
 275 280 285
 Ile Pro Phe His Ile Ala Met Ser Ser Val Val Val Ala Phe Thr Ser
 290 295 300
 Leu Leu Trp Ala Gln Gly Arg Ile Arg Val Gly Gly Lys Ala Thr Val
 305 310 315 320
 Thr Gly Ser Val Asp Gly Asp Ile Lys Asn Glu Ile Ile Thr Asn Pro
 325 330 335
 Phe Glu Lys Lys Ser Lys Gln Pro Val Lys
 340 345

<210> 671

<211> 444

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(421)

<223> RXA01227

<400> 671

ggataatcga aaatatgtgc cccttggtga agggtcgggg agctaataagg atgacagtga 60
 acctattttc cacgtcttta tccgtagtat tggagatccg atg acc tac aca atc 115

	Met	Thr	Tyr	Thr	Ile	
	1				5	
gcc cag ccc tgc gtt gat gtc ctg gat cga gcc tgc gtc gag gaa tgt						163
Ala Gln Pro Cys Val Asp Val Leu Asp Arg Ala Cys Val Glu Glu Cys						
ccc gtg gac tgc atc tac gag ggc aaa cgg atg ctc tac atc cac ccc						211
Pro Val Asp Cys Ile Tyr Glu Gly Lys Arg Met Leu Tyr Ile His Pro						
gat gag tgc gtc gac tgc ggt gcc tgc gag ccc gtc tgc ccg gtt gaa						259
Asp Glu Cys Val Asp Cys Gly Ala Cys Glu Pro Val Cys Pro Val Glu						
gcc atc ttc tac gaa gat gat gtt ccc cac gaa tgg tgg gac tac acc						307
Ala Ile Phe Tyr Glu Asp Asp Val Pro His Glu Trp Trp Asp Tyr Thr						
ggc gct aac gcc gcc ttt ttc gac gac ctc ggt tcg cca ggc ggt gcc						355
Gly Ala Asn Ala Ala Phe Phe Asp Asp Leu Gly Ser Pro Gly Gly Ala						
gcc agc ctg ggt ccg cag gac ttc gac gcc cag ctc gtc gcg gtg ctg						403
Ala Ser Leu Gly Pro Gln Asp Phe Asp Ala Gln Leu Val Ala Val Leu						
ccg cca cag aac cag aac taggacctga tatcggccct aaa						444
Pro Pro Gln Asn Gln Asn						

<210> 672

<211> 107

<212> PRT

<213> Corynebacterium glutamicum

<400> 672

Met Thr Tyr Thr Ile Ala Gln Pro Cys Val Asp Val Leu Asp Arg Ala																
1				5				10					15			
Cys Val Glu Glu Cys Pro Val Asp Cys Ile Tyr Glu Gly Lys Arg Met																
				20				25					30			
Leu Tyr Ile His Pro Asp Glu Cys Val Asp Cys Gly Ala Cys Glu Pro																
				35				40					45			
Val Cys Pro Val Glu Ala Ile Phe Tyr Glu Asp Asp Val Pro His Glu																
				50				55					60			
Trp Trp Asp Tyr Thr Gly Ala Asn Ala Ala Phe Phe Asp Asp Leu Gly																
				65				70					75			80
Ser Pro Gly Gly Ala Ala Ser Leu Gly Pro Gln Asp Phe Asp Ala Gln																
				85				90					95			
Leu Val Ala Val Leu Pro Pro Gln Asn Gln Asn																
				100				105								

<210> 673

<211> 438
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(415)
 <223> RXA01865

<400> 673
 ggtggaattt ggcctgcggt caaggggaag tagcataata agcctaaagc tttcccatat 60

ttattagcct cttagagttc tcaggagaaa acgaaatccc atg aca tac aca atc 115
 Met Thr Tyr Thr Ile
 1 5

gca cag ccc tgc gtt gac gtc ttg gat cgt gcc tgc gtt gaa gaa tgc 163
 Ala Gln Pro Cys Val Asp Val Leu Asp Arg Ala Cys Val Glu Glu Cys
 10 15 20

cca gta gat tgc atc tac gaa ggt aag cgc atg ctg tac atc cac ccg 211
 Pro Val Asp Cys Ile Tyr Glu Gly Lys Arg Met Leu Tyr Ile His Pro
 25 30 35

gat gag tgc gtt gac tgt ggt gca tgt gag cct gct tgc cca gtt gag 259
 Asp Glu Cys Val Asp Cys Gly Ala Cys Glu Pro Ala Cys Pro Val Glu
 40 45 50

gca atc ttc tac gag gac gat gtc cca gac gaa tgg ctt gac tac aac 307
 Ala Ile Phe Tyr Glu Asp Asp Val Pro Asp Glu Trp Leu Asp Tyr Asn
 55 60 65

gat gcc aac gct gca ttc ttc gat gat ctg ggc tcc cca ggt ggt gcg 355
 Asp Ala Asn Ala Ala Phe Phe Asp Asp Leu Gly Ser Pro Gly Gly Ala
 70 75 80 85

gct aag ctt gga cca caa gat ttt gat cac cca atg atc gct gcg ctg 403
 Ala Lys Leu Gly Pro Gln Asp Phe Asp His Pro Met Ile Ala Ala Leu
 90 95 100

ccg cct cag gca taatctaacg catgacctct cgc 438
 Pro Pro Gln Ala
 105

<210> 674
 <211> 105
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 674
 Met Thr Tyr Thr Ile Ala Gln Pro Cys Val Asp Val Leu Asp Arg Ala
 1 5 10 15

Cys Val Glu Glu Cys Pro Val Asp Cys Ile Tyr Glu Gly Lys Arg Met
 20 25 30

Leu Tyr Ile His Pro Asp Glu Cys Val Asp Cys Gly Ala Cys Glu Pro
 35 40 45

Ala Cys Pro Val Glu Ala Ile Phe Tyr Glu Asp Asp Val Pro Asp Glu

50				55				60							
Trp	Leu	Asp	Tyr	Asn	Asp	Ala	Asn	Ala	Ala	Phe	Phe	Asp	Asp	Leu	Gly
65					70					75					80
Ser	Pro	Gly	Gly	Ala	Ala	Lys	Leu	Gly	Pro	Gln	Asp	Phe	Asp	His	Pro
				85					90					95	
Met	Ile	Ala	Ala	Leu	Pro	Pro	Gln	Ala							
			100					105							

```
<210> 675
<211> 441
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(418)  
<223> RXA00680
```

<400> 675																	
ttcttgc	atc	cccagaagcc	gaatacatca	ctggggcaa	aac	actcatcg	tt	gatggtg	ggcc	60							
gacagttcat ctaagtacta aaagtttctaa ggagaagatc										atg	tct	act	att	cat	115		
										Met	Ser	Thr	Ile	His	5		
										1							
ttc	att	gat	cat	gct	ggc	aaa	acc	cgc	acc	atc	gag	gcg	act	gtt	ggt	163	
Phe	Ile	Asp	His	Ala	Gly	Lys	Thr	Arg	Thr	Ile	Glu	Ala	Thr	Val	Gly		
				10					15					20			
gat	tca	gta	atg	gag	acc	gca	gtc	cga	aac	gga	gtg	cct	gga	att	gtt	211	
Asp	Ser	Val	Met	Glu	Thr	Ala	Val	Arg	Asn	Gly	Val	Pro	Gly	Ile	Val		
				25					30					35			
gct	gaa	tgc	ggc	ggg	tcc	tta	tcg	tgt	gca	acc	tgc	cat	gtg	ttt	gtt	259	
Ala	Glu	Cys	Gly	Gly	Ser	Leu	Ser	Cys	Ala	Thr	Cys	His	Val	Phe	Val		
				40					45					50			
gac	cct	gca	cag	tat	gat	gcg	ctt	ccc	cca	atg	gag	gag	atg	gaa	gat	307	
Asp	Pro	Ala	Gln	Tyr	Asp	Ala	Leu	Pro	Pro	Met	Glu	Glu	Met	Glu	Asp		
				55					60					65			
gaa	atg	ctg	tgg	ggg	gct	gcc	gtg	gac	cgt	gag	gat	tgc	tcc	cgt	ttg	355	
Glu	Met	Leu	Trp	Gly	Ala	Ala	Val	Asp	Arg	Glu	Asp	Cys	Ser	Arg	Leu		
				70					75					80			
tct	tgc	caa	atc	aag	gtc	acc	gaa	ggc	atg	gat	ctt	tcg	ttg	acc	acg	403	
Ser	Cys	Gln	Ile	Lys	Val	Thr	Glu	Gly	Met	Asp	Leu	Ser	Leu	Thr	Thr		
				90					95					100			
cca	gaa	acg	caa	gtg	tgaggttg	aa	tcatga	atac	ttc							441	
Pro	Glu	Thr	Gln	Val													
				105													

```
<210> 676
<211> 106
<212> PRT
```

<213> Corynebacterium glutamicum

<400> 676

```

Met Ser Thr Ile His Phe Ile Asp His Ala Gly Lys Thr Arg Thr Ile
 1             5             10             15

Glu Ala Thr Val Gly Asp Ser Val Met Glu Thr Ala Val Arg Asn Gly
      20             25             30

Val Pro Gly Ile Val Ala Glu Cys Gly Gly Ser Leu Ser Cys Ala Thr
      35             40             45

Cys His Val Phe Val Asp Pro Ala Gln Tyr Asp Ala Leu Pro Pro Met
      50             55             60

Glu Glu Met Glu Asp Glu Met Leu Trp Gly Ala Ala Val Asp Arg Glu
      65             70             75             80

Asp Cys Ser Arg Leu Ser Cys Gln Ile Lys Val Thr Glu Gly Met Asp
      85             90             95

Leu Ser Leu Thr Thr Pro Glu Thr Gln Val
      100             105

```

<210> 677

<211> 1389

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1366)

<223> RXA00679

<400> 677

```

ggaccgtgag gattgctccc gtttgtcttg ccaaatacaag gtcaccgaag gcatggatct 60

ttcgttgacc acgccagaaa cgcaagtgtg aggttgaatc atg aat act tca gct 115
                               Met Asn Thr Ser Ala
                               1             5

gaa act gga atc ttg atc atc ggt gca aac caa tcg ggt gtg cag ctg 163
Glu Thr Gly Ile Leu Ile Ile Gly Ala Asn Gln Ser Gly Val Gln Leu
      10             15             20

gcg att tcc ctg cgg gcc acg ggt ttc acc gaa tcg atc acg ctt cta 211
Ala Ile Ser Leu Arg Ala Thr Gly Phe Thr Glu Ser Ile Thr Leu Leu
      25             30             35

ggc gag gag gat cac cgc ccc tac cag cgt ccc gcc ttg tcc aag gag 259
Gly Glu Glu Asp His Arg Pro Tyr Gln Arg Pro Ala Leu Ser Lys Glu
      40             45             50

ttc ctc cag gac aag atc gac aaa gag cgt ctg att ttc cgt tcc aat 307
Phe Leu Gln Asp Lys Ile Asp Lys Glu Arg Leu Ile Phe Arg Ser Asn
      55             60             65

gag tat tgg gaa gaa aat aat att cgc ctg gtc aag ggc gtg cgc atc 355
Glu Tyr Trp Glu Glu Asn Asn Ile Arg Leu Val Lys Gly Val Arg Ile
      70             75             80             85

```


gaa cgc att gaa aag aac gac gac gga tca ggg gtc gcc tac ggc gcc	403
Glu Arg Ile Glu Lys Asn Asp Asp Gly Ser Gly Val Ala Tyr Gly Ala	
90 95 100	
gga caa gaa ttc gct ttt cga cgt ctc gct cta gcg gtt ggt gcc cgc	451
Gly Gln Glu Phe Ala Phe Arg Arg Leu Ala Leu Ala Val Gly Ala Arg	
105 110 115	
cct cgc cac ctc gac ctc ccg ggc gcc acc ttg gag ggt gtc acc tac	499
Pro Arg His Leu Asp Leu Pro Gly Ala Thr Leu Glu Gly Val Thr Tyr	
120 125 130	
ctg cgc aac gcg gac gac gcc ttg gcg ctc aaa gcg atg att ggt tct	547
Leu Arg Asn Ala Asp Asp Ala Leu Ala Leu Lys Ala Met Ile Gly Ser	
135 140 145	
gtc acc gat gcc gtt gta gtc ggt ggt ggg ttc atc gga ttg gaa gct	595
Val Thr Asp Ala Val Val Val Gly Gly Gly Phe Ile Gly Leu Glu Ala	
150 155 160 165	
gcg tgt tcg ctt cat gac ctc ggc aaa aat gtc acc gtc ctg gaa tat	643
Ala Cys Ser Leu His Asp Leu Gly Lys Asn Val Thr Val Leu Glu Tyr	
170 175 180	
ggt ccg cgt ctg att ggc cga gcg gtg ggt gaa gaa acc gca gca ttc	691
Gly Pro Arg Leu Ile Gly Arg Ala Val Gly Glu Glu Thr Ala Ala Phe	
185 190 195	
ttc ctc gaa caa cac cgt tcc cgt ggc gta aat atc gtg ctt gat gcc	739
Phe Leu Glu Gln His Arg Ser Arg Gly Val Asn Ile Val Leu Asp Ala	
200 205 210	
cgc atg aaa cag ttt gtg ggc aag gat gga aag ctc agc ggc att gag	787
Arg Met Lys Gln Phe Val Gly Lys Asp Gly Lys Leu Ser Gly Ile Glu	
215 220 225	
cta gaa gat ggc aca gta att cct gcc caa cta gtc att gtg ggc atc	835
Leu Glu Asp Gly Thr Val Ile Pro Ala Gln Leu Val Ile Val Gly Ile	
230 235 240 245	
ggt gtc att ccg aac aca gaa ctt gcc gct gtt ctg ggc tta gac atc	883
Gly Val Ile Pro Asn Thr Glu Leu Ala Ala Val Leu Gly Leu Asp Ile	
250 255 260	
aac aac ggc atc gtg gtg gat aaa cat gcc gtc gcg tca gat ggc acc	931
Asn Asn Gly Ile Val Val Asp Lys His Ala Val Ala Ser Asp Gly Thr	
265 270 275	
acc att gcg att ggc gat gtc gcc aac att ccc aat cca atc cct ggt	979
Thr Ile Ala Ile Gly Asp Val Ala Asn Ile Pro Asn Pro Ile Pro Gly	
280 285 290	
tcc ccc gct gat gaa cgc atc cga cta gaa agc gtc aat aac gcc atc	1027
Ser Pro Ala Asp Glu Arg Ile Arg Leu Glu Ser Val Asn Asn Ala Ile	
295 300 305	
gag cac gca aag atc gct gca tac tca ctc gtc ggc cag ccc gaa gcc	1075
Glu His Ala Lys Ile Ala Ala Tyr Ser Leu Val Gly Gln Pro Glu Ala	
310 315 320 325	

tac gcc gga atc ccc tgg ttc tgg tcc aac caa ggc gat ctc aaa cta 1123
 Tyr Ala Gly Ile Pro Trp Phe Trp Ser Asn Gln Gly Asp Leu Lys Leu
 330 335 340

caa att gca gga ctt acc ctt ggt tat gac agc aca gta atc cga cag 1171
 Gln Ile Ala Gly Leu Thr Leu Gly Tyr Asp Ser Thr Val Ile Arg Gln
 345 350 355

gat ccc gag aaa aag aag ttc tct gtc ctt tat tac cgt ggc gac aac 1219
 Asp Pro Glu Lys Lys Lys Phe Ser Val Leu Tyr Tyr Arg Gly Asp Asn
 360 365 370

atc atc gcc gcc gat tgt gtc aac gct cca ctg gat ttc atg gct gtg 1267
 Ile Ile Ala Ala Asp Cys Val Asn Ala Pro Leu Asp Phe Met Ala Val
 375 380 385

cgc agt gca ctt tcc agg aac caa aat atc ccc gcc gac ctt gct gca 1315
 Arg Ser Ala Leu Ser Arg Asn Gln Asn Ile Pro Ala Asp Leu Ala Ala
 390 395 400 405

gat att tcg cag ccg ctg aaa aaa cta gcc gtt gac ctg gag gtt acc 1363
 Asp Ile Ser Gln Pro Leu Lys Lys Leu Ala Val Asp Leu Glu Val Thr
 410 415 420

cga tgactcgacag taatttaccc gct 1389
 Arg

<210> 678

<211> 422

<212> PRT

<213> Corynebacterium glutamicum

<400> 678

Met Asn Thr Ser Ala Glu Thr Gly Ile Leu Ile Ile Gly Ala Asn Gln
 1 5 10 15

Ser Gly Val Gln Leu Ala Ile Ser Leu Arg Ala Thr Gly Phe Thr Glu
 20 25 30

Ser Ile Thr Leu Leu Gly Glu Glu Asp His Arg Pro Tyr Gln Arg Pro
 35 40 45

Ala Leu Ser Lys Glu Phe Leu Gln Asp Lys Ile Asp Lys Glu Arg Leu
 50 55 60

Ile Phe Arg Ser Asn Glu Tyr Trp Glu Glu Asn Asn Ile Arg Leu Val
 65 70 75 80

Lys Gly Val Arg Ile Glu Arg Ile Glu Lys Asn Asp Asp Gly Ser Gly
 85 90 95

Val Ala Tyr Gly Ala Gly Gln Glu Phe Ala Phe Arg Arg Leu Ala Leu
 100 105 110

Ala Val Gly Ala Arg Pro Arg His Leu Asp Leu Pro Gly Ala Thr Leu
 115 120 125

Glu Gly Val Thr Tyr Leu Arg Asn Ala Asp Asp Ala Leu Ala Leu Lys
 130 135 140

Ala Met Ile Gly Ser Val Thr Asp Ala Val Val Val Gly Gly Gly Phe
 145 150 155 160
 Ile Gly Leu Glu Ala Ala Cys Ser Leu His Asp Leu Gly Lys Asn Val
 165 170 175
 Thr Val Leu Glu Tyr Gly Pro Arg Leu Ile Gly Arg Ala Val Gly Glu
 180 185 190
 Glu Thr Ala Ala Phe Phe Leu Glu Gln His Arg Ser Arg Gly Val Asn
 195 200 205
 Ile Val Leu Asp Ala Arg Met Lys Gln Phe Val Gly Lys Asp Gly Lys
 210 215 220
 Leu Ser Gly Ile Glu Leu Glu Asp Gly Thr Val Ile Pro Ala Gln Leu
 225 230 235 240
 Val Ile Val Gly Ile Gly Val Ile Pro Asn Thr Glu Leu Ala Ala Val
 245 250 255
 Leu Gly Leu Asp Ile Asn Asn Gly Ile Val Val Asp Lys His Ala Val
 260 265 270
 Ala Ser Asp Gly Thr Thr Ile Ala Ile Gly Asp Val Ala Asn Ile Pro
 275 280 285
 Asn Pro Ile Pro Gly Ser Pro Ala Asp Glu Arg Ile Arg Leu Glu Ser
 290 295 300
 Val Asn Asn Ala Ile Glu His Ala Lys Ile Ala Ala Tyr Ser Leu Val
 305 310 315 320
 Gly Gln Pro Glu Ala Tyr Ala Gly Ile Pro Trp Phe Trp Ser Asn Gln
 325 330 335
 Gly Asp Leu Lys Leu Gln Ile Ala Gly Leu Thr Leu Gly Tyr Asp Ser
 340 345 350
 Thr Val Ile Arg Gln Asp Pro Glu Lys Lys Lys Phe Ser Val Leu Tyr
 355 360 365
 Tyr Arg Gly Asp Asn Ile Ile Ala Ala Asp Cys Val Asn Ala Pro Leu
 370 375 380
 Asp Phe Met Ala Val Arg Ser Ala Leu Ser Arg Asn Gln Asn Ile Pro
 385 390 395 400
 Ala Asp Leu Ala Ala Asp Ile Ser Gln Pro Leu Lys Lys Leu Ala Val
 405 410 415
 Asp Leu Glu Val Thr Arg
 420

<210> 679

<211> 1074

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1051)

<223> RXA00224

<400> 679

```

gtgatgtcat tgggtgcatcg ggtgctgctg aaaagattgc tgagtacctc gcttcagaga 60
acctcatcta gccactatct tcacaaagga gaacatttaa atg tct att tct tat 115
                                     Met Ser Ile Ser Tyr
                                     1 5

gtg ctg gtt gag cag cta gat ggc cgc cca gaa cca gtt acc ctt gaa 163
Val Leu Val Glu Gln Leu Asp Gly Arg Pro Glu Pro Val Thr Leu Glu
          10          15          20

ttg atc act gct gct cgc gca ctc ggt gac gtc gtt gcc gtt gtc gtt 211
Leu Ile Thr Ala Ala Arg Ala Leu Gly Asp Val Val Ala Val Val Val
          25          30          35

ggc gag cca ggt gcc ggc gta aac ctt gct gct gag ctc ggc aat tgg 259
Gly Glu Pro Gly Ala Gly Val Asn Leu Ala Ala Glu Leu Gly Asn Trp
          40          45          50

ggt gca gca cag gtt gtt tcc gct gaa atc tct ggc gct tcc aac cgt 307
Gly Ala Ala Gln Val Val Ser Ala Glu Ile Ser Gly Ala Ser Asn Arg
          55          60          65

ttg atc ttg cct gct gtt gat gcg ctg cac att ttg gct gcg aac aac 355
Leu Ile Leu Pro Ala Val Asp Ala Leu His Ile Leu Ala Ala Asn Asn
          70          75          80          85

cca ggt cca att gtt atc gct gca act gca agc ggt aat gag atc gct 403
Pro Gly Pro Ile Val Ile Ala Ala Thr Ala Ser Gly Asn Glu Ile Ala
          90          95          100

ggt cgt ttg gct gcc cgt ttg gct tct ggt gtg ctc acc gat gtc gtc 451
Gly Arg Leu Ala Ala Arg Leu Ala Ser Gly Val Leu Thr Asp Val Val
          105          110          115

gga atc aat gcc gac cgc acc gca cag cag tcc att ttc ggc gac acc 499
Gly Ile Asn Ala Asp Arg Thr Ala Gln Gln Ser Ile Phe Gly Asp Thr
          120          125          130

att cag gtg tcc gct gca gtt ggt ggc gct tca ccg ctg tac acc ctg 547
Ile Gln Val Ser Ala Ala Val Gly Gly Ala Ser Pro Leu Tyr Thr Leu
          135          140          145

cgt cca ggt gcc ctt gat ggc gtg gcc gtt cct gca acc ggt gaa ttg 595
Arg Pro Gly Ala Leu Asp Gly Val Ala Val Pro Ala Thr Gly Glu Leu
          150          155          160          165

gca acc att gag atc cca ggc gca acc gcc aag gat gtc acc atc acc 643
Ala Thr Ile Glu Ile Pro Gly Ala Thr Ala Lys Asp Val Thr Ile Thr
          170          175          180

tcc ttc acg cca agc acc cag agc gat cgc cct gag ctg cca cag gca 691
Ser Phe Thr Pro Ser Thr Gln Ser Asp Arg Pro Glu Leu Pro Gln Ala
          185          190          195

aag gtc gtt atc gca ggt gga cgt ggt gtc gga agc gaa gaa aac ttc 739

```

Lys Val Val Ile Ala Gly Gly Arg Gly Val Gly Ser Glu Glu Asn Phe
 200 205 210
 cgc agc atc gtt gaa cca ctg gca gat gca ttg ggc ggt gcc gtt ggc 787
 Arg Ser Ile Val Glu Pro Leu Ala Asp Ala Leu Gly Gly Ala Val Gly
 215 220 225
 gca acc cgc gac gcc gtt gat ctg ggc tac tac cca ggc gag tac cag 835
 Ala Thr Arg Asp Ala Val Asp Leu Gly Tyr Tyr Pro Gly Glu Tyr Gln
 230 235 240 245
 gtt ggt cag acc ggt gtc acc gtg tcc cca gac ctc tac atc ggc ctc 883
 Val Gly Gln Thr Gly Val Thr Val Ser Pro Asp Leu Tyr Ile Gly Leu
 250 255 260
 ggc att tcc ggt gca att cag cac act tct ggt atg cag acc gca aag 931
 Gly Ile Ser Gly Ala Ile Gln His Thr Ser Gly Met Gln Thr Ala Lys
 265 270 275
 aag gtt att gtg atc aac aac gat gag gac gcg ccg atc ttc cag att 979
 Lys Val Ile Val Ile Asn Asn Asp Glu Asp Ala Pro Ile Phe Gln Ile
 280 285 290
 gcg gac ctc ggt gtc gtt ggc gac ctc ttt gac atc gcc cct gcg ctc 1027
 Ala Asp Leu Gly Val Val Gly Asp Leu Phe Asp Ile Ala Pro Ala Leu
 295 300 305
 atc gaa gag atc aac aag cgc aag taggagtttt gaacactttt tat 1074
 Ile Glu Glu Ile Asn Lys Arg Lys
 310 315

<210> 680

<211> 317

<212> PRT

<213> Corynebacterium glutamicum

<400> 680

Met Ser Ile Ser Tyr Val Leu Val Glu Gln Leu Asp Gly Arg Pro Glu
 1 5 10 15
 Pro Val Thr Leu Glu Leu Ile Thr Ala Ala Arg Ala Leu Gly Asp Val
 20 25 30
 Val Ala Val Val Val Gly Glu Pro Gly Ala Gly Val Asn Leu Ala Ala
 35 40 45
 Glu Leu Gly Asn Trp Gly Ala Ala Gln Val Val Ser Ala Glu Ile Ser
 50 55 60
 Gly Ala Ser Asn Arg Leu Ile Leu Pro Ala Val Asp Ala Leu His Ile
 65 70 75 80
 Leu Ala Ala Asn Asn Pro Gly Pro Ile Val Ile Ala Ala Thr Ala Ser
 85 90 95
 Gly Asn Glu Ile Ala Gly Arg Leu Ala Ala Arg Leu Ala Ser Gly Val
 100 105 110
 Leu Thr Asp Val Val Gly Ile Asn Ala Asp Arg Thr Ala Gln Gln Ser
 115 120 125

Ile Phe Gly Asp Thr Ile Gln Val Ser Ala Ala Val Gly Gly Ala Ser
 130 135 140
 Pro Leu Tyr Thr Leu Arg Pro Gly Ala Leu Asp Gly Val Ala Val Pro
 145 150 155 160
 Ala Thr Gly Glu Leu Ala Thr Ile Glu Ile Pro Gly Ala Thr Ala Lys
 165 170 175
 Asp Val Thr Ile Thr Ser Phe Thr Pro Ser Thr Gln Ser Asp Arg Pro
 180 185 190
 Glu Leu Pro Gln Ala Lys Val Val Ile Ala Gly Gly Arg Gly Val Gly
 195 200 205
 Ser Glu Glu Asn Phe Arg Ser Ile Val Glu Pro Leu Ala Asp Ala Leu
 210 215 220
 Gly Gly Ala Val Gly Ala Thr Arg Asp Ala Val Asp Leu Gly Tyr Tyr
 225 230 235 240
 Pro Gly Glu Tyr Gln Val Gly Gln Thr Gly Val Thr Val Ser Pro Asp
 245 250 255
 Leu Tyr Ile Gly Leu Gly Ile Ser Gly Ala Ile Gln His Thr Ser Gly
 260 265 270
 Met Gln Thr Ala Lys Lys Val Ile Val Ile Asn Asn Asp Glu Asp Ala
 275 280 285
 Pro Ile Phe Gln Ile Ala Asp Leu Gly Val Val Gly Asp Leu Phe Asp
 290 295 300
 Ile Ala Pro Ala Leu Ile Glu Glu Ile Asn Lys Arg Lys
 305 310 315

<210> 681
 <211> 909
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(886)
 <223> RXA00225

<400> 681
 gtaggcgtcg aaaagcaatg ggcgaagccc gcgtagtatg ggcgggcaac gctaaaagcg 60
 ccaaaaacgc caaaaatcgt gaattgaaag gtgagtgtgg atg tcc aca atc gtg 115
 Met Ser Thr Ile Val
 1 5
 gtt ctg gtt aaa aat gtt cca gac acc tgg tct aag agg act ctg gaa 163
 Val Leu Val Lys Asn Val Pro Asp Thr Trp Ser Lys Arg Thr Leu Glu
 10 15 20
 gct gat ttc acc ctt gac cgt gag ggt gta gat cga gtc ttg gat gag 211
 Ala Asp Phe Thr Leu Asp Arg Glu Gly Val Asp Arg Val Leu Asp Glu

25	30	35	
atc aat gag ttt gct ctg gag cag gca ctg cgc ttg cgg gag tcc aac Ile Asn Glu Phe Ala Leu Glu Gln Ala Leu Arg Leu Arg Glu Ser Asn 40 45 50			259
ccg gat gct ggt tac cgc gtt gtt gcg ctg agc gcc ggc cct gcc ggt Pro Asp Ala Gly Tyr Arg Val Val Ala Leu Ser Ala Gly Pro Ala Gly 55 60 65			307
ggg gaa gag gcg ctg cgt aag gcg ctg tcc atg ggt gct gat gaa gca Gly Glu Glu Ala Leu Arg Lys Ala Leu Ser Met Gly Ala Asp Glu Ala 70 75 80 85			355
atc cag ctc agt gat gat gcc ttg gct ggt tct gat ctt ttg gga acc Ile Gln Leu Ser Asp Asp Ala Leu Ala Gly Ser Asp Leu Leu Gly Thr 90 95 100			403
gct tgg gcg ctg aac aac gct atc aac acc atc gcg ggt gtt gct ctc Ala Trp Ala Leu Asn Asn Ala Ile Asn Thr Ile Ala Gly Val Ala Leu 105 110 115			451
atc gtg acg ggt tcg gct tct tcc gat ggt tcc atg ggt gcg ctt cct Ile Val Thr Gly Ser Ala Ser Ser Asp Gly Ser Met Gly Ala Leu Pro 120 125 130			499
ggc gtg tta gct gag tac cgc cag gtc cca gcg ttg act aac ttg tct Gly Val Leu Ala Glu Tyr Arg Gln Val Pro Ala Leu Thr Asn Leu Ser 135 140 145			547
gcg ctg aag gtc gag ggt gca tct att act gcc act cgc att gat aac Ala Leu Lys Val Glu Gly Ala Ser Ile Thr Ala Thr Arg Ile Asp Asn 150 155 160 165			595
cac ggc acc tat gag ttg cag gct gca ctt cct gcg gtt gtg tcg att His Gly Thr Tyr Glu Leu Gln Ala Ala Leu Pro Ala Val Val Ser Ile 170 175 180			643
tcc gat aag gct gac aag cca cgt ttc cct aac ttc aag ggc atc atg Ser Asp Lys Ala Asp Lys Pro Arg Phe Pro Asn Phe Lys Gly Ile Met 185 190 195			691
gct gct aag aag gct gag atc aag aag ctt tcc ttg gct gaa atc ggc Ala Ala Lys Lys Ala Glu Ile Lys Lys Leu Ser Leu Ala Glu Ile Gly 200 205 210			739
gtg gct cca gag cag gtt ggt ctg tct cac gcg gca act gct gtt act Val Ala Pro Glu Gln Val Gly Leu Ser His Ala Ala Thr Ala Val Thr 215 220 225			787
gct gca gct gat cgt cct gag cgc tcc caa ggt gat gtc att ggt gca Ala Ala Ala Asp Arg Pro Glu Arg Ser Gln Gly Asp Val Ile Gly Ala 230 235 240 245			835
tcg ggt gct gct gaa aag att gct gag tac ctc gct tca gag aac ctc Ser Gly Ala Ala Glu Lys Ile Ala Glu Tyr Leu Ala Ser Glu Asn Leu 250 255 260			883
atc tagccactat cttcacaag gag Ile			909

<210> 682
 <211> 262
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 682

```

Met Ser Thr Ile Val Val Leu Val Lys Asn Val Pro Asp Thr Trp Ser
  1           5           10           15

Lys Arg Thr Leu Glu Ala Asp Phe Thr Leu Asp Arg Glu Gly Val Asp
      20           25           30

Arg Val Leu Asp Glu Ile Asn Glu Phe Ala Leu Glu Gln Ala Leu Arg
      35           40           45

Leu Arg Glu Ser Asn Pro Asp Ala Gly Tyr Arg Val Val Ala Leu Ser
      50           55           60

Ala Gly Pro Ala Gly Gly Glu Glu Ala Leu Arg Lys Ala Leu Ser Met
      65           70           75           80

Gly Ala Asp Glu Ala Ile Gln Leu Ser Asp Asp Ala Leu Ala Gly Ser
      85           90           95

Asp Leu Leu Gly Thr Ala Trp Ala Leu Asn Asn Ala Ile Asn Thr Ile
      100          105          110

Ala Gly Val Ala Leu Ile Val Thr Gly Ser Ala Ser Ser Asp Gly Ser
      115          120          125

Met Gly Ala Leu Pro Gly Val Leu Ala Glu Tyr Arg Gln Val Pro Ala
      130          135          140

Leu Thr Asn Leu Ser Ala Leu Lys Val Glu Gly Ala Ser Ile Thr Ala
      145          150          155          160

Thr Arg Ile Asp Asn His Gly Thr Tyr Glu Leu Gln Ala Ala Leu Pro
      165          170          175

Ala Val Val Ser Ile Ser Asp Lys Ala Asp Lys Pro Arg Phe Pro Asn
      180          185          190

Phe Lys Gly Ile Met Ala Ala Lys Lys Ala Glu Ile Lys Lys Leu Ser
      195          200          205

Leu Ala Glu Ile Gly Val Ala Pro Glu Gln Val Gly Leu Ser His Ala
      210          215          220

Ala Thr Ala Val Thr Ala Ala Ala Asp Arg Pro Glu Arg Ser Gln Gly
      225          230          235          240

Asp Val Ile Gly Ala Ser Gly Ala Ala Glu Lys Ile Ala Glu Tyr Leu
      245          250          255

Ala Ser Glu Asn Leu Ile
      260

```

<210> 683

<211> 2378
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (82)..(2355)
 <223> RXN00606

<400> 683

```

tgcggtggcg attgctgcga cccaagctgg caccaccagc ctcgatggta ttttgcactc 60
tgatttctgg cggagaagcc agtg ctc acg ggt gtt att gcg gtg ctg att 111
                    Val Leu Thr Gly Val Ile Ala Val Leu Ile
                      1                      5                      10

gca atg tcc gcg ttc act aag tcc gca cag ttc ccg ttc cac ttc tgg 159
Ala Met Ser Ala Phe Thr Lys Ser Ala Gln Phe Pro Phe His Phe Trp
                      15                      20                      25

ctg cct gag gcg atg gct gcg gcc acc cca gtg tcg gcg ttc ctg cac 207
Leu Pro Glu Ala Met Ala Ala Ala Thr Pro Val Ser Ala Phe Leu His
                      30                      35                      40

gct gcg gcc gtg gtc aag gcg ggt att tac ctg ttg ctg cgc ttt agc 255
Ala Ala Ala Val Val Lys Ala Gly Ile Tyr Leu Leu Leu Arg Phe Ser
                      45                      50                      55

att gtg ttc cat gat gtt gcg gtc tgg aat tgg ttg ctg att atc gtc 303
Ile Val Phe His Asp Val Ala Val Trp Asn Trp Leu Leu Ile Ile Val
                      60                      65                      70

ggc atg ggt acg gcc atc atg tcg gcg tat ttc gcg gtg cag aag acc 351
Gly Met Gly Thr Ala Ile Met Ser Ala Tyr Phe Ala Val Gln Lys Thr
                      75                      80                      85                      90

gat ctg aag aag ctc acg gca tat tcc acg gtg tcg cat ttg ggt tgg 399
Asp Leu Lys Lys Leu Thr Ala Tyr Ser Thr Val Ser His Leu Gly Trp
                      95                      100                      105

atc gta gcg acc atc ggc gtg ggc act cct ttc gcg ctc ggc gct gcc 447
Ile Val Ala Thr Ile Gly Val Gly Thr Pro Phe Ala Leu Gly Ala Ala
                      110                      115                      120

att gtg cac acg ctc agc cac gcg ctg ttt aag tcc tcg ttg ttc atg 495
Ile Val His Thr Leu Ser His Ala Leu Phe Lys Ser Ser Leu Phe Met
                      125                      130                      135

ctc att ggc gtg att gat cac cag act ggc acg cgc gat att cgt cgc 543
Leu Ile Gly Val Ile Asp His Gln Thr Gly Thr Arg Asp Ile Arg Arg
                      140                      145                      150

ctc ggt ttc ctg gtc aag aag atg ccg ttc acg ttt gtg tct gta tta 591
Leu Gly Phe Leu Val Lys Lys Met Pro Phe Thr Phe Val Ser Val Leu
                      155                      160                      165                      170

ata ggt gcg ttg tcg atg gca tcg gtt ccg ccg ttg ctc ggc ttc gtg 639
Ile Gly Ala Leu Ser Met Ala Ser Val Pro Pro Leu Leu Gly Phe Val
                      175                      180                      185

tcc aaa gaa ggc atg atc aca gcg ttc atg gac gcc ccc atc ggc aac 687

```

Ser	Lys	Glu	Gly	Met	Ile	Thr	Ala	Phe	Met	Asp	Ala	Pro	Ile	Gly	Asn	
			190					195					200			
tcc	tat	gtt	gta	tta	ctg	ctg	gtc	ggc	gca	gca	atc	ggc	gcg	gtc	cta	735
Ser	Tyr	Val	Val	Leu	Leu	Leu	Val	Gly	Ala	Ala	Ile	Gly	Ala	Val	Leu	
		205					210					215				
acc	ttc	aca	tac	tcc	gcg	aaa	ctc	gtg	ctc	ggc	gca	ttc	gtc	gac	ggc	783
Thr	Phe	Thr	Tyr	Ser	Ala	Lys	Leu	Val	Leu	Gly	Ala	Phe	Val	Asp	Gly	
	220					225					230					
cca	cgc	gac	atg	tca	cac	gtc	aag	gaa	gcc	ccc	gtc	tcc	ctc	tgg	ctt	831
Pro	Arg	Asp	Met	Ser	His	Val	Lys	Glu	Ala	Pro	Val	Ser	Leu	Trp	Leu	
	235				240					245					250	
ccg	gcc	gcc	ctg	cct	gga	ctt	atg	tct	ctg	cca	cta	gtc	cta	gta	ctt	879
Pro	Ala	Ala	Leu	Pro	Gly	Leu	Met	Ser	Leu	Pro	Leu	Val	Leu	Val	Leu	
				255					260					265		
tcg	ctt	ttc	gac	gcc	ccc	gtc	tcc	gcc	gca	gcc	acc	tcc	gcc	gcg	ggg	927
Ser	Leu	Phe	Asp	Ala	Pro	Val	Ser	Ala	Ala	Ala	Thr	Ser	Ala	Ala	Gly	
			270					275					280			
gaa	gcg	gcg	cac	atg	cac	ctg	gca	ttg	tgg	cac	ggc	atc	aac	acc	cca	975
Glu	Ala	Ala	His	Met	His	Leu	Ala	Leu	Trp	His	Gly	Ile	Asn	Thr	Pro	
		285					290					295				
ctg	ttg	att	tcc	ttg	ggt	gtg	ctg	gtg	gcc	gga	atc	ctt	ggt	gtg	ctg	1023
Leu	Leu	Ile	Ser	Leu	Gly	Val	Leu	Val	Ala	Gly	Ile	Leu	Gly	Val	Leu	
	300					305					310					
ttc	cgc	aaa	gag	ctg	tgg	aaa	atc	gcc	gag	acc	agc	cct	ttc	ccc	atc	1071
Phe	Arg	Lys	Glu	Leu	Trp	Lys	Ile	Ala	Glu	Thr	Ser	Pro	Phe	Pro	Ile	
	315				320				325						330	
gcc	aca	ggc	aac	gac	atc	cta	tcg	atg	ctg	gtt	tac	cga	gcc	aac	ttg	1119
Ala	Thr	Gly	Asn	Asp	Ile	Leu	Ser	Met	Leu	Val	Tyr	Arg	Ala	Asn	Leu	
				335					340					345		
ctg	ggt	aaa	ttc	ttc	ggt	cgc	atg	gct	gat	tcg	atg	agc	cca	cgc	agg	1167
Leu	Gly	Lys	Phe	Phe	Gly	Arg	Met	Ala	Asp	Ser	Met	Ser	Pro	Arg	Arg	
			350					355					360			
cac	ttg	gtc	agc	ctc	atc	gtg	ctg	ctc	tgg	gcg	ctg	gct	gct	ttt	gcc	1215
His	Leu	Val	Ser	Leu	Ile	Val	Leu	Leu	Trp	Ala	Leu	Ala	Ala	Phe	Ala	
		365					370					375				
acc	att	cac	ccc	tcg	gtt	cag	ctt	gca	cca	aag	caa	ccg	gga	att	gat	1263
Thr	Ile	His	Pro	Ser	Val	Gln	Leu	Ala	Pro	Lys	Gln	Pro	Gly	Ile	Asp	
	380					385					390					
cgt	tgg	atc	gac	ctc	att	ccg	ctt	gcc	atc	atc	gcg	cta	tct	gtc	ttc	1311
Arg	Trp	Ile	Asp	Leu	Ile	Pro	Leu	Ala	Ile	Ile	Ala	Leu	Ser	Val	Phe	
	395				400				405					410		
ggc	ctg	ctc	acc	acc	cga	aac	cgc	ctc	agc	gca	gcc	gtg	ctt	gtg	ggt	1359
Gly	Leu	Leu	Thr	Thr	Arg	Asn	Arg	Leu	Ser	Ala	Ala	Val	Leu	Val	Gly	
				415					420					425		
acc	gtt	ggt	gtg	ggt	gtt	tcc	ttc	cag	atg	cta	ctt	ctg	ggc	gct	ccc	1407
Thr	Val	Gly	Val	Gly	Val	Ser	Phe	Gln	Met	Leu	Leu	Leu	Gly	Ala	Pro	

430							435					440					
gat	gtt	gca	ctt	acc	cag	ttc	ctg	gta	gaa	ggc	ctc	gtc	gtg	gta	atc	1455	
Asp	Val	Ala	Leu	Thr	Gln	Phe	Leu	Val	Glu	Gly	Leu	Val	Val	Val	Ile		
		445					450					455					
atc	atg	atg	gtt	gtc	cgg	cac	cag	cct	gcc	aac	ttc	aag	cgc	atc	aag	1503	
Ile	Met	Met	Val	Val	Arg	His	Gln	Pro	Ala	Asn	Phe	Lys	Arg	Ile	Lys		
	460					465					470						
ccc	agc	aga	agg	cgc	agc	acc	gtt	ctt	gtc	gcc	gtc	ctt	gct	gcc	ttc	1551	
Pro	Ser	Arg	Arg	Arg	Ser	Thr	Val	Leu	Val	Ala	Val	Leu	Ala	Ala	Phe		
475					480					485					490		
gcc	gca	ttc	atg	gcg	gtg	tgg	gga	ttg	ctt	ggc	cgt	cac	gaa	cgt	tct	1599	
Ala	Ala	Phe	Met	Ala	Val	Trp	Gly	Leu	Leu	Gly	Arg	His	Glu	Arg	Ser		
				495				500						505			
gag	ctg	gcc	atg	tgg	tac	ctc	aac	caa	ggg	cca	gag	atc	acc	tct	ggc	1647	
Glu	Leu	Ala	Met	Trp	Tyr	Leu	Asn	Gln	Gly	Pro	Glu	Ile	Thr	Ser	Gly		
			510					515					520				
gcc	aac	gtg	gtg	aac	acc	atc	ctc	gtg	gaa	ttc	cgt	gca	ctg	gat	acg	1695	
Ala	Asn	Val	Val	Asn	Thr	Ile	Leu	Val	Glu	Phe	Arg	Ala	Leu	Asp	Thr		
		525					530					535					
ttg	ggc	gag	ctc	tcc	gtg	ctt	ggc	atg	gca	gct	gtc	gtc	atc	ggg	gcg	1743	
Leu	Gly	Glu	Leu	Ser	Val	Leu	Gly	Met	Ala	Ala	Val	Val	Ile	Gly	Ala		
	540					545					550						
atg	gtg	gct	tcc	atg	cct	cgt	cat	ccg	ttt	gcc	aag	ggc	acc	cac	cct	1791	
Met	Val	Ala	Ser	Met	Pro	Arg	His	Pro	Phe	Ala	Lys	Gly	Thr	His	Pro		
555					560					565					570		
cgc	ccc	ttt	ggc	caa	tca	cag	ttg	aac	tcc	att	ccg	ctg	cgc	atg	ctg	1839	
Arg	Pro	Phe	Gly	Gln	Ser	Gln	Leu	Asn	Ser	Ile	Pro	Leu	Arg	Met	Leu		
				575				580						585			
ctt	aag	gtg	ctg	gtt	cca	gcg	cta	tgc	ttc	ttg	agc	ttc	atg	gtg	ttc	1887	
Leu	Lys	Val	Leu	Val	Pro	Ala	Leu	Cys	Phe	Leu	Ser	Phe	Met	Val	Phe		
			590					595					600				
atg	cgt	gga	cac	aat	gat	ccg	gga	ggc	ggg	ttc	atc	gca	gcc	cta	att	1935	
Met	Arg	Gly	His	Asn	Asp	Pro	Gly	Gly	Gly	Phe	Ile	Ala	Ala	Leu	Ile		
		605					610					615					
gcc	ggg	ggc	gcg	ctg	atg	ctc	ctg	tac	ctg	tcc	aag	gcc	aaa	gat	ggc	1983	
Ala	Gly	Gly	Ala	Leu	Met	Leu	Leu	Tyr	Leu	Ser	Lys	Ala	Lys	Asp	Gly		
		620				625					630						
cgc	att	ttc	cgc	ccg	aat	gtt	cct	ttc	att	ctc	act	ggg	gcg	ggc	atc	2031	
Arg	Ile	Phe	Arg	Pro	Asn	Val	Pro	Phe	Ile	Leu	Thr	Gly	Ala	Gly	Ile		
635					640					645					650		
ttg	atg	gca	gtg	ttc	tcg	ggc	gta	ctg	gga	ctc	acc	cac	ggg	tct	ttc	2079	
Leu	Met	Ala	Val	Phe	Ser	Gly	Val	Leu	Gly	Leu	Thr	His	Gly	Ser	Phe		
				655				660						665			
ctg	tac	gcc	atc	cac	ttc	aac	ttc	gta	ggc	cag	cac	tgg	acc	acc	tcg	2127	
Leu	Tyr	Ala	Ile	His	Phe	Asn	Phe	Val	Gly	Gln	His	Trp	Thr	Thr	Ser		
			670					675					680				

atg atc ttc gac ctc ggc gtg tac ctg gcc gtg ttg ggc atg gtg tcc 2175
 Met Ile Phe Asp Leu Gly Val Tyr Leu Ala Val Leu Gly Met Val Ser
 685 690 695

atg gca atc aac ggc ctg ggc gga tac ctg cgc cca ggt acc gac aat 2223
 Met Ala Ile Asn Gly Leu Gly Gly Tyr Leu Arg Pro Gly Thr Asp Asn
 700 705 710

gca gat ctg gac tac gcc cgc cga agt ggc cca ctg cca gca acg cca 2271
 Ala Asp Leu Asp Tyr Ala Arg Arg Ser Gly Pro Leu Pro Ala Thr Pro
 715 720 725 730

acg gtt gaa ccc gaa cca gaa ggc gat gaa gac tgg ccc gaa ccc atc 2319
 Thr Val Glu Pro Glu Pro Glu Gly Asp Glu Asp Trp Pro Glu Pro Ile
 735 740 745

aac ccc gca ggc gat aac aaa gag gag gca aac cga tgattctcgc 2365
 Asn Pro Ala Gly Asp Asn Lys Glu Glu Ala Asn Arg
 750 755

actgacagtc gcg 2378

<210> 684

<211> 758

<212> PRT

<213> Corynebacterium glutamicum

<400> 684

Val Leu Thr Gly Val Ile Ala Val Leu Ile Ala Met Ser Ala Phe Thr
 1 5 10 15

Lys Ser Ala Gln Phe Pro Phe His Phe Trp Leu Pro Glu Ala Met Ala
 20 25 30

Ala Ala Thr Pro Val Ser Ala Phe Leu His Ala Ala Ala Val Val Lys
 35 40 45

Ala Gly Ile Tyr Leu Leu Leu Arg Phe Ser Ile Val Phe His Asp Val
 50 55 60

Ala Val Trp Asn Trp Leu Leu Ile Ile Val Gly Met Gly Thr Ala Ile
 65 70 75 80

Met Ser Ala Tyr Phe Ala Val Gln Lys Thr Asp Leu Lys Lys Leu Thr
 85 90 95

Ala Tyr Ser Thr Val Ser His Leu Gly Trp Ile Val Ala Thr Ile Gly
 100 105 110

Val Gly Thr Pro Phe Ala Leu Gly Ala Ala Ile Val His Thr Leu Ser
 115 120 125

His Ala Leu Phe Lys Ser Ser Leu Phe Met Leu Ile Gly Val Ile Asp
 130 135 140

His Gln Thr Gly Thr Arg Asp Ile Arg Arg Leu Gly Phe Leu Val Lys
 145 150 155 160

Lys Met Pro Phe Thr Phe Val Ser Val Leu Ile Gly Ala Leu Ser Met

165					170					175					
Ala	Ser	Val	Pro	Pro	Leu	Leu	Gly	Phe	Val	Ser	Lys	Glu	Gly	Met	Ile
			180					185						190	
Thr	Ala	Phe	Met	Asp	Ala	Pro	Ile	Gly	Asn	Ser	Tyr	Val	Val	Leu	Leu
		195					200					205			
Leu	Val	Gly	Ala	Ala	Ile	Gly	Ala	Val	Leu	Thr	Phe	Thr	Tyr	Ser	Ala
	210					215					220				
Lys	Leu	Val	Leu	Gly	Ala	Phe	Val	Asp	Gly	Pro	Arg	Asp	Met	Ser	His
225					230					235					240
Val	Lys	Glu	Ala	Pro	Val	Ser	Leu	Trp	Leu	Pro	Ala	Ala	Leu	Pro	Gly
				245					250					255	
Leu	Met	Ser	Leu	Pro	Leu	Val	Leu	Val	Leu	Ser	Leu	Phe	Asp	Ala	Pro
			260					265					270		
Val	Ser	Ala	Ala	Ala	Thr	Ser	Ala	Ala	Gly	Glu	Ala	Ala	His	Met	His
		275					280					285			
Leu	Ala	Leu	Trp	His	Gly	Ile	Asn	Thr	Pro	Leu	Leu	Ile	Ser	Leu	Gly
	290					295					300				
Val	Leu	Val	Ala	Gly	Ile	Leu	Gly	Val	Leu	Phe	Arg	Lys	Glu	Leu	Trp
305					310					315					320
Lys	Ile	Ala	Glu	Thr	Ser	Pro	Phe	Pro	Ile	Ala	Thr	Gly	Asn	Asp	Ile
				325					330					335	
Leu	Ser	Met	Leu	Val	Tyr	Arg	Ala	Asn	Leu	Leu	Gly	Lys	Phe	Phe	Gly
			340					345					350		
Arg	Met	Ala	Asp	Ser	Met	Ser	Pro	Arg	Arg	His	Leu	Val	Ser	Leu	Ile
		355					360					365			
Val	Leu	Leu	Trp	Ala	Leu	Ala	Ala	Phe	Ala	Thr	Ile	His	Pro	Ser	Val
	370					375					380				
Gln	Leu	Ala	Pro	Lys	Gln	Pro	Gly	Ile	Asp	Arg	Trp	Ile	Asp	Leu	Ile
385					390					395					400
Pro	Leu	Ala	Ile	Ile	Ala	Leu	Ser	Val	Phe	Gly	Leu	Leu	Thr	Thr	Arg
				405					410					415	
Asn	Arg	Leu	Ser	Ala	Ala	Val	Leu	Val	Gly	Thr	Val	Gly	Val	Gly	Val
			420					425					430		
Ser	Phe	Gln	Met	Leu	Leu	Leu	Gly	Ala	Pro	Asp	Val	Ala	Leu	Thr	Gln
		435					440					445			
Phe	Leu	Val	Glu	Gly	Leu	Val	Val	Val	Ile	Ile	Met	Met	Val	Val	Arg
	450					455					460				
His	Gln	Pro	Ala	Asn	Phe	Lys	Arg	Ile	Lys	Pro	Ser	Arg	Arg	Arg	Ser
465					470					475					480
Thr	Val	Leu	Val	Ala	Val	Leu	Ala	Ala	Phe	Ala	Ala	Phe	Met	Ala	Val
				485					490					495	

Trp Gly Leu Leu Gly Arg His Glu Arg Ser Glu Leu Ala Met Trp Tyr
 500 505 510
 Leu Asn Gln Gly Pro Glu Ile Thr Ser Gly Ala Asn Val Val Asn Thr
 515 520 525
 Ile Leu Val Glu Phe Arg Ala Leu Asp Thr Leu Gly Glu Leu Ser Val
 530 535 540
 Leu Gly Met Ala Ala Val Val Ile Gly Ala Met Val Ala Ser Met Pro
 545 550 555 560
 Arg His Pro Phe Ala Lys Gly Thr His Pro Arg Pro Phe Gly Gln Ser
 565 570 575
 Gln Leu Asn Ser Ile Pro Leu Arg Met Leu Leu Lys Val Leu Val Pro
 580 585 590
 Ala Leu Cys Phe Leu Ser Phe Met Val Phe Met Arg Gly His Asn Asp
 595 600 605
 Pro Gly Gly Gly Phe Ile Ala Ala Leu Ile Ala Gly Gly Ala Leu Met
 610 615 620
 Leu Leu Tyr Leu Ser Lys Ala Lys Asp Gly Arg Ile Phe Arg Pro Asn
 625 630 635 640
 Val Pro Phe Ile Leu Thr Gly Ala Gly Ile Leu Met Ala Val Phe Ser
 645 650 655
 Gly Val Leu Gly Leu Thr His Gly Ser Phe Leu Tyr Ala Ile His Phe
 660 665 670
 Asn Phe Val Gly Gln His Trp Thr Thr Ser Met Ile Phe Asp Leu Gly
 675 680 685
 Val Tyr Leu Ala Val Leu Gly Met Val Ser Met Ala Ile Asn Gly Leu
 690 695 700
 Gly Gly Tyr Leu Arg Pro Gly Thr Asp Asn Ala Asp Leu Asp Tyr Ala
 705 710 715 720
 Arg Arg Ser Gly Pro Leu Pro Ala Thr Pro Thr Val Glu Pro Glu Pro
 725 730 735
 Glu Gly Asp Glu Asp Trp Pro Glu Pro Ile Asn Pro Ala Gly Asp Asn
 740 745 750
 Lys Glu Glu Ala Asn Arg
 755

<210> 685

<211> 1872

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1849)

<223> FRXA00606

<400> 685

```

atggataacc agactggcac gcgcgatatt cgtcgcctcg gtttcctggt caagaaaaat 60

gccgttcacg tttgtgtctg tattaatagg tgcgttgctcg atg gca tcg gtt ccg 115
                                         Met Ala Ser Val Pro
                                         1           5

ccg ttg ctc ggc ttc gtg tcc aaa gaa ggc atg atc aca gcg ttc atg 163
Pro Leu Leu Gly Phe Val Ser Lys Glu Gly Met Ile Thr Ala Phe Met
              10              15              20

gac gcc ccc atc ggc aac tcc tat gtt gta tta ctg ctg gtc ggc gca 211
Asp Ala Pro Ile Gly Asn Ser Tyr Val Val Leu Leu Leu Val Gly Ala
              25              30              35

gca atc ggc gcg gtc cta acc ttc aca tac tcc gcg aaa ctc gtg ctc 259
Ala Ile Gly Ala Val Leu Thr Phe Thr Tyr Ser Ala Lys Leu Val Leu
              40              45              50

ggc gca ttc gtc gac ggc cca cgc gac atg tca cac gtc aag gaa gcc 307
Gly Ala Phe Val Asp Gly Pro Arg Asp Met Ser His Val Lys Glu Ala
              55              60              65

ccc gtc tcc ctc tgg ctt ccg gcc gcc ctg cct gga ctt atg tct ctg 355
Pro Val Ser Leu Trp Leu Pro Ala Ala Leu Pro Gly Leu Met Ser Leu
              70              75              80              85

cca cta gtc cta gta ctt tcg ctt ttc gac gcc ccc gtc tcc gcc gca 403
Pro Leu Val Leu Val Leu Ser Leu Phe Asp Ala Pro Val Ser Ala Ala
              90              95              100

gcc acc tcc gcc gcg ggg gaa gcg gcg cac atg cac ctg gca ttg tgg 451
Ala Thr Ser Ala Ala Gly Glu Ala Ala His Met His Leu Ala Leu Trp
              105              110              115

cac ggc atc aac acc cca ctg ttg att tcc ttg ggt gtg ctg gtg gcc 499
His Gly Ile Asn Thr Pro Leu Leu Ile Ser Leu Gly Val Leu Val Ala
              120              125              130

gga atc ctt ggt gtg ctg ttc cgc aaa gag ctg tgg aaa atc gcc gag 547
Gly Ile Leu Gly Val Leu Phe Arg Lys Glu Leu Trp Lys Ile Ala Glu
              135              140              145

acc agc cct ttc ccc atc gcc aca ggc aac gac atc cta tcg atg ctg 595
Thr Ser Pro Phe Pro Ile Ala Thr Gly Asn Asp Ile Leu Ser Met Leu
              150              155              160              165

gtt tac cga gcc aac ttg ctg ggt aaa ttc ttc ggt cgc atg gct gat 643
Val Tyr Arg Ala Asn Leu Leu Gly Lys Phe Phe Gly Arg Met Ala Asp
              170              175              180

tcg atg agc cca cgc agg cac ttg gtc agc ctc atc gtg ctg ctc tgg 691
Ser Met Ser Pro Arg Arg His Leu Val Ser Leu Ile Val Leu Leu Trp
              185              190              195

gcg ctg gct gct ttt gcc acc att cac ccc tcg gtt cag ctt gca cca 739
Ala Leu Ala Ala Phe Ala Thr Ile His Pro Ser Val Gln Leu Ala Pro
              200              205              210

```

aag caa ccg gga att gat cgt tgg atc gac ctc att ccg ctt gcc atc	787
Lys Gln Pro Gly Ile Asp Arg Trp Ile Asp Leu Ile Pro Leu Ala Ile	
215 220 225	
atc gcg cta tct gtc ttc ggc ctg ctc acc acc cga aac cgc ctc agc	835
Ile Ala Leu Ser Val Phe Gly Leu Leu Thr Thr Arg Asn Arg Leu Ser	
230 235 240 245	
gca gcc gtg ctt gtg ggt acc gtt ggt gtg ggt gtt tcc ttc cag atg	883
Ala Ala Val Leu Val Gly Thr Val Gly Val Gly Val Ser Phe Gln Met	
250 255 260	
cta ctt ctg ggc gct ccc gat gtt gca ctt acc cag ttc ctg gta gaa	931
Leu Leu Leu Gly Ala Pro Asp Val Ala Leu Thr Gln Phe Leu Val Glu	
265 270 275	
ggc ctc gtc gtg gta atc atc atg atg gtt gtc cgg cac cag cct gcc	979
Gly Leu Val Val Val Ile Ile Met Met Val Val Arg His Gln Pro Ala	
280 285 290	
aac ttc aag cgc atc aag ccc agc aga agg cgc agc acc gtt ctt gtc	1027
Asn Phe Lys Arg Ile Lys Pro Ser Arg Arg Arg Ser Thr Val Leu Val	
295 300 305	
gcc gtc ctt gct gcc ttc gcc gca ttc atg gcg gtg tgg gga ttg ctt	1075
Ala Val Leu Ala Ala Phe Ala Ala Phe Met Ala Val Trp Gly Leu Leu	
310 315 320 325	
ggc cgt cac gaa cgt tct gag ctg gcc atg tgg tac ctc aac caa ggt	1123
Gly Arg His Glu Arg Ser Glu Leu Ala Met Trp Tyr Leu Asn Gln Gly	
330 335 340	
cca gag atc acc tct ggc gcc aac gtg gtg aac acc atc ctc gtg gaa	1171
Pro Glu Ile Thr Ser Gly Ala Asn Val Val Asn Thr Ile Leu Val Glu	
345 350 355	
ttc cgt gca ctg gat acg ttg ggc gag ctc tcc gtg ctt ggc atg gca	1219
Phe Arg Ala Leu Asp Thr Leu Gly Glu Leu Ser Val Leu Gly Met Ala	
360 365 370	
gct gtc gtc atc ggt gcg atg gtg gct tcc atg cct cgt cat ccg ttt	1267
Ala Val Val Ile Gly Ala Met Val Ala Ser Met Pro Arg His Pro Phe	
375 380 385	
gcc aag ggc acc cac cct cgc ccc ttt ggc caa tca cag ttg aac tcc	1315
Ala Lys Gly Thr His Pro Arg Pro Phe Gly Gln Ser Gln Leu Asn Ser	
390 395 400 405	
att ccg ctg cgc atg ctg ctt aag gtg ctg gtt cca gcg cta tgc ttc	1363
Ile Pro Leu Arg Met Leu Leu Lys Val Leu Val Pro Ala Leu Cys Phe	
410 415 420	
ttg agc ttc atg gtg ttc atg cgt gga cac aat gat ccg gga ggc ggt	1411
Leu Ser Phe Met Val Phe Met Arg Gly His Asn Asp Pro Gly Gly Gly	
425 430 435	
ttc atc gca gcc cta att gcc ggt ggc gcg ctg atg ctc ctg tac ctg	1459
Phe Ile Ala Ala Leu Ile Ala Gly Gly Ala Leu Met Leu Leu Tyr Leu	
440 445 450	
tcc aag gcc aaa gat ggc cgc att ttc cgc ccg aat gtt cct ttc att	1507

Ser Lys Ala Lys Asp Gly Arg Ile Phe Arg Pro Asn Val Pro Phe Ile
 455 460 465

ctc act ggt gcg ggc atc ttg atg gca gtg ttc tcg ggc gta ctg gga 1555
 Leu Thr Gly Ala Gly Ile Leu Met Ala Val Phe Ser Gly Val Leu Gly
 470 475 480 485

ctc acc cac ggt tct ttc ctg tac gcc atc cac ttc aac ttc gta ggc 1603
 Leu Thr His Gly Ser Phe Leu Tyr Ala Ile His Phe Asn Phe Val Gly
 490 495 500

cag cac tgg acc acc tcg atg atc ttc gac ctc ggc gtg tac ctg gcc 1651
 Gln His Trp Thr Thr Ser Met Ile Phe Asp Leu Gly Val Tyr Leu Ala
 505 510 515

gtg ttg ggc atg gtg tcc atg gca atc aac ggc ctg ggc gga tac ctg 1699
 Val Leu Gly Met Val Ser Met Ala Ile Asn Gly Leu Gly Gly Tyr Leu
 520 525 530

cgc cca ggt acc gac aat gca gat ctg gac tac gcc cgc cga agt ggc 1747
 Arg Pro Gly Thr Asp Asn Ala Asp Leu Asp Tyr Ala Arg Arg Ser Gly
 535 540 545

cca ctg cca gca acg cca acg gtt gaa ccc gaa cca gaa ggc gat gaa 1795
 Pro Leu Pro Ala Thr Pro Thr Val Glu Pro Glu Pro Glu Gly Asp Glu
 550 555 560 565

gac tgg ccc gaa ccc atc aac ccc gca ggc gat aac aaa gag gag gca 1843
 Asp Trp Pro Glu Pro Ile Asn Pro Ala Gly Asp Asn Lys Glu Glu Ala
 570 575 580

aac cga tgattctcgc actgacagtc gcg 1872
 Asn Arg

<210> 686

<211> 583

<212> PRT

<213> Corynebacterium glutamicum

<400> 686

Met Ala Ser Val Pro Pro Leu Leu Gly Phe Val Ser Lys Glu Gly Met
 1 5 10 15

Ile Thr Ala Phe Met Asp Ala Pro Ile Gly Asn Ser Tyr Val Val Leu
 20 25 30

Leu Leu Val Gly Ala Ala Ile Gly Ala Val Leu Thr Phe Thr Tyr Ser
 35 40 45

Ala Lys Leu Val Leu Gly Ala Phe Val Asp Gly Pro Arg Asp Met Ser
 50 55 60

His Val Lys Glu Ala Pro Val Ser Leu Trp Leu Pro Ala Ala Leu Pro
 65 70 75 80

Gly Leu Met Ser Leu Pro Leu Val Leu Val Leu Ser Leu Phe Asp Ala
 85 90 95

Pro Val Ser Ala Ala Ala Thr Ser Ala Ala Gly Glu Ala Ala His Met

100					105					110						
His	Leu	Ala	Leu	Trp	His	Gly	Ile	Asn	Thr	Pro	Leu	Leu	Ile	Ser	Leu	
115					120					125						
Gly	Val	Leu	Val	Ala	Gly	Ile	Leu	Gly	Val	Leu	Phe	Arg	Lys	Glu	Leu	
130					135					140						
Trp	Lys	Ile	Ala	Glu	Thr	Ser	Pro	Phe	Pro	Ile	Ala	Thr	Gly	Asn	Asp	
145					150					155					160	
Ile	Leu	Ser	Met	Leu	Val	Tyr	Arg	Ala	Asn	Leu	Leu	Gly	Lys	Phe	Phe	
165					170					175						
Gly	Arg	Met	Ala	Asp	Ser	Met	Ser	Pro	Arg	Arg	His	Leu	Val	Ser	Leu	
180					185					190						
Ile	Val	Leu	Leu	Trp	Ala	Leu	Ala	Ala	Phe	Ala	Thr	Ile	His	Pro	Ser	
195					200					205						
Val	Gln	Leu	Ala	Pro	Lys	Gln	Pro	Gly	Ile	Asp	Arg	Trp	Ile	Asp	Leu	
210					215					220						
Ile	Pro	Leu	Ala	Ile	Ile	Ala	Leu	Ser	Val	Phe	Gly	Leu	Leu	Thr	Thr	
225					230					235					240	
Arg	Asn	Arg	Leu	Ser	Ala	Ala	Val	Leu	Val	Gly	Thr	Val	Gly	Val	Gly	
245					250					255						
Val	Ser	Phe	Gln	Met	Leu	Leu	Leu	Gly	Ala	Pro	Asp	Val	Ala	Leu	Thr	
260					265					270						
Gln	Phe	Leu	Val	Glu	Gly	Leu	Val	Val	Val	Ile	Ile	Met	Met	Val	Val	
275					280					285						
Arg	His	Gln	Pro	Ala	Asn	Phe	Lys	Arg	Ile	Lys	Pro	Ser	Arg	Arg	Arg	
290					295					300						
Ser	Thr	Val	Leu	Val	Ala	Val	Leu	Ala	Ala	Phe	Ala	Ala	Phe	Met	Ala	
305					310					315					320	
Val	Trp	Gly	Leu	Leu	Gly	Arg	His	Glu	Arg	Ser	Glu	Leu	Ala	Met	Trp	
325					330					335						
Tyr	Leu	Asn	Gln	Gly	Pro	Glu	Ile	Thr	Ser	Gly	Ala	Asn	Val	Val	Asn	
340					345					350						
Thr	Ile	Leu	Val	Glu	Phe	Arg	Ala	Leu	Asp	Thr	Leu	Gly	Glu	Leu	Ser	
355					360					365						
Val	Leu	Gly	Met	Ala	Ala	Val	Val	Ile	Gly	Ala	Met	Val	Ala	Ser	Met	
370					375					380						
Pro	Arg	His	Pro	Phe	Ala	Lys	Gly	Thr	His	Pro	Arg	Pro	Phe	Gly	Gln	
385					390					395					400	
Ser	Gln	Leu	Asn	Ser	Ile	Pro	Leu	Arg	Met	Leu	Leu	Lys	Val	Leu	Val	
405					410					415						
Pro	Ala	Leu	Cys	Phe	Leu	Ser	Phe	Met	Val	Phe	Met	Arg	Gly	His	Asn	
420					425					430						

Asp Pro Gly Gly Gly Phe Ile Ala Ala Leu Ile Ala Gly Gly Ala Leu
 435 440 445
 Met Leu Leu Tyr Leu Ser Lys Ala Lys Asp Gly Arg Ile Phe Arg Pro
 450 455 460
 Asn Val Pro Phe Ile Leu Thr Gly Ala Gly Ile Leu Met Ala Val Phe
 465 470 475 480
 Ser Gly Val Leu Gly Leu Thr His Gly Ser Phe Leu Tyr Ala Ile His
 485 490 495
 Phe Asn Phe Val Gly Gln His Trp Thr Thr Ser Met Ile Phe Asp Leu
 500 505 510
 Gly Val Tyr Leu Ala Val Leu Gly Met Val Ser Met Ala Ile Asn Gly
 515 520 525
 Leu Gly Gly Tyr Leu Arg Pro Gly Thr Asp Asn Ala Asp Leu Asp Tyr
 530 535 540
 Ala Arg Arg Ser Gly Pro Leu Pro Ala Thr Pro Thr Val Glu Pro Glu
 545 550 555 560
 Pro Glu Gly Asp Glu Asp Trp Pro Glu Pro Ile Asn Pro Ala Gly Asp
 565 570 575
 Asn Lys Glu Glu Ala Asn Arg
 580

<210> 687
 <211> 1653
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1630)
 <223> RXN00595

<400> 687
 cgacgacacc cgggtccatcg aaccagatga cgatcaatcg cctttgacta ctagcgctcg 60
 ttcagtcacc aacccaacag atcaggagga taaagcttaa atg gcc atg gat gtt 115
 Met Ala Met Asp Val
 1 5
 ctc ctt cct att ttc gtt gca gtt ccc ctt gct gcc tct gcc att gcg 163
 Leu Leu Pro Ile Phe Val Ala Val Pro Leu Ala Ala Ser Ala Ile Ala
 10 15 20
 gtg ctt ctg ccg tgg cgt ctc atc cgc gat att ttg cac atc atc gtg 211
 Val Leu Leu Pro Trp Arg Leu Ile Arg Asp Ile Leu His Ile Ile Val
 25 30 35
 cct ttc gcg ggt att ttt gct ggc atc tgg ttg ttt gca cac acc gct 259
 Pro Phe Ala Gly Ile Phe Ala Gly Ile Trp Leu Phe Ala His Thr Ala
 40 45 50

gaa cac ggc ccg att gct cac aac gtg ggc ctt tat gtc ggt ggc gtg	307
Glu His Gly Pro Ile Ala His Asn Val Gly Leu Tyr Val Gly Gly Val	
55 60 65	
gca atc ccc ttt gct gcc gat acg ttc agc gcc atc atg ttg atc acc	355
Ala Ile Pro Phe Ala Ala Asp Thr Phe Ser Ala Ile Met Leu Ile Thr	
70 75 80 85	
acc tcg atc gtt gcg gtg gct gcc aac tgg ttt gcc acc atc gtc ggt	403
Thr Ser Ile Val Ala Val Ala Asn Trp Phe Ala Thr Ile Val Gly	
90 95 100	
gaa acc cgc gcg cgt ttc tat cca gcg ctc aca ttg atg ctg atc acg	451
Glu Thr Arg Ala Arg Phe Tyr Pro Ala Leu Thr Leu Met Leu Ile Thr	
105 110 115	
ggc gtc aac ggt gct ctg ctg act gcc gat ctg ttc aac ttc ttt gtg	499
Gly Val Asn Gly Ala Leu Leu Thr Ala Asp Leu Phe Asn Phe Phe Val	
120 125 130	
ttc atc gaa gtg atg ctg ctg cct tcc tat ggt ttg atc gcc atg acc	547
Phe Ile Glu Val Met Leu Leu Pro Ser Tyr Gly Leu Ile Ala Met Thr	
135 140 145	
gga acg tgg gcg cgc cta gcc tct gga cga atc ttc gta cta gtc aat	595
Gly Thr Trp Ala Arg Leu Ala Ser Gly Arg Ile Phe Val Leu Val Asn	
150 155 160 165	
ctc tct gcc tcc aca ttg ctg gtt gca ggt gtg gga atc gtc tac ggt	643
Leu Ser Ala Ser Thr Leu Leu Val Ala Gly Val Gly Ile Val Tyr Gly	
170 175 180	
gtc ata ggc tca gtc aac atc gca gct ctg caa gat gtc gta gag ggc	691
Val Ile Gly Ser Val Asn Ile Ala Ala Leu Gln Asp Val Val Glu Gly	
185 190 195	
aac ccc ctg gtt gcc agc gca atg ggc atc gtg gtt att gcc atc gcg	739
Asn Pro Leu Val Ala Ser Ala Met Gly Ile Val Val Ile Ala Ile Ala	
200 205 210	
gtt aaa gcc ggt gta ttc cca gtg cac aca tgg ctg cca cgc acc tat	787
Val Lys Ala Gly Val Phe Pro Val His Thr Trp Leu Pro Arg Thr Tyr	
215 220 225	
cct ggt aca tca gca gct gtg atg ggg ttg ttc tcc ggt ttg cac acc	835
Pro Gly Thr Ser Ala Ala Val Met Gly Leu Phe Ser Gly Leu His Thr	
230 235 240 245	
aaa gtc gcg gta tac atg ctc tat cgc att tgg gtc cac att ttt aac	883
Lys Val Ala Val Tyr Met Leu Tyr Arg Ile Trp Val His Ile Phe Asn	
250 255 260	
atg gat ccc acg tgg aat tgg ctg att gtc gca ttc atg gtg ata tcc	931
Met Asp Pro Thr Trp Asn Trp Leu Ile Val Ala Phe Met Val Ile Ser	
265 270 275	
atg ctg gtc ggt ggc ttc gct gga ctt gct gaa aac tcc atc cgt cgc	979
Met Leu Val Gly Gly Phe Ala Gly Leu Ala Glu Asn Ser Ile Arg Arg	
280 285 290	
gtc ctt gcc tac caa atg gtc aac ggc atg cca ttt att ctc atc atg	1027

Val	Leu	Ala	Tyr	Gln	Met	Val	Asn	Gly	Met	Pro	Phe	Ile	Leu	Ile	Met	
295						300					305					
atg	gcg	ttt	acc	tct	gac	gat	cca	cag	cg	gca	ctt	gcc	gct	gg	ctg	1075
Met	Ala	Phe	Thr	Ser	Asp	Asp	Pro	Gln	Arg	Ala	Leu	Ala	Ala	Gly	Leu	
310					315					320					325	
ttg	tac	acc	ctg	cac	cac	atg	atc	acc	atc	gcc	gca	ttg	gtg	ctc	act	1123
Leu	Tyr	Thr	Leu	His	His	Met	Ile	Thr	Ile	Ala	Ala	Leu	Val	Leu	Thr	
				330					335					340		
tcc	ggc	gca	atc	gaa	gaa	acc	tac	ggc	acc	gg	atg	ttg	tcc	aag	ctg	1171
Ser	Gly	Ala	Ile	Glu	Glu	Thr	Tyr	Gly	Thr	Gly	Met	Leu	Ser	Lys	Leu	
			345					350					355			
tct	ggc	ctt	gca	cg	cg	gaa	ccc	gtc	gtc	gca	gca	gtg	ttc	gct	gca	1219
Ser	Gly	Leu	Ala	Arg	Arg	Glu	Pro	Val	Val	Ala	Ala	Val	Phe	Ala	Ala	
		360					365					370				
gg	gcc	ttc	tct	gtt	gtc	gg	ttc	cca	ccg	ttt	tcc	gg	atg	tgg	gg	1267
Gly	Ala	Phe	Ser	Val	Val	Gly	Phe	Pro	Pro	Phe	Ser	Gly	Met	Trp	Gly	
	375					380					385					
aaa	gcg	ctc	atc	ctg	ctc	gag	atc	gcc	cg	gtc	ggc	aat	att	gca	gca	1315
Lys	Ala	Leu	Ile	Leu	Leu	Glu	Ile	Ala	Arg	Val	Gly	Asn	Ile	Ala	Ala	
390					395					400					405	
tgg	atc	gca	atc	gcc	gcc	atc	atc	atc	gcc	agc	ctg	ggc	gca	ctg	ctc	1363
Trp	Ile	Ala	Ile	Ala	Ala	Ile	Ile	Ile	Ala	Ser	Leu	Gly	Ala	Leu	Leu	
				410					415					420		
tcg	atg	atc	cg	gtg	tgg	cgt	gaa	gtc	ttc	tgg	gg	ggc	gca	atg	cac	1411
Ser	Met	Ile	Arg	Val	Trp	Arg	Glu	Val	Phe	Trp	Gly	Gly	Ala	Met	His	
			425					430					435			
cag	cg	ggc	gtc	tcg	ccg	cag	ctg	cg	atc	agc	cca	gca	aaa	atc	gcc	1459
Gln	Arg	Gly	Val	Ser	Pro	Gln	Leu	Arg	Ile	Ser	Pro	Ala	Lys	Ile	Ala	
		440					445					450				
cca	gcg	ctc	agc	ctg	atc	att	tta	tcg	gta	ggc	atg	ttc	atc	ttc	gcg	1507
Pro	Ala	Leu	Ser	Leu	Ile	Ile	Leu	Ser	Val	Gly	Met	Phe	Ile	Phe	Ala	
	455					460					465					
ggc	ccg	ctt	atc	gac	gcg	acc	ctc	acc	gcc	acc	gac	ggc	ctc	ttg	aac	1555
Gly	Pro	Leu	Ile	Asp	Ala	Thr	Leu	Thr	Ala	Thr	Asp	Gly	Leu	Leu	Asn	
470					475				480						485	
acc	gat	gca	tac	caa	cag	gct	gtg	ctc	gg	gaa	aat	gcc	atc	gga	gtg	1603
Thr	Asp	Ala	Tyr	Gln	Gln	Ala	Val	Leu	Gly	Glu	Asn	Ala	Ile	Gly	Val	
				490					495					500		
cca	agc	cct	agc	tac	cag	gga	gga	aac	taatgcttaa	cgccctgaaa						1650
Pro	Ser	Pro	Ser	Tyr	Gln	Gly	Gly	Asn								
			505					510								
ttc																1653

<210> 688
 <211> 510
 <212> PRT

<213> Corynebacterium glutamicum

<400> 688

Met Ala Met Asp Val Leu Leu Pro Ile Phe Val Ala Val Pro Leu Ala
 1 5 10 15
 Ala Ser Ala Ile Ala Val Leu Leu Pro Trp Arg Leu Ile Arg Asp Ile
 20 25 30
 Leu His Ile Ile Val Pro Phe Ala Gly Ile Phe Ala Gly Ile Trp Leu
 35 40 45
 Phe Ala His Thr Ala Glu His Gly Pro Ile Ala His Asn Val Gly Leu
 50 55 60
 Tyr Val Gly Gly Val Ala Ile Pro Phe Ala Ala Asp Thr Phe Ser Ala
 65 70 75 80
 Ile Met Leu Ile Thr Thr Ser Ile Val Ala Val Ala Ala Asn Trp Phe
 85 90 95
 Ala Thr Ile Val Gly Glu Thr Arg Ala Arg Phe Tyr Pro Ala Leu Thr
 100 105 110
 Leu Met Leu Ile Thr Gly Val Asn Gly Ala Leu Leu Thr Ala Asp Leu
 115 120 125
 Phe Asn Phe Phe Val Phe Ile Glu Val Met Leu Leu Pro Ser Tyr Gly
 130 135 140
 Leu Ile Ala Met Thr Gly Thr Trp Ala Arg Leu Ala Ser Gly Arg Ile
 145 150 155 160
 Phe Val Leu Val Asn Leu Ser Ala Ser Thr Leu Leu Val Ala Gly Val
 165 170 175
 Gly Ile Val Tyr Gly Val Ile Gly Ser Val Asn Ile Ala Ala Leu Gln
 180 185 190
 Asp Val Val Glu Gly Asn Pro Leu Val Ala Ser Ala Met Gly Ile Val
 195 200 205
 Val Ile Ala Ile Ala Val Lys Ala Gly Val Phe Pro Val His Thr Trp
 210 215 220
 Leu Pro Arg Thr Tyr Pro Gly Thr Ser Ala Ala Val Met Gly Leu Phe
 225 230 235 240
 Ser Gly Leu His Thr Lys Val Ala Val Tyr Met Leu Tyr Arg Ile Trp
 245 250 255
 Val His Ile Phe Asn Met Asp Pro Thr Trp Asn Trp Leu Ile Val Ala
 260 265 270
 Phe Met Val Ile Ser Met Leu Val Gly Gly Phe Ala Gly Leu Ala Glu
 275 280 285
 Asn Ser Ile Arg Arg Val Leu Ala Tyr Gln Met Val Asn Gly Met Pro
 290 295 300
 Phe Ile Leu Ile Met Met Ala Phe Thr Ser Asp Asp Pro Gln Arg Ala

305		310		315		320
Leu Ala Ala Gly	Leu Leu Tyr Thr	Leu His His Met	Ile Thr	Ile Ala		
	325			330		335
Ala Leu Val Leu	Thr Ser Gly Ala	Ile Glu Glu Thr	Tyr Gly	Thr Gly		
	340		345	350		
Met Leu Ser Lys	Leu Ser Gly Leu	Ala Arg Arg Glu	Pro Val	Val Ala		
	355		360	365		
Ala Val Phe Ala	Ala Gly Ala Phe	Ser Val Val Gly	Phe Pro	Pro Phe		
	370		375	380		
Ser Gly Met Trp	Gly Lys Ala Leu	Ile Leu Leu Glu	Ile Ala	Arg Val		
	385		390	395		400
Gly Asn Ile Ala	Ala Trp Ile Ala	Ile Ala Ala Ile	Ile Ile	Ala Ser		
	405		410	415		
Leu Gly Ala Leu	Leu Ser Met Ile	Arg Val Trp	Arg Glu	Val Phe	Trp	
	420		425	430		
Gly Gly Ala Met	His Gln Arg Gly	Val Ser Pro Gln	Leu Arg	Ile Ser		
	435		440	445		
Pro Ala Lys Ile	Ala Pro Ala Leu	Ser Leu Ile Ile	Leu Ser	Val Gly		
	450		455	460		
Met Phe Ile Phe	Ala Gly Pro Leu	Ile Asp Ala Thr	Leu Thr	Ala Thr		
	465		470	475		480
Asp Gly Leu Leu	Asn Thr Asp Ala	Tyr Gln Gln Ala	Val Leu	Gly Glu		
	485		490	495		
Asn Ala Ile Gly	Val Pro Ser Pro	Ser Tyr Gln Gly	Gly Asn			
	500		505	510		

<210> 689

<211> 865

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(865)

<223> FRXA00608

<400> 689

cgacgacacc cgggtccatcg aaccagatga cgatcaatcg cctttgacta ctagcgctcg 60

ttcagtcacc aacccaacag atcaggagga taaagcttaa	atg gcc atg gat gtt	115
	Met Ala Met Asp Val	
	1 5	

ctc ctt cct att ttc gtt gca gtt ccc ctt gct gcc tct gcc att gcg	163
Leu Leu Pro Ile Phe Val Ala Val Pro Leu Ala Ala Ser Ala Ile Ala	
10 15 20	

gtg ctt ctg ccg tgg cgt ctc atc cgc gat att ttg cac atc atc gtg	211
---	-----

Val	Leu	Leu	Pro	Trp	Arg	Leu	Ile	Arg	Asp	Ile	Leu	His	Ile	Ile	Val	
			25					30					35			
cct	ttc	gcg	ggt	att	ttt	gct	ggc	atc	tgg	ttg	ttt	gca	cac	acc	gct	259
Pro	Phe	Ala	Gly	Ile	Phe	Ala	Gly	Ile	Trp	Leu	Phe	Ala	His	Thr	Ala	
		40					45					50				
gaa	cac	ggc	ccg	att	gct	cac	aac	gtg	ggc	ctt	tat	gtc	ggg	ggc	gtg	307
Glu	His	Gly	Pro	Ile	Ala	His	Asn	Val	Gly	Leu	Tyr	Val	Gly	Gly	Val	
	55					60					65					
gca	atc	ccc	ttt	gct	gcc	gat	acg	ttc	agc	gcc	atc	atg	ttg	atc	acc	355
Ala	Ile	Pro	Phe	Ala	Ala	Asp	Thr	Phe	Ser	Ala	Ile	Met	Leu	Ile	Thr	
	70				75					80					85	
acc	tgc	atc	gtt	gcg	gtg	gct	gcc	aac	tgg	ttt	gcc	acc	atc	gtc	ggg	403
Thr	Ser	Ile	Val	Ala	Val	Ala	Ala	Asn	Trp	Phe	Ala	Thr	Ile	Val	Gly	
				90					95					100		
gaa	acc	cgc	gcg	cgt	ttc	tat	cca	gcg	ctc	aca	ttg	atg	ctg	atc	acg	451
Glu	Thr	Arg	Ala	Arg	Phe	Tyr	Pro	Ala	Leu	Thr	Leu	Met	Leu	Ile	Thr	
			105					110					115			
ggc	gtc	aac	ggt	gct	ctg	ctg	act	gcc	gat	ctg	ttc	aac	ttc	ttt	gtg	499
Gly	Val	Asn	Gly	Ala	Leu	Leu	Thr	Ala	Asp	Leu	Phe	Asn	Phe	Phe	Val	
		120					125					130				
ttc	atc	gaa	gtg	atg	ctg	ctg	cct	tcc	tat	ggg	ttg	atc	gcc	atg	acc	547
Phe	Ile	Glu	Val	Met	Leu	Leu	Pro	Ser	Tyr	Gly	Leu	Ile	Ala	Met	Thr	
	135					140					145					
gga	acg	tgg	gcg	cgc	cta	gcc	tct	gga	cga	atc	ttc	gta	cta	gtc	aat	595
Gly	Thr	Trp	Ala	Arg	Leu	Ala	Ser	Gly	Arg	Ile	Phe	Val	Leu	Val	Asn	
	150				155					160					165	
ctc	tct	gcc	tcc	aca	ttg	ctg	gtt	gca	ggg	gtg	gga	atc	gtc	tac	ggg	643
Leu	Ser	Ala	Ser	Thr	Leu	Leu	Val	Ala	Gly	Val	Gly	Ile	Val	Tyr	Gly	
				170					175					180		
gtc	ata	ggc	tca	gtc	aac	atc	gca	gct	ctg	caa	gat	gtc	gta	gag	ggc	691
Val	Ile	Gly	Ser	Val	Asn	Ile	Ala	Ala	Leu	Gln	Asp	Val	Val	Glu	Gly	
			185					190					195			
aac	ccc	ctg	gtt	gcc	agc	gca	atg	ggc	atc	gtg	gtt	att	gcc	atc	gcg	739
Asn	Pro	Leu	Val	Ala	Ser	Ala	Met	Gly	Ile	Val	Val	Ile	Ala	Ile	Ala	
		200					205					210				
gtt	aaa	gcc	ggt	gta	ttc	cca	gtg	cac	aca	tgg	ctg	cca	cgc	acc	tat	787
Val	Lys	Ala	Gly	Val	Phe	Pro	Val	His	Thr	Trp	Leu	Pro	Arg	Thr	Tyr	
	215					220					225					
cct	ggt	aca	tca	gca	gct	gtg	atg	ggg	ttg	ttc	tcc	ggg	ttg	cac	acc	835
Pro	Gly	Thr	Ser	Ala	Ala	Val	Met	Gly	Leu	Phe	Ser	Gly	Leu	His	Thr	
	230				235				240					245		
aaa	gtc	gcg	gta	tac	atg	ctc	tat	cgc	att							865
Lys	Val	Ala	Val	Tyr	Met	Leu	Tyr	Arg	Ile							
				250				255								

<210> 690

<211> 255

<212> PRT

<213> Corynebacterium glutamicum

<400> 690

Met Ala Met Asp Val Leu Leu Pro Ile Phe Val Ala Val Pro Leu Ala
 1 5 10 15

Ala Ser Ala Ile Ala Val Leu Leu Pro Trp Arg Leu Ile Arg Asp Ile
 20 25 30

Leu His Ile Ile Val Pro Phe Ala Gly Ile Phe Ala Gly Ile Trp Leu
 35 40 45

Phe Ala His Thr Ala Glu His Gly Pro Ile Ala His Asn Val Gly Leu
 50 55 60

Tyr Val Gly Gly Val Ala Ile Pro Phe Ala Ala Asp Thr Phe Ser Ala
 65 70 75 80

Ile Met Leu Ile Thr Thr Ser Ile Val Ala Val Ala Ala Asn Trp Phe
 85 90 95

Ala Thr Ile Val Gly Glu Thr Arg Ala Arg Phe Tyr Pro Ala Leu Thr
 100 105 110

Leu Met Leu Ile Thr Gly Val Asn Gly Ala Leu Leu Thr Ala Asp Leu
 115 120 125

Phe Asn Phe Phe Val Phe Ile Glu Val Met Leu Leu Pro Ser Tyr Gly
 130 135 140

Leu Ile Ala Met Thr Gly Thr Trp Ala Arg Leu Ala Ser Gly Arg Ile
 145 150 155 160

Phe Val Leu Val Asn Leu Ser Ala Ser Thr Leu Leu Val Ala Gly Val
 165 170 175

Gly Ile Val Tyr Gly Val Ile Gly Ser Val Asn Ile Ala Ala Leu Gln
 180 185 190

Asp Val Val Glu Gly Asn Pro Leu Val Ala Ser Ala Met Gly Ile Val
 195 200 205

Val Ile Ala Ile Ala Val Lys Ala Gly Val Phe Pro Val His Thr Trp
 210 215 220

Leu Pro Arg Thr Tyr Pro Gly Thr Ser Ala Ala Val Met Gly Leu Phe
 225 230 235 240

Ser Gly Leu His Thr Lys Val Ala Val Tyr Met Leu Tyr Arg Ile
 245 250 255

<210> 691

<211> 2118

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(2118)

<223> RXA00913

<400> 691

att att tcc gtg gtg ggc att ggt acc cgc gaa gct ttg ctg gca ggt	48
Ile Ile Ser Val Val Gly Ile Gly Thr Arg Glu Ala Leu Leu Ala Gly	
1 5 10 15	
ctt gca ctg acc gtt gcg cac tcc ttg ttt aag gca aca ttg ttc atg	96
Leu Ala Leu Thr Val Ala His Ser Leu Phe Lys Ala Thr Leu Phe Met	
20 25 30	
aca gtt ggt gcc att gac cac acc acc gga act cgt gat att cgt aaa	144
Thr Val Gly Ala Ile Asp His Thr Thr Gly Thr Arg Asp Ile Arg Lys	
35 40 45	
ctc tcc ggt ctg tgg cgt aaa caa ccg atc ctg ttc gcc gtt gct gct	192
Leu Ser Gly Leu Trp Arg Lys Gln Pro Ile Leu Phe Ala Val Ala Ala	
50 55 60	
gtt tcg gcg gcg tcc atg gct ggt att ccg cca ctg ttt ggt ttt atc	240
Val Ser Ala Ala Ser Met Ala Gly Ile Pro Pro Leu Phe Gly Phe Ile	
65 70 75 80	
gcc aag gaa aca gcg ctg gat acc gtg ttg aat gag cag atg ttg cat	288
Ala Lys Glu Thr Ala Leu Asp Thr Val Leu Asn Glu Gln Met Leu His	
85 90 95	
ggc atg cca ggt cga ttg atg ctg gct ggc atc gtt ttg ggt tcc atc	336
Gly Met Pro Gly Arg Leu Met Leu Ala Gly Ile Val Leu Gly Ser Ile	
100 105 110	
ttc acc atg gca tat tcc tgc tac ttc ctg tac gaa gcc ttt gcc acg	384
Phe Thr Met Ala Tyr Ser Cys Tyr Phe Leu Tyr Glu Ala Phe Ala Thr	
115 120 125	
aag cac tcc aaa ttc cca gag gcc aac ggt gtc tca cct gca gtg gag	432
Lys His Ser Lys Phe Pro Glu Ala Asn Gly Val Ser Pro Ala Val Glu	
130 135 140	
gca atg cat ccg gtg aag ttt aag ctg tgg atc gca cct gtc atc ctg	480
Ala Met His Pro Val Lys Phe Lys Leu Trp Ile Ala Pro Val Ile Leu	
145 150 155 160	
gct att ttg acc gta gtg ttt ggt gtt ttc ccc aag cca gtg tcg gaa	528
Ala Ile Leu Thr Val Val Phe Gly Val Phe Pro Lys Pro Val Ser Glu	
165 170 175	
gca att gtc acg cat ctt gat aac gtc acg cca tcg ctt gat gat gtc	576
Ala Ile Val Thr His Leu Asp Asn Val Thr Pro Ser Leu Asp Asp Val	
180 185 190	
cac acc aaa ctg gcc ttg tgg cat ggt ctg aat cta ccg ctg ctg ctg	624
His Thr Lys Leu Ala Leu Trp His Gly Leu Asn Leu Pro Leu Leu Leu	
195 200 205	
tct gtg gtg atc atc att tcc gga ttc atc atc ttc tgg gag cga gac	672
Ser Val Val Ile Ile Ile Ser Gly Phe Ile Ile Phe Trp Glu Arg Asp	
210 215 220	
acc gtc gaa cgt ttg cgc cct aac acc gca gcg ttt ggc agt gcc gat	720

Thr 225	Val	Glu	Arg	Leu	Arg 230	Pro	Asn	Thr	Ala	Ala 235	Phe	Gly	Ser	Ala	Asp 240	
acc	gcc	tac	gac	gcc	att	ctt	gat	gca	ctg	cgt	gtg	ctc	tcc	cac	cgc	768
Thr	Ala	Tyr	Asp	Ala	Ile	Leu	Asp	Ala	Leu	Arg	Val	Leu	Ser	His	Arg	
				245					250					255		
ctg	act	gca	tcc	acc	cag	cgt	ggc	tct	ttg	acc	ctg	aac	gtc	ggc	gtg	816
Leu	Thr	Ala	Ser	Thr	Gln	Arg	Gly	Ser	Leu	Thr	Leu	Asn	Val	Gly	Val	
			260					265					270			
atc	ttc	ttc	gtc	ctc	acg	att	gtt	ccg	ctg	atc	gct	ttg	atc	act	ggc	864
Ile	Phe	Phe	Val	Leu	Thr	Ile	Val	Pro	Leu	Ile	Ala	Leu	Ile	Thr	Gly	
		275					280					285				
gaa	caa	agc	gat	gtc	cgc	atg	gag	ctg	tgg	gat	agc	cct	att	cag	ggc	912
Glu	Gln	Ser	Asp	Val	Arg	Met	Glu	Leu	Trp	Asp	Ser	Pro	Ile	Gln	Gly	
	290					295					300					
ttc	atc	gcg	gcc	atc	att	atc	gtc	gtt	gcg	att	gtg	gca	acc	acc	atg	960
Phe	Ile	Ala	Ala	Ile	Ile	Ile	Val	Val	Ala	Ile	Val	Ala	Thr	Thr	Met	
305					310				315						320	
gat	aac	cgt	ttg	tct	gcg	ctg	att	ttg	gtg	ggc	gtg	aca	ggc	tat	ggc	1008
Asp	Asn	Arg	Leu	Ser	Ala	Leu	Ile	Leu	Val	Gly	Val	Thr	Gly	Tyr	Gly	
				325					330					335		
att	gcc	gtt	atc	ttc	gcg	cta	cat	ggc	gca	ccg	gac	ttg	gcg	cta	acc	1056
Ile	Ala	Val	Ile	Phe	Ala	Leu	His	Gly	Ala	Pro	Asp	Leu	Ala	Leu	Thr	
			340					345					350			
cag	gtg	ctg	gtg	gag	acc	atc	gtc	atg	gtg	gta	ttc	atg	ctg	gtg	ctg	1104
Gln	Val	Leu	Val	Glu	Thr	Ile	Val	Met	Val	Val	Phe	Met	Leu	Val	Leu	
		355					360					365				
cgt	aaa	atg	ccg	aca	gaa	gtt	gcg	tgg	aag	gca	gaa	cct	aaa	cag	tct	1152
Arg	Lys	Met	Pro	Thr	Glu	Val	Ala	Trp	Lys	Ala	Glu	Pro	Lys	Gln	Ser	
	370					375					380					
cgc	gtg	cga	gcg	tgg	ctt	gct	ggc	gcc	acc	gga	ttg	tcc	gtt	gtt	att	1200
Arg	Val	Arg	Ala	Trp	Leu	Ala	Gly	Ala	Thr	Gly	Leu	Ser	Val	Val	Ile	
385					390					395					400	
gtc	acc	att	ttt	gcc	atg	aat	gct	cgc	acc	act	gaa	ccg	atc	tct	gta	1248
Val	Thr	Ile	Phe	Ala	Met	Asn	Ala	Arg	Thr	Thr	Glu	Pro	Ile	Ser	Val	
				405					410					415		
tac	atg	cag	gat	ctg	gcc	tat	gag	atc	gga	cat	ggc	gca	aac	acc	gtc	1296
Tyr	Met	Gln	Asp	Leu	Ala	Tyr	Glu	Ile	Gly	His	Gly	Ala	Asn	Thr	Val	
			420					425					430			
aac	gta	ctg	ctc	gta	gac	ctg	cgt	ggc	ttt	gat	acc	ttc	ggc	gaa	att	1344
Asn	Val	Leu	Leu	Val	Asp	Leu	Arg	Gly	Phe	Asp	Thr	Phe	Gly	Glu	Ile	
		435					440					445				
tcc	gtc	ctt	gtg	atc	gcg	gca	acc	ggc	atc	gcc	tcc	ctg	gtc	tac	cga	1392
Ser	Val	Leu	Val	Ile	Ala	Ala	Thr	Gly	Ile	Ala	Ser	Leu	Val	Tyr	Arg	
	450					455					460					
aac	cgc	agc	ttc	cgc	aag	gat	tct	cgc	aga	cca	acc	ctg	gct	acc	act	1440
Asn	Arg	Ser	Phe	Arg	Lys	Asp	Ser	Arg	Arg	Pro	Thr	Leu	Ala	Thr	Thr	

465	470	475	480	
ggt cgc cgt tgg ttg gct gct gct gtt gat acc gaa agg gcg cag aac				1488
Gly Arg Arg Trp Leu Ala Ala Ala Val Asp Thr Glu Arg Ala Gln Asn				
	485	490	495	
cgc tcg ctg atg gtt gat gtg gca acg cgc atc ctc ttc cct gcc atg				1536
Arg Ser Leu Met Val Asp Val Ala Thr Arg Ile Leu Phe Pro Ala Met				
	500	505	510	
atc atg ttg tct gtg tac ttc ttc ttc gcc gga cac aac gcg ccg ggc				1584
Ile Met Leu Ser Val Tyr Phe Phe Phe Ala Gly His Asn Ala Pro Gly				
	515	520	525	
ggc gga ttc gcc ggc ggc ctt gtt gcc tcc ttg gcg ttc gcc ttg cgc				1632
Gly Gly Phe Ala Gly Gly Leu Val Ala Ser Leu Ala Phe Ala Leu Arg				
	530	535	540	
tac ctt gcc ggt gga cgt gaa gaa ctt gaa gaa gcg ttg cct atc gac				1680
Tyr Leu Ala Gly Gly Arg Glu Glu Leu Glu Glu Ala Leu Pro Ile Asp				
	545	550	555	560
gcc ggc cgt atc ttg gga act gga cta ttt gtt tct gca act gca gtg				1728
Ala Gly Arg Ile Leu Gly Thr Gly Leu Phe Val Ser Ala Thr Ala Val				
	565	570	575	
ctg tgg ccc atg gtt ctt ctt ggt gaa cca ccg ctg acc tcc cat att				1776
Leu Trp Pro Met Val Leu Leu Gly Glu Pro Pro Leu Thr Ser His Ile				
	580	585	590	
tgg gat ctc aca ctg cca ctt atc ggt gag att cac att gca tcc gcg				1824
Trp Asp Leu Thr Leu Pro Leu Ile Gly Glu Ile His Ile Ala Ser Ala				
	595	600	605	
ctg ctc ttt gac ctt ggt gtc tac ctg atc gtc atc ggt ttg acc atg				1872
Leu Leu Phe Asp Leu Gly Val Tyr Leu Ile Val Ile Gly Leu Thr Met				
	610	615	620	
cac att ctc aac agt ttg ggc ggc cag ctc gac cgc gat gag gaa atg				1920
His Ile Leu Asn Ser Leu Gly Gly Gln Leu Asp Arg Asp Glu Glu Met				
	625	630	635	640
cgt aag cag cgt gcg cgc gac cga gct cga cgc ttg gcg cgc aac cag				1968
Arg Lys Gln Arg Ala Arg Asp Arg Ala Arg Arg Leu Ala Arg Asn Gln				
	645	650	655	
cgt cga gaa gca gca acc gtc ggc gca cgc agg tcg aac gag aaa tcg				2016
Arg Arg Glu Ala Ala Thr Val Gly Ala Arg Arg Ser Asn Glu Lys Ser				
	660	665	670	
aca cgc caa atg ccg acg att cgg cct cca ggg gca gac aca gaa tcg				2064
Thr Arg Gln Met Pro Thr Ile Arg Pro Pro Gly Ala Asp Thr Glu Ser				
	675	680	685	
gtg gag cag aac ggt gag aac cag acg tcg ata agc aca aag cgt tta				2112
Val Glu Gln Asn Gly Glu Asn Gln Thr Ser Ile Ser Thr Lys Arg Leu				
	690	695	700	
aag cag				2118
Lys Gln				
705				

<210> 692
 <211> 706
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 692

```

Ile Ile Ser Val Val Gly Ile Gly Thr Arg Glu Ala Leu Leu Ala Gly
 1             5             10             15

Leu Ala Leu Thr Val Ala His Ser Leu Phe Lys Ala Thr Leu Phe Met
      20             25             30

Thr Val Gly Ala Ile Asp His Thr Thr Gly Thr Arg Asp Ile Arg Lys
      35             40             45

Leu Ser Gly Leu Trp Arg Lys Gln Pro Ile Leu Phe Ala Val Ala Ala
 50             55             60

Val Ser Ala Ala Ser Met Ala Gly Ile Pro Pro Leu Phe Gly Phe Ile
 65             70             75             80

Ala Lys Glu Thr Ala Leu Asp Thr Val Leu Asn Glu Gln Met Leu His
      85             90             95

Gly Met Pro Gly Arg Leu Met Leu Ala Gly Ile Val Leu Gly Ser Ile
      100            105            110

Phe Thr Met Ala Tyr Ser Cys Tyr Phe Leu Tyr Glu Ala Phe Ala Thr
      115            120            125

Lys His Ser Lys Phe Pro Glu Ala Asn Gly Val Ser Pro Ala Val Glu
      130            135            140

Ala Met His Pro Val Lys Phe Lys Leu Trp Ile Ala Pro Val Ile Leu
      145            150            155            160

Ala Ile Leu Thr Val Val Phe Gly Val Phe Pro Lys Pro Val Ser Glu
      165            170            175

Ala Ile Val Thr His Leu Asp Asn Val Thr Pro Ser Leu Asp Asp Val
      180            185            190

His Thr Lys Leu Ala Leu Trp His Gly Leu Asn Leu Pro Leu Leu Leu
      195            200            205

Ser Val Val Ile Ile Ile Ser Gly Phe Ile Ile Phe Trp Glu Arg Asp
      210            215            220

Thr Val Glu Arg Leu Arg Pro Asn Thr Ala Ala Phe Gly Ser Ala Asp
      225            230            235            240

Thr Ala Tyr Asp Ala Ile Leu Asp Ala Leu Arg Val Leu Ser His Arg
      245            250            255

Leu Thr Ala Ser Thr Gln Arg Gly Ser Leu Thr Leu Asn Val Gly Val
      260            265            270

Ile Phe Phe Val Leu Thr Ile Val Pro Leu Ile Ala Leu Ile Thr Gly
      275            280            285

```

Glu Gln Ser Asp Val Arg Met Glu Leu Trp Asp Ser Pro Ile Gln Gly
 290 295 300
 Phe Ile Ala Ala Ile Ile Ile Val Val Ala Ile Val Ala Thr Thr Met
 305 310 315 320
 Asp Asn Arg Leu Ser Ala Leu Ile Leu Val Gly Val Thr Gly Tyr Gly
 325 330 335
 Ile Ala Val Ile Phe Ala Leu His Gly Ala Pro Asp Leu Ala Leu Thr
 340 345 350
 Gln Val Leu Val Glu Thr Ile Val Met Val Val Phe Met Leu Val Leu
 355 360 365
 Arg Lys Met Pro Thr Glu Val Ala Trp Lys Ala Glu Pro Lys Gln Ser
 370 375 380
 Arg Val Arg Ala Trp Leu Ala Gly Ala Thr Gly Leu Ser Val Val Ile
 385 390 395 400
 Val Thr Ile Phe Ala Met Asn Ala Arg Thr Thr Glu Pro Ile Ser Val
 405 410 415
 Tyr Met Gln Asp Leu Ala Tyr Glu Ile Gly His Gly Ala Asn Thr Val
 420 425 430
 Asn Val Leu Leu Val Asp Leu Arg Gly Phe Asp Thr Phe Gly Glu Ile
 435 440 445
 Ser Val Leu Val Ile Ala Ala Thr Gly Ile Ala Ser Leu Val Tyr Arg
 450 455 460
 Asn Arg Ser Phe Arg Lys Asp Ser Arg Arg Pro Thr Leu Ala Thr Thr
 465 470 475 480
 Gly Arg Arg Trp Leu Ala Ala Ala Val Asp Thr Glu Arg Ala Gln Asn
 485 490 495
 Arg Ser Leu Met Val Asp Val Ala Thr Arg Ile Leu Phe Pro Ala Met
 500 505 510
 Ile Met Leu Ser Val Tyr Phe Phe Phe Ala Gly His Asn Ala Pro Gly
 515 520 525
 Gly Gly Phe Ala Gly Gly Leu Val Ala Ser Leu Ala Phe Ala Leu Arg
 530 535 540
 Tyr Leu Ala Gly Gly Arg Glu Glu Leu Glu Glu Ala Leu Pro Ile Asp
 545 550 555 560
 Ala Gly Arg Ile Leu Gly Thr Gly Leu Phe Val Ser Ala Thr Ala Val
 565 570 575
 Leu Trp Pro Met Val Leu Leu Gly Glu Pro Pro Leu Thr Ser His Ile
 580 585 590
 Trp Asp Leu Thr Leu Pro Leu Ile Gly Glu Ile His Ile Ala Ser Ala
 595 600 605

Leu Leu Phe Asp Leu Gly Val Tyr Leu Ile Val Ile Gly Leu Thr Met
 610 615 620
 His Ile Leu Asn Ser Leu Gly Gly Gln Leu Asp Arg Asp Glu Glu Met
 625 630 635 640
 Arg Lys Gln Arg Ala Arg Asp Arg Ala Arg Arg Leu Ala Arg Asn Gln
 645 650 655
 Arg Arg Glu Ala Ala Thr Val Gly Ala Arg Arg Ser Asn Glu Lys Ser
 660 665 670
 Thr Arg Gln Met Pro Thr Ile Arg Pro Pro Gly Ala Asp Thr Glu Ser
 675 680 685
 Val Glu Gln Asn Gly Glu Asn Gln Thr Ser Ile Ser Thr Lys Arg Leu
 690 695 700
 Lys Gln
 705

<210> 693
 <211> 955
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(955)
 <223> RXA00909

<400> 693
 tcgatgtgtg ttgctaactg ggggtggcac gcacgttggc gttgttgttt ggtgtggctc 60
 cagagtaatc cacaacgcgc aaaggggaac tggagaacac gtg ctc att ctt ttt 115
 Val Leu Ile Leu Phe
 1 5
 ctc gcg ctc act gca gcc gca gta gtc gcc ccc atc ctg atc cga act 163
 Leu Ala Leu Thr Ala Ala Ala Val Val Ala Pro Ile Leu Ile Arg Thr
 10 15 20
 ctc ggt cga cca gct ttt ggt ctg ctg gcg ctt gta cct ggc att ggt 211
 Leu Gly Arg Pro Ala Phe Gly Leu Leu Ala Leu Val Pro Gly Ile Gly
 25 30 35
 ttt ttc tgg gtg ctt tcg gag ttc atc aaa ggc act ttc aag gat gga 259
 Phe Phe Trp Val Leu Ser Glu Phe Ile Lys Gly Thr Phe Lys Asp Gly
 40 45 50
 ggt gaa ctc ctc ctc cac tat gcc tgg atg cct tcg gct cac ctc aat 307
 Gly Glu Leu Leu Leu His Tyr Ala Trp Met Pro Ser Ala His Leu Asn
 55 60 65
 atc gat ttc cgt atg gat tcc ctc gcg gcg ctg ttc tca ctc atc gtc 355
 Ile Asp Phe Arg Met Asp Ser Leu Ala Ala Leu Phe Ser Leu Ile Val
 70 75 80 85
 tta ggc gtg ggc gcc cta gtg ctg ctg tac tgc tgg gga tat ttt gat 403
 Leu Gly Val Gly Ala Leu Val Leu Leu Tyr Cys Trp Gly Tyr Phe Asp

	90	95	100	
tcc aac gcg ggt cgc ctc agt gcc ttt ggt gct gaa ctg gtg gcc ttc				451
Ser Asn Ala Gly Arg Leu Ser Ala Phe Gly Ala Glu Leu Val Ala Phe				
	105	110	115	
gcc atg gcg atg ttt ggt ctt gtc att tca gac aac atc ctg ctg atg				499
Ala Met Ala Met Phe Gly Leu Val Ile Ser Asp Asn Ile Leu Leu Met				
	120	125	130	
tac gtc ttc tgg gaa atc acc tcc gtt tta tcc ttc ctc ctg gtt ggt				547
Tyr Val Phe Trp Glu Ile Thr Ser Val Leu Ser Phe Leu Leu Val Gly				
	135	140	145	
tat tac ggc gaa cgc gca tct tca cgt cgc tct gca ggt caa gcc ttg				595
Tyr Tyr Gly Glu Arg Ala Ser Ser Arg Arg Ser Ala Gly Gln Ala Leu				
	150	155	160	165
atg gtg acc acc ctg ggt gga ttg gcc atg ctg gtg ggc atc att ttg				643
Met Val Thr Thr Leu Gly Gly Leu Ala Met Leu Val Gly Ile Ile Leu				
	170	175	180	
atg ggt acc caa act ggc gtg tgg cga ttc tct gag atc cct gcc tac				691
Met Gly Thr Gln Thr Gly Val Trp Arg Phe Ser Glu Ile Pro Ala Tyr				
	185	190	195	
tca agc tcc tgg gca gat gtg ccg tat att tcc gct gct gct gcc ctt				739
Ser Ser Ser Trp Ala Asp Val Pro Tyr Ile Ser Ala Ala Ala Leu				
	200	205	210	
atc ttg gct ggc gca cta tcc aaa tcg gct atc gca cca acc cac ttc				787
Ile Leu Ala Gly Ala Leu Ser Lys Ser Ala Ile Ala Pro Thr His Phe				
	215	220	225	
tgg ctt ccc ggc gcg atg gcc gca cca acg ccg gtg tct gct tac ctg				835
Trp Leu Pro Gly Ala Met Ala Ala Pro Thr Pro Val Ser Ala Tyr Leu				
	230	235	240	245
cac tcc gca gcg atg gtg aag gcg ggt att tac ctt gtg gct cgc ctc				883
His Ser Ala Ala Met Val Lys Ala Gly Ile Tyr Leu Val Ala Arg Leu				
	250	255	260	
tct cca gac ctc aac gta gtt ggt tcg tgg tac ctg atc atc atc ccg				931
Ser Pro Asp Leu Asn Val Val Gly Ser Trp Tyr Leu Ile Ile Ile Pro				
	265	270	275	
ttg ggc atg ttg acc atg ctc atg				955
Leu Gly Met Leu Thr Met Leu Met				
	280	285		

<210> 694

<211> 285

<212> PRT

<213> Corynebacterium glutamicum

<400> 694

Val	Leu	Ile	Leu	Phe	Leu	Ala	Leu	Thr	Ala	Ala	Ala	Val	Val	Ala	Pro
1				5				10						15	

Ile Leu Ile Arg Thr Leu Gly Arg Pro Ala Phe Gly Leu Leu Ala Leu

20										25					30															
Val	Pro	Gly	Ile	Gly	Phe	Phe	Trp	Val	Leu	Ser	Glu	Phe	Ile	Lys	Gly															
		35					40					45																		
Thr	Phe	Lys	Asp	Gly	Gly	Glu	Leu	Leu	Leu	His	Tyr	Ala	Trp	Met	Pro															
		50				55					60																			
Ser	Ala	His	Leu	Asn	Ile	Asp	Phe	Arg	Met	Asp	Ser	Leu	Ala	Ala	Leu															
		65			70					75					80															
Phe	Ser	Leu	Ile	Val	Leu	Gly	Val	Gly	Ala	Leu	Val	Leu	Leu	Tyr	Cys															
			85					90						95																
Trp	Gly	Tyr	Phe	Asp	Ser	Asn	Ala	Gly	Arg	Leu	Ser	Ala	Phe	Gly	Ala															
			100					105					110																	
Glu	Leu	Val	Ala	Phe	Ala	Met	Ala	Met	Phe	Gly	Leu	Val	Ile	Ser	Asp															
		115					120					125																		
Asn	Ile	Leu	Leu	Met	Tyr	Val	Phe	Trp	Glu	Ile	Thr	Ser	Val	Leu	Ser															
		130				135					140																			
Phe	Leu	Leu	Val	Gly	Tyr	Tyr	Gly	Glu	Arg	Ala	Ser	Ser	Arg	Arg	Ser															
		145			150				155					160																
Ala	Gly	Gln	Ala	Leu	Met	Val	Thr	Thr	Leu	Gly	Gly	Leu	Ala	Met	Leu															
			165					170						175																
Val	Gly	Ile	Ile	Leu	Met	Gly	Thr	Gln	Thr	Gly	Val	Trp	Arg	Phe	Ser															
		180						185					190																	
Glu	Ile	Pro	Ala	Tyr	Ser	Ser	Ser	Trp	Ala	Asp	Val	Pro	Tyr	Ile	Ser															
		195					200					205																		
Ala	Ala	Ala	Ala	Leu	Ile	Leu	Ala	Gly	Ala	Leu	Ser	Lys	Ser	Ala	Ile															
		210				215					220																			
Ala	Pro	Thr	His	Phe	Trp	Leu	Pro	Gly	Ala	Met	Ala	Ala	Pro	Thr	Pro															
		225			230				235					240																
Val	Ser	Ala	Tyr	Leu	His	Ser	Ala	Ala	Met	Val	Lys	Ala	Gly	Ile	Tyr															
			245					250						255																
Leu	Val	Ala	Arg	Leu	Ser	Pro	Asp	Leu	Asn	Val	Val	Gly	Ser	Trp	Tyr															
		260						265					270																	
Leu	Ile	Ile	Ile	Pro	Leu	Gly	Met	Leu	Thr	Met	Leu	Met																		
		275					280					285																		

<210> 695

<211> 927

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(904)

<223> RXA00700

<400> 695

```

acgccccaca agtcgcaaaa atcaccgccg gcattccaaga ggaatcacac tggctcacag 60

tctcggccgt gaaagctgcg ctagggcatg gtgaaatctc atg atc aac gcc atc 115
                                         Met Ile Asn Ala Ile
                                         1           5

aca ctc aag ccc aaa acc ttc ctc acc tta agc ttc ctt gcg gtt ttg 163
Thr Leu Lys Pro Lys Thr Phe Leu Thr Leu Ser Phe Leu Ala Val Leu
          10                15                20

agc atc gtg att ttc ttc tgg ccg ctg atc gtc aac ccg gaa tcc ttc 211
Ser Ile Val Ile Phe Phe Trp Pro Leu Ile Val Asn Pro Glu Ser Phe
          25                30                35

ctg tcc gac aaa gcc caa gcg ccc ctc tac atc gcg atc gtc att ccc 259
Leu Ser Asp Lys Ala Gln Ala Pro Leu Tyr Ile Ala Ile Val Ile Pro
          40                45                50

ctc gtg ctg gcc gct gtc atc gcc gaa atc agt gaa aac gga ttc gac 307
Leu Val Leu Ala Ala Val Ile Ala Glu Ile Ser Glu Asn Gly Phe Asp
          55                60                65

gtt aaa gcc gta gcc atg ctc ggc gtc ctc acc gcc atg gtt gcc gta 355
Val Lys Ala Val Ala Met Leu Gly Val Leu Thr Ala Met Val Ala Val
          70                75                80                85

gtc cga cca ttc ggt gcc ggc gca gca ggc ttt gaa gca gtc ttc ttt 403
Val Arg Pro Phe Gly Ala Gly Ala Ala Gly Phe Glu Ala Val Phe Phe
          90                95                100

gtc ctc atc ctc ggc gga cga gcc ttc gga ccc ggc ttc gga ttc atc 451
Val Leu Ile Leu Gly Gly Arg Ala Phe Gly Pro Gly Phe Gly Phe Ile
          105                110                115

ctc ggc aac acc gga ctg ttc gca tcc gcg ctg ctc acc gca gga atc 499
Leu Gly Asn Thr Gly Leu Phe Ala Ser Ala Leu Leu Thr Ala Gly Ile
          120                125                130

gga ccg tgg ctc ccc tac caa atg ctc gca gcc gcc tgg gtc agc ttc 547
Gly Pro Trp Leu Pro Tyr Gln Met Leu Ala Ala Ala Trp Val Ser Phe
          135                140                145

ggc gcc ggc cta ctc ccc caa gta cgc ggc aaa aag gaa atg ctc atc 595
Gly Ala Gly Leu Leu Pro Gln Val Arg Gly Lys Lys Glu Met Leu Ile
          150                155                160                165

atc gtc cta tac gcc atc gtc tct tca ctc ggc tac gga acc atg atg 643
Ile Val Leu Tyr Ala Ile Val Ser Ser Leu Gly Tyr Gly Thr Met Met
          170                175                180

aac atg agc ttc tgg ccc tac gcc atc ggt gtc acc agc ggg ctt tcc 691
Asn Met Ser Phe Trp Pro Tyr Ala Ile Gly Val Thr Ser Gly Leu Ser
          185                190                195

ttc aca ccc ggc gcg ccc gtc ctg gaa aac ctc cac acc ttc atg ctg 739
Phe Thr Pro Gly Ala Pro Val Leu Glu Asn Leu His Thr Phe Met Leu
          200                205                210

ttc tgc ctc acc aca tcc atg ggt tgg gat ctc ggc cgc gcc ttc ttc 787
Phe Cys Leu Thr Thr Ser Met Gly Trp Asp Leu Gly Arg Ala Phe Phe

```

215 220 225
 acc tca gtg cta tta ctg ctc aca gcc aaa ccc gtt tta ggt gct tta 835
 Thr Ser Val Leu Leu Leu Leu Thr Ala Lys Pro Val Leu Gly Ala Leu
 230 235 240 245
 cga cgc gcc agc cgc cgc gcc gct ttc ggc gtc gag cgt gac ttc ggg 883
 Arg Arg Ala Ser Arg Arg Ala Ala Phe Gly Val Glu Arg Asp Phe Gly
 250 255 260
 gag gcc ggg gtg cct cgg gtc taaagatttt gttggcttgc ttc 927
 Glu Ala Gly Val Pro Arg Val
 265

 <210> 696
 <211> 268
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 696
 Met Ile Asn Ala Ile Thr Leu Lys Pro Lys Thr Phe Leu Thr Leu Ser
 1 5 10 15
 Phe Leu Ala Val Leu Ser Ile Val Ile Phe Phe Trp Pro Leu Ile Val
 20 25 30
 Asn Pro Glu Ser Phe Leu Ser Asp Lys Ala Gln Ala Pro Leu Tyr Ile
 35 40 45
 Ala Ile Val Ile Pro Leu Val Leu Ala Ala Val Ile Ala Glu Ile Ser
 50 55 60
 Glu Asn Gly Phe Asp Val Lys Ala Val Ala Met Leu Gly Val Leu Thr
 65 70 75 80
 Ala Met Val Ala Val Val Arg Pro Phe Gly Ala Gly Ala Ala Gly Phe
 85 90 95
 Glu Ala Val Phe Phe Val Leu Ile Leu Gly Gly Arg Ala Phe Gly Pro
 100 105 110
 Gly Phe Gly Phe Ile Leu Gly Asn Thr Gly Leu Phe Ala Ser Ala Leu
 115 120 125
 Leu Thr Ala Gly Ile Gly Pro Trp Leu Pro Tyr Gln Met Leu Ala Ala
 130 135 140
 Ala Trp Val Ser Phe Gly Ala Gly Leu Leu Pro Gln Val Arg Gly Lys
 145 150 155 160
 Lys Glu Met Leu Ile Ile Val Leu Tyr Ala Ile Val Ser Ser Leu Gly
 165 170 175
 Tyr Gly Thr Met Met Asn Met Ser Phe Trp Pro Tyr Ala Ile Gly Val
 180 185 190
 Thr Ser Gly Leu Ser Phe Thr Pro Gly Ala Pro Val Leu Glu Asn Leu
 195 200 205
 His Thr Phe Met Leu Phe Cys Leu Thr Thr Ser Met Gly Trp Asp Leu

	210				215				220							
Gly	Arg	Ala	Phe	Phe	Thr	Ser	Val	Leu	Leu	Leu	Leu	Thr	Ala	Lys	Pro	
225					230					235					240	
Val	Leu	Gly	Ala	Leu	Arg	Arg	Ala	Ser	Arg	Arg	Ala	Ala	Phe	Gly	Val	
				245					250					255		
Glu	Arg	Asp	Phe	Gly	Glu	Ala	Gly	Val	Pro	Arg	Val					
			260					265								

```
<210> 697
<211> 1587
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(1564)  
<223> RXN00483
```

<400> 697																
agaccaaga	gtaaaatccc	aggatttgct	tatacttgcg	ctcatggata	atcaacttcg	60										
tcccactttg	cattatcaag	ctcaaaaacc	gcaccggcga	gtg	ctg	gtc	acc	ggt	115							
				Val	Leu	Val	Thr	Gly	5							
				1												
gcg	aca	ggc	tac	att	ggc	ggc	agg	ttg	att	act	gag	tta	ctt	gct	gcc	163
Ala	Thr	Gly	Tyr	Ile	Gly	Gly	Arg	Leu	Ile	Thr	Glu	Leu	Leu	Ala	Ala	20
			10					15								
ggt	ttc	caa	gtt	cgg	gcc	acc	tcg	agg	aaa	aaa	aca	agt	ctt	cag	cgc	211
Gly	Phe	Gln	Val	Arg	Ala	Thr	Ser	Arg	Lys	Lys	Thr	Ser	Leu	Gln	Arg	35
			25					30								
ttt	gac	tgg	tac	gag	gac	gtc	gag	gca	gtg	gaa	gcg	gat	ctg	act	gac	259
Phe	Asp	Trp	Tyr	Glu	Asp	Val	Glu	Ala	Val	Glu	Ala	Asp	Leu	Thr	Asp	50
		40					45									
gcg	act	gag	tta	gat	acg	tta	ttt	aag	gat	gta	gac	gtt	gtt	tac	tat	307
Ala	Thr	Glu	Leu	Asp	Thr	Leu	Phe	Lys	Asp	Val	Asp	Val	Val	Tyr	Tyr	55
						60					65					
cta	gtg	cat	tcc	atg	gga	ggg	aag	aat	gtt	gat	ttt	gaa	gag	caa	gag	355
Leu	Val	His	Ser	Met	Gly	Gly	Lys	Asn	Val	Asp	Phe	Glu	Glu	Gln	Glu	70
					75					80					85	
caa	cgc	act	gct	gaa	aat	gta	att	caa	gct	gct	gat	caa	gcc	ggg	ata	403
Gln	Arg	Thr	Ala	Glu	Asn	Val	Ile	Gln	Ala	Ala	Asp	Gln	Ala	Gly	Ile	90
									95					100		
aaa	cag	att	gtc	tac	ctt	tcc	ggc	tta	cac	ccg	cgt	aat	cga	aaa	ata	451
Lys	Gln	Ile	Val	Tyr	Leu	Ser	Gly	Leu	His	Pro	Arg	Asn	Arg	Lys	Ile	105
								110					115			
gaa	gaa	cta	tct	aag	cac	atg	cgc	tca	cgg	gaa	aag	gtc	gcc	cag	att	499
Glu	Glu	Leu	Ser	Lys	His	Met	Arg	Ser	Arg	Glu	Lys	Val	Ala	Gln	Ile	120
							125					130				

ttg ctg gca ggc cag aca cca gct tta att tta agg gct gcc aca att	547
Leu Leu Ala Gly Gln Thr Pro Ala Leu Ile Leu Arg Ala Ala Thr Ile	
135 140 145	
att ggt tcc ggc tct gca tca ttt gaa ata atc cgt cat ctc acg gag	595
Ile Gly Ser Gly Ser Ala Ser Phe Glu Ile Ile Arg His Leu Thr Glu	
150 155 160 165	
cgt ttg cct aga atg ata gcg cct cag tgg att act aat cag att gag	643
Arg Leu Pro Arg Met Ile Ala Pro Gln Trp Ile Thr Asn Gln Ile Glu	
170 175 180	
cct tta gca ata cgg gat gtt ttg cat tac cta atc tcg gcg gct gat	691
Pro Leu Ala Ile Arg Asp Val Leu His Tyr Leu Ile Ser Ala Ala Asp	
185 190 195	
tta aag gat cca gtc aac cgc tcc tgc gat att ggg tgt gga aag tcg	739
Leu Lys Asp Pro Val Asn Arg Ser Cys Asp Ile Gly Cys Gly Lys Ser	
200 205 210	
tat gaa ttt gcg gat cta ttg cgt atc tat gcc gat gtt cgg gga ctg	787
Tyr Glu Phe Ala Asp Leu Leu Arg Ile Tyr Ala Asp Val Arg Gly Leu	
215 220 225	
aaa cgt cat gta aat tcc gta cct ctc aat ttg ccc atg gac aag cta	835
Lys Arg His Val Asn Ser Val Pro Leu Asn Leu Pro Met Asp Lys Leu	
230 235 240 245	
tcc ggt ctt tgg att agt cta gtg aca cct gtt cca ttt caa ttg tct	883
Ser Gly Leu Trp Ile Ser Leu Val Thr Pro Val Pro Phe Gln Leu Ser	
250 255 260	
ttc cct tta gct caa tca atg gct gag gat gcc gtc act gaa gag cac	931
Phe Pro Leu Ala Gln Ser Met Ala Glu Asp Ala Val Thr Glu Glu His	
265 270 275	
agc att aaa gat att att tca gat cca ccc gat ggt ttt att gag tat	979
Ser Ile Lys Asp Ile Ile Ser Asp Pro Pro Asp Gly Phe Ile Glu Tyr	
280 285 290	
cgg gaa gca gtg gag ctg gca tta gct gca gaa ttt gat cgt gga gtt	1027
Arg Glu Ala Val Glu Leu Ala Leu Ala Glu Phe Asp Arg Gly Val	
295 300 305	
cca acg tca tgg gat cga agc tgg act gta caa caa ccg tgg gct ggc	1075
Pro Thr Ser Trp Asp Arg Ser Trp Thr Val Gln Gln Pro Trp Ala Gly	
310 315 320 325	
cag cct acc gat cca gag tgg gcg ggc aaa gct gta tat gaa gac gtc	1123
Gln Pro Thr Asp Pro Glu Trp Ala Gly Lys Ala Val Tyr Glu Asp Val	
330 335 340	
cgc aca gaa gat act gat ctc cga gca gcg cag gtc tgg ccg atc att	1171
Arg Thr Glu Asp Thr Asp Leu Arg Ala Ala Gln Val Trp Pro Ile Ile	
345 350 355	
gaa ggt ttg ggt ggc gtg aac ggc tgg tat tct gca cca ctg cta tgg	1219
Glu Gly Leu Gly Gly Val Asn Gly Trp Tyr Ser Ala Pro Leu Leu Trp	
360 365 370	
cga ttg cgg ggt atc gct gac aga ctc atc ggc ggt cca ggt ttg ggc	1267

Arg Leu Arg Gly Ile Ala Asp Arg Leu Ile Gly Gly Pro Gly Leu Gly
 375 380 385

gga cgg cgg gat ccc cgt cat ttg aaa ctt ggg gat cgc att gat tgg 1315
 Gly Arg Arg Asp Pro Arg His Leu Lys Leu Gly Asp Arg Ile Asp Trp
 390 395 400 405

tgg cgg gtt act gag atc gat cca cca cat aga tta gtg ctc acc gca 1363
 Trp Arg Val Thr Glu Ile Asp Pro Pro His Arg Leu Val Leu Thr Ala
 410 415 420

gag atg aaa gta gat ggt ggc gct tgg ctg atc ctg gaa gtt gcg gac 1411
 Glu Met Lys Val Asp Gly Gly Ala Trp Leu Ile Leu Glu Val Ala Asp
 425 430 435

aag gaa aat ggc gga tgt act tat acc cag cgc gca ata ttt gag ccg 1459
 Lys Glu Asn Gly Gly Cys Thr Tyr Thr Gln Arg Ala Ile Phe Glu Pro
 440 445 450

aag ggt ttg ccc ggt tat ctc tat tgg tgg gtt gtt tca ccg ttc cat 1507
 Lys Gly Leu Pro Gly Tyr Leu Tyr Trp Trp Val Val Ser Pro Phe His
 455 460 465

gcg att att ttt cct tat atg cgt tcg aat att tta aaa gct gcg cgt 1555
 Ala Ile Ile Phe Pro Tyr Met Arg Ser Asn Ile Leu Lys Ala Ala Arg
 470 475 480 485

aaa ctc act taatcgcaga gtaggcgtct aaa 1587
 Lys Leu Thr

<210> 698

<211> 488

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 698

Val Leu Val Thr Gly Ala Thr Gly Tyr Ile Gly Gly Arg Leu Ile Thr
 1 5 10 15

Glu Leu Leu Ala Ala Gly Phe Gln Val Arg Ala Thr Ser Arg Lys Lys
 20 25 30

Thr Ser Leu Gln Arg Phe Asp Trp Tyr Glu Asp Val Glu Ala Val Glu
 35 40 45

Ala Asp Leu Thr Asp Ala Thr Glu Leu Asp Thr Leu Phe Lys Asp Val
 50 55 60

Asp Val Val Tyr Tyr Leu Val His Ser Met Gly Gly Lys Asn Val Asp
 65 70 75 80

Phe Glu Glu Gln Glu Gln Arg Thr Ala Glu Asn Val Ile Gln Ala Ala
 85 90 95

Asp Gln Ala Gly Ile Lys Gln Ile Val Tyr Leu Ser Gly Leu His Pro
 100 105 110

Arg Asn Arg Lys Ile Glu Glu Leu Ser Lys His Met Arg Ser Arg Glu
 115 120 125

Lys Val Ala Gln Ile Leu Leu Ala Gly Gln Thr Pro Ala Leu Ile Leu
 130 135 140
 Arg Ala Ala Thr Ile Ile Gly Ser Gly Ser Ala Ser Phe Glu Ile Ile
 145 150 155 160
 Arg His Leu Thr Glu Arg Leu Pro Arg Met Ile Ala Pro Gln Trp Ile
 165 170 175
 Thr Asn Gln Ile Glu Pro Leu Ala Ile Arg Asp Val Leu His Tyr Leu
 180 185 190
 Ile Ser Ala Ala Asp Leu Lys Asp Pro Val Asn Arg Ser Cys Asp Ile
 195 200 205
 Gly Cys Gly Lys Ser Tyr Glu Phe Ala Asp Leu Leu Arg Ile Tyr Ala
 210 215 220
 Asp Val Arg Gly Leu Lys Arg His Val Asn Ser Val Pro Leu Asn Leu
 225 230 235 240
 Pro Met Asp Lys Leu Ser Gly Leu Trp Ile Ser Leu Val Thr Pro Val
 245 250 255
 Pro Phe Gln Leu Ser Phe Pro Leu Ala Gln Ser Met Ala Glu Asp Ala
 260 265 270
 Val Thr Glu Glu His Ser Ile Lys Asp Ile Ile Ser Asp Pro Pro Asp
 275 280 285
 Gly Phe Ile Glu Tyr Arg Glu Ala Val Glu Leu Ala Leu Ala Ala Glu
 290 295 300
 Phe Asp Arg Gly Val Pro Thr Ser Trp Asp Arg Ser Trp Thr Val Gln
 305 310 315 320
 Gln Pro Trp Ala Gly Gln Pro Thr Asp Pro Glu Trp Ala Gly Lys Ala
 325 330 335
 Val Tyr Glu Asp Val Arg Thr Glu Asp Thr Asp Leu Arg Ala Ala Gln
 340 345 350
 Val Trp Pro Ile Ile Glu Gly Leu Gly Gly Val Asn Gly Trp Tyr Ser
 355 360 365
 Ala Pro Leu Leu Trp Arg Leu Arg Gly Ile Ala Asp Arg Leu Ile Gly
 370 375 380
 Gly Pro Gly Leu Gly Gly Arg Arg Asp Pro Arg His Leu Lys Leu Gly
 385 390 395 400
 Asp Arg Ile Asp Trp Trp Arg Val Thr Glu Ile Asp Pro Pro His Arg
 405 410 415
 Leu Val Leu Thr Ala Glu Met Lys Val Asp Gly Gly Ala Trp Leu Ile
 420 425 430
 Leu Glu Val Ala Asp Lys Glu Asn Gly Gly Cys Thr Tyr Thr Gln Arg
 435 440 445

Ala Ile Phe Glu Pro Lys Gly Leu Pro Gly Tyr Leu Tyr Trp Trp Val
 450 455 460

Val Ser Pro Phe His Ala Ile Ile Phe Pro Tyr Met Arg Ser Asn Ile
 465 470 475 480

Leu Lys Ala Ala Arg Lys Leu Thr
 485

<210> 699

<211> 1587

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1564)

<223> FRXA00483

<400> 699

agacccaaga gtaaaatccc aggatttgct tatacttgcg ctcatggata atcaacttcg 60

tcccactttg cattatcaag ctcaaaaccc gcaccggcga gtg ctg gtc acc ggt 115
 Val Leu Val Thr Gly
 1 5

gcg aca ggc tac att ggc ggc agg ttg att act gag tta ctt gct gcc 163
 Ala Thr Gly Tyr Ile Gly Gly Arg Leu Ile Thr Glu Leu Leu Ala Ala
 10 15 20

ggt ttc caa gtt cgg gcc acc tcg agg aaa aaa aca agt ctt cag cgc 211
 Gly Phe Gln Val Arg Ala Thr Ser Arg Lys Lys Thr Ser Leu Gln Arg
 25 30 35

ttt gac tgg tac gag gac gtc gag gca gtg gaa gcg gat ctg act gac 259
 Phe Asp Trp Tyr Glu Asp Val Glu Ala Val Glu Ala Asp Leu Thr Asp
 40 45 50

gcg act gag tta gat acg tta ttt aag gat gta gac gtt gtt tac tat 307
 Ala Thr Glu Leu Asp Thr Leu Phe Lys Asp Val Asp Val Val Tyr Tyr
 55 60 65

cta gtg cat tcc atg gga ggt aag aat gtt gat ttt gaa gag caa gag 355
 Leu Val His Ser Met Gly Gly Lys Asn Val Asp Phe Glu Glu Gln Glu
 70 75 80 85

caa cgc act gct gaa aat gta att caa gct gct gat caa gcc ggg ata 403
 Gln Arg Thr Ala Glu Asn Val Ile Gln Ala Ala Asp Gln Ala Gly Ile
 90 95 100

aaa cag att gtc tac ctt tcc ggc tta cac ccg cgt aat cga aaa ata 451
 Lys Gln Ile Val Tyr Leu Ser Gly Leu His Pro Arg Asn Arg Lys Ile
 105 110 115

gaa gaa cta tct aag cac atg cgc tca cgg gaa aag gtc gcc cag att 499
 Glu Glu Leu Ser Lys His Met Arg Ser Arg Glu Lys Val Ala Gln Ile
 120 125 130

ttg ctg gca ggc cag aca cca gct tta att tta agg gct gcc aca att 547
 Leu Leu Ala Gly Gln Thr Pro Ala Leu Ile Leu Arg Ala Ala Thr Ile

135	140	145	
att ggt tcc ggc tct gca tca ttt gaa ata atc cgt cat ctc acg gag Ile Gly Ser Gly Ser Ala Ser Phe Glu Ile Ile Arg His Leu Thr Glu 150 155 160 165			595
cgt ttg cct aga atg ata gcg cct cag tgg att act aat cag att gag Arg Leu Pro Arg Met Ile Ala Pro Gln Trp Ile Thr Asn Gln Ile Glu 170 175 180			643
cct tta gca ata cgg gat gtt ttg cat tac cta atc tcg gcg gct gat Pro Leu Ala Ile Arg Asp Val Leu His Tyr Leu Ile Ser Ala Ala Asp 185 190 195			691
tta aag gat cca gtc aac cgc tcc tgc gat att ggg tgt gga aag tcg Leu Lys Asp Pro Val Asn Arg Ser Cys Asp Ile Gly Cys Gly Lys Ser 200 205 210			739
tat gaa ttt gcg gat cta ttg cgt atc tat gcc gat gtt cgg gga ctg Tyr Glu Phe Ala Asp Leu Leu Arg Ile Tyr Ala Asp Val Arg Gly Leu 215 220 225			787
aaa cgt cat gta aat tcc gta cct ctc aat ttg ccc atg gac aag cta Lys Arg His Val Asn Ser Val Pro Leu Asn Leu Pro Met Asp Lys Leu 230 235 240 245			835
tcc ggt ctt tgg att agt cta gtg aca cct gtt cca ttt caa ttg tct Ser Gly Leu Trp Ile Ser Leu Val Thr Pro Val Pro Phe Gln Leu Ser 250 255 260			883
ttc cct tta gct caa tca atg gct gag gat gcc gtc act gaa gag cac Phe Pro Leu Ala Gln Ser Met Ala Glu Asp Ala Val Thr Glu Glu His 265 270 275			931
agc att aaa gat att att tca gat cca ccc gat ggt ttt att gag tat Ser Ile Lys Asp Ile Ile Ser Asp Pro Pro Asp Gly Phe Ile Glu Tyr 280 285 290			979
cgg gaa gca gtg gag ctg gca tta gct gca gaa ttt gat cgt gga gtt Arg Glu Ala Val Glu Leu Ala Leu Ala Glu Phe Asp Arg Gly Val 295 300 305			1027
cca acg tca tgg gat cga agc tgg act gta caa caa ccg tgg gct ggc Pro Thr Ser Trp Asp Arg Ser Trp Thr Val Gln Gln Pro Trp Ala Gly 310 315 320 325			1075
cag cct acc gat cca gag tgg gcg ggc aaa gct gta tat gaa gac gtc Gln Pro Thr Asp Pro Glu Trp Ala Gly Lys Ala Val Tyr Glu Asp Val 330 335 340			1123
cgc aca gaa gat act gat ctc cga gca gcg cag gtc tgg ccg atc att Arg Thr Glu Asp Thr Asp Leu Arg Ala Ala Gln Val Trp Pro Ile Ile 345 350 355			1171
gaa ggt ttg ggt ggc gtg aac ggc tgg tat tct gca cca ctg cta tgg Glu Gly Leu Gly Gly Val Asn Gly Trp Tyr Ser Ala Pro Leu Leu Trp 360 365 370			1219
cga ttg cgg ggt atc gct gac aga ctc atc ggc ggt cca ggt ttg ggc Arg Leu Arg Gly Ile Ala Asp Arg Leu Ile Gly Gly Pro Gly Leu Gly 375 380 385			1267

gga cgg cgg gat ccc cgt cat ttg aaa ctt ggg gat cgc att gat tgg 1315
 Gly Arg Arg Asp Pro Arg His Leu Lys Leu Gly Asp Arg Ile Asp Trp
 390 395 400 405
 tgg cgg gtt act gag atc gat cca cca cat aga tta gtg ctc acc gca 1363
 Trp Arg Val Thr Glu Ile Asp Pro Pro His Arg Leu Val Leu Thr Ala
 410 415 420
 gag atg aaa gta gat ggt ggc gct tgg ctg atc ctg gaa gtt gcg gac 1411
 Glu Met Lys Val Asp Gly Gly Ala Trp Leu Ile Leu Glu Val Ala Asp
 425 430 435
 aag gaa aat ggc gga tgt act tat acc cag cgc gca ata ttt gag ccg 1459
 Lys Glu Asn Gly Gly Cys Thr Tyr Thr Gln Arg Ala Ile Phe Glu Pro
 440 445 450
 aag ggt ttg ccc ggt tat ctc tat tgg tgg gtt gtt tca ccg ttc cat 1507
 Lys Gly Leu Pro Gly Tyr Leu Tyr Trp Trp Val Val Ser Pro Phe His
 455 460 465
 gcg att att ttt cct tat atg cgt tcg aat att tta aaa gct gcg cgt 1555
 Ala Ile Ile Phe Pro Tyr Met Arg Ser Asn Ile Leu Lys Ala Ala Arg
 470 475 480 485
 aaa ctc act taatcgacaga gtaggcgtct aaa 1587
 Lys Leu Thr

<210> 700

<211> 488

<212> PRT

<213> Corynebacterium glutamicum

<400> 700

Val Leu Val Thr Gly Ala Thr Gly Tyr Ile Gly Gly Arg Leu Ile Thr
 1 5 10 15
 Glu Leu Leu Ala Ala Gly Phe Gln Val Arg Ala Thr Ser Arg Lys Lys
 20 25 30
 Thr Ser Leu Gln Arg Phe Asp Trp Tyr Glu Asp Val Glu Ala Val Glu
 35 40 45
 Ala Asp Leu Thr Asp Ala Thr Glu Leu Asp Thr Leu Phe Lys Asp Val
 50 55 60
 Asp Val Val Tyr Tyr Leu Val His Ser Met Gly Gly Lys Asn Val Asp
 65 70 75 80
 Phe Glu Glu Gln Glu Gln Arg Thr Ala Glu Asn Val Ile Gln Ala Ala
 85 90 95
 Asp Gln Ala Gly Ile Lys Gln Ile Val Tyr Leu Ser Gly Leu His Pro
 100 105 110
 Arg Asn Arg Lys Ile Glu Glu Leu Ser Lys His Met Arg Ser Arg Glu
 115 120 125
 Lys Val Ala Gln Ile Leu Leu Ala Gly Gln Thr Pro Ala Leu Ile Leu

130	135	140
Arg Ala Ala Thr Ile Ile Gly Ser Gly Ser Ala Ser Phe Glu Ile Ile 145 150 155 160		
Arg His Leu Thr Glu Arg Leu Pro Arg Met Ile Ala Pro Gln Trp Ile 165 170 175		
Thr Asn Gln Ile Glu Pro Leu Ala Ile Arg Asp Val Leu His Tyr Leu 180 185 190		
Ile Ser Ala Ala Asp Leu Lys Asp Pro Val Asn Arg Ser Cys Asp Ile 195 200 205		
Gly Cys Gly Lys Ser Tyr Glu Phe Ala Asp Leu Leu Arg Ile Tyr Ala 210 215 220		
Asp Val Arg Gly Leu Lys Arg His Val Asn Ser Val Pro Leu Asn Leu 225 230 235 240		
Pro Met Asp Lys Leu Ser Gly Leu Trp Ile Ser Leu Val Thr Pro Val 245 250 255		
Pro Phe Gln Leu Ser Phe Pro Leu Ala Gln Ser Met Ala Glu Asp Ala 260 265 270		
Val Thr Glu Glu His Ser Ile Lys Asp Ile Ile Ser Asp Pro Pro Asp 275 280 285		
Gly Phe Ile Glu Tyr Arg Glu Ala Val Glu Leu Ala Leu Ala Ala Glu 290 295 300		
Phe Asp Arg Gly Val Pro Thr Ser Trp Asp Arg Ser Trp Thr Val Gln 305 310 315 320		
Gln Pro Trp Ala Gly Gln Pro Thr Asp Pro Glu Trp Ala Gly Lys Ala 325 330 335		
Val Tyr Glu Asp Val Arg Thr Glu Asp Thr Asp Leu Arg Ala Ala Gln 340 345 350		
Val Trp Pro Ile Ile Glu Gly Leu Gly Gly Val Asn Gly Trp Tyr Ser 355 360 365		
Ala Pro Leu Leu Trp Arg Leu Arg Gly Ile Ala Asp Arg Leu Ile Gly 370 375 380		
Gly Pro Gly Leu Gly Gly Arg Arg Asp Pro Arg His Leu Lys Leu Gly 385 390 395 400		
Asp Arg Ile Asp Trp Trp Arg Val Thr Glu Ile Asp Pro Pro His Arg 405 410 415		
Leu Val Leu Thr Ala Glu Met Lys Val Asp Gly Gly Ala Trp Leu Ile 420 425 430		
Leu Glu Val Ala Asp Lys Glu Asn Gly Gly Cys Thr Tyr Thr Gln Arg 435 440 445		
Ala Ile Phe Glu Pro Lys Gly Leu Pro Gly Tyr Leu Tyr Trp Trp Val 450 455 460		

Val Ser Pro Phe His Ala Ile Ile Phe Pro Tyr Met Arg Ser Asn Ile
 465 470 475 480

Leu Lys Ala Ala Arg Lys Leu Thr
 485

<210> 701
 <211> 612
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(589)
 <223> RXA01534

<400> 701
 attgctctca tcggttcgat atagactgaa ttgtctaggt taatatccaa tatggaagaa 60
 aaactagaca gttaagtaga ctgaatggcc tactaggtgc atg act tca gca atc 115
 Met Thr Ser Ala Ile
 1 5
 acc acc gca act gat ctt cgc tcc gta ctg cga aac gta cca acc cca 163
 Thr Thr Ala Thr Asp Leu Arg Ser Val Leu Arg Asn Val Pro Thr Pro
 10 15 20
 att agc ttc att gca acc cac acc gat cag cct ctg ggc atg atc gtt 211
 Ile Ser Phe Ile Ala Thr His Thr Asp Gln Pro Leu Gly Met Ile Val
 25 30 35
 ggt tca ttc gtc agc att agc gcc gaa cca cca ttg gta ggc atc ttc 259
 Gly Ser Phe Val Ser Ile Ser Ala Glu Pro Pro Leu Val Gly Ile Phe
 40 45 50
 ttg cag aag agc tct tct tca tgg cca gct atc gag cag gca tta gtt 307
 Leu Gln Lys Ser Ser Ser Ser Trp Pro Ala Ile Glu Gln Ala Leu Val
 55 60 65
 acc ggc caa gag cta ggc att tct atc ctc ggc ggg gca cac gca gac 355
 Thr Gly Gln Glu Leu Gly Ile Ser Ile Leu Gly Gly Ala His Ala Asp
 70 75 80 85
 cat gtg cgt aag ctt tct ggc cca tcc gac cag cgc ttt gaa aac ctt 403
 His Val Arg Lys Leu Ser Gly Pro Ser Asp Gln Arg Phe Glu Asn Leu
 90 95 100
 ggg tgg gca tcc acc gaa aac ggt gcg att cac ctt gaa ggc gct gat 451
 Gly Trp Ala Ser Thr Glu Asn Gly Ala Ile His Leu Glu Gly Ala Asp
 105 110 115
 gca caa cta acc acg aaa ctt cat gat ctc cag gaa atc ggc gat cac 499
 Ala Gln Leu Thr Thr Lys Leu His Asp Leu Gln Glu Ile Gly Asp His
 120 125 130
 ttc ttt gca gtt cta gaa gtt att gac gct tcc gct gac caa gac ttc 547
 Phe Phe Ala Val Leu Glu Val Ile Asp Ala Ser Ala Asp Gln Asp Phe
 135 140 145

agc tca gcg ctg gtg tac cac cgc tca cag gtg tcc tcg ctg 589
 Ser Ser Ala Leu Val Tyr His Arg Ser Gln Val Ser Ser Leu
 150 155 160

taggacacta aattttaaga ggg 612

<210> 702

<211> 163

<212> PRT

<213> Corynebacterium glutamicum

<400> 702

Met Thr Ser Ala Ile Thr Thr Ala Thr Asp Leu Arg Ser Val Leu Arg
 1 5 10 15

Asn Val Pro Thr Pro Ile Ser Phe Ile Ala Thr His Thr Asp Gln Pro
 20 25 30

Leu Gly Met Ile Val Gly Ser Phe Val Ser Ile Ser Ala Glu Pro Pro
 35 40 45

Leu Val Gly Ile Phe Leu Gln Lys Ser Ser Ser Ser Trp Pro Ala Ile
 50 55 60

Glu Gln Ala Leu Val Thr Gly Gln Glu Leu Gly Ile Ser Ile Leu Gly
 65 70 75 80

Gly Ala His Ala Asp His Val Arg Lys Leu Ser Gly Pro Ser Asp Gln
 85 90 95

Arg Phe Glu Asn Leu Gly Trp Ala Ser Thr Glu Asn Gly Ala Ile His
 100 105 110

Leu Glu Gly Ala Asp Ala Gln Leu Thr Thr Lys Leu His Asp Leu Gln
 115 120 125

Glu Ile Gly Asp His Phe Phe Ala Val Leu Glu Val Ile Asp Ala Ser
 130 135 140

Ala Asp Gln Asp Phe Ser Ser Ala Leu Val Tyr His Arg Ser Gln Val
 145 150 155 160

Ser Ser Leu

<210> 703

<211> 1134

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1111)

<223> RXA00288

<400> 703

ggcgtgctaa aaaagcacgt caaatacaga atcggcagat tacatcgctg agcagagaaa 60

acacggggcat gaaacgtacc caagggctaa catcggggggc atg agc gcg caa atg 115

																Met Ser Ala Gln Met	
																1	5
gat	acc	cct	gat	ccc	act	atg	tct	gct	gtt	gca	atg	tta	gat	tcc	atc	163	
Asp	Thr	Pro	Asp	Pro	Thr	Met	Ser	Ala	Val	Ala	Met	Leu	Asp	Ser	Ile		
				10					15					20			
cct	tct	gat	caa	cca	gat	ttc	ctg	atc	gat	gta	gaa	gta	gat	cga	cca	211	
Pro	Ser	Asp	Gln	Pro	Asp	Phe	Leu	Ile	Asp	Val	Glu	Val	Asp	Arg	Pro		
				25					30					35			
act	ccc	gga	cca	cat	gat	ctg	cta	gtc	cac	att	gag	gcg	gtc	tca	att	259	
Thr	Pro	Gly	Pro	His	Asp	Leu	Leu	Val	His	Ile	Glu	Ala	Val	Ser	Ile		
				40					45					50			
aac	cct	gtt	gat	acc	aag	gta	cgc	atg	cgg	gcc	ggg	aag	caa	aag	cat	307	
Asn	Pro	Val	Asp	Thr	Lys	Val	Arg	Met	Arg	Ala	Gly	Lys	Gln	Lys	His		
				55					60					65			
cct	aaa	att	tta	ggg	ttt	gat	gct	gca	ggg	gag	gtg	gtg	gct	gtt	gga	355	
Pro	Lys	Ile	Leu	Gly	Phe	Asp	Ala	Ala	Gly	Glu	Val	Val	Ala	Val	Gly		
				70					75					80			
tcg	cag	gtc	acg	ctc	ttc	aat	gtt	ggg	gac	aaa	gtg	ttc	tac	gca	gga	403	
Ser	Gln	Val	Thr	Leu	Phe	Asn	Val	Gly	Asp	Lys	Val	Phe	Tyr	Ala	Gly		
				90					95					100			
tcc	aat	cag	cgt	cca	gga	agt	aac	gca	gag	tac	cag	gtg	gtg	gat	gaa	451	
Ser	Asn	Gln	Arg	Pro	Gly	Ser	Asn	Ala	Glu	Tyr	Gln	Val	Val	Asp	Glu		
				105					110					115			
cgg	ctg	gtg	ggg	cac	gca	cca	caa	agc	ttg	ggg	gca	cac	gac	gcc	gct	499	
Arg	Leu	Val	Gly	His	Ala	Pro	Gln	Ser	Leu	Gly	Ala	His	Asp	Ala	Ala		
				120					125					130			
gct	ctc	cca	ctt	gtc	gcg	ctc	act	gca	tg	gag	tca	ctt	ttt	gac	cga	547	
Ala	Leu	Pro	Leu	Val	Ala	Leu	Thr	Ala	Trp	Glu	Ser	Leu	Phe	Asp	Arg		
				135					140					145			
ttg	gga	gta	act	cag	tca	act	act	gga	aca	ctg	ttg	gtc	ttg	ggc	ggg	595	
Leu	Gly	Val	Thr	Gln	Ser	Thr	Thr	Gly	Thr	Leu	Leu	Val	Leu	Gly	Gly		
				150					155					160			
tca	gga	ggg	gtg	cct	tca	gct	ctt	att	caa	ctt	gct	cga	gct	ctc	act	643	
Ser	Gly	Gly	Val	Pro	Ser	Ala	Leu	Ile	Gln	Leu	Ala	Arg	Ala	Leu	Thr		
				170					175					180			
ggg	ctg	aaa	gta	gtg	gca	aca	gct	tct	cgc	cct	gaa	tca	caa	gaa	tg	691	
Gly	Leu	Lys	Val	Val	Ala	Thr	Ala	Ser	Arg	Pro	Glu	Ser	Gln	Glu	Trp		
				185					190					195			
gtg	aca	aag	ctc	ggg	gct	cat	gag	gtg	att	gat	cac	tcc	aag	gat	ttg	739	
Val	Thr	Lys	Leu	Gly	Ala	His	Glu	Val	Ile	Asp	His	Ser	Lys	Asp	Leu		
				200					205					210			
agt	gag	caa	atc	tcc	gac	gtg	gat	ttt	gtt	ttc	agc	tcg	tg	act	act	787	
Ser	Glu	Gln	Ile	Ser	Asp	Val	Asp	Phe	Val	Phe	Ser	Ser	Trp	Thr	Thr		
				215					220					225			
ggg	cgt	gaa	gta	gag	ctc	gcc	acg	ttg	atg	aaa	ccc	cag	tcc	cac	cta	835	
Gly	Arg	Glu	Val	Glu	Leu	Ala	Thr	Leu	Met	Lys	Pro	Gln	Ser	His	Leu		

230	235	240	245	
gtg ctc atc gat gat cca gtg gat ccc aat ttg ggc gct ttt aag caa				883
Val Leu Ile Asp Asp Pro Val Asp Pro Asn Leu Gly Ala Phe Lys Gln	250	255	260	
aaa gcg atc gct ttg cac tgg gag ttc atg ttt acc cgc gct atg ttc				931
Lys Ala Ile Ala Leu His Trp Glu Phe Met Phe Thr Arg Ala Met Phe	265	270	275	
aac act cct gat atg ggt gaa caa ggg aaa att ctg aat aag atc gcc				979
Asn Thr Pro Asp Met Gly Glu Gln Gly Lys Ile Leu Asn Lys Ile Ala	280	285	290	
gac atg gtt gat cgg ggt cag ttt gag tcc gtg aca gca acg gtg ctg				1027
Asp Met Val Asp Arg Gly Gln Phe Glu Ser Val Thr Ala Thr Val Leu	295	300	305	
gat ggg ctc aac gct gca aac atc atg gag ggg cac cgg ctc gtt gag				1075
Asp Gly Leu Asn Ala Ala Asn Ile Met Glu Gly His Arg Leu Val Glu	310	315	320	325
cag ggt aaa acc tca gga aaa att gtt gtg agg gta taaagaggac				1121
Gln Gly Lys Thr Ser Gly Lys Ile Val Val Arg Val	330	335		
ttgaaaaatg cac				1134
<210> 704				
<211> 337				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 704				
Met Ser Ala Gln Met Asp Thr Pro Asp Pro Thr Met Ser Ala Val Ala				
1 5 10 15				
Met Leu Asp Ser Ile Pro Ser Asp Gln Pro Asp Phe Leu Ile Asp Val				
20 25 30				
Glu Val Asp Arg Pro Thr Pro Gly Pro His Asp Leu Leu Val His Ile				
35 40 45				
Glu Ala Val Ser Ile Asn Pro Val Asp Thr Lys Val Arg Met Arg Ala				
50 55 60				
Gly Lys Gln Lys His Pro Lys Ile Leu Gly Phe Asp Ala Ala Gly Glu				
65 70 75 80				
Val Val Ala Val Gly Ser Gln Val Thr Leu Phe Asn Val Gly Asp Lys				
85 90 95				
Val Phe Tyr Ala Gly Ser Asn Gln Arg Pro Gly Ser Asn Ala Glu Tyr				
100 105 110				
Gln Val Val Asp Glu Arg Leu Val Gly His Ala Pro Gln Ser Leu Gly				
115 120 125				
Ala His Asp Ala Ala Ala Leu Pro Leu Val Ala Leu Thr Ala Trp Glu				
130 135 140				

Ser Leu Phe Asp Arg Leu Gly Val Thr Gln Ser Thr Thr Gly Thr Leu
 145 150 155 160
 Leu Val Leu Gly Gly Ser Gly Gly Val Pro Ser Ala Leu Ile Gln Leu
 165 170 175
 Ala Arg Ala Leu Thr Gly Leu Lys Val Val Ala Thr Ala Ser Arg Pro
 180 185 190
 Glu Ser Gln Glu Trp Val Thr Lys Leu Gly Ala His Glu Val Ile Asp
 195 200 205
 His Ser Lys Asp Leu Ser Glu Gln Ile Ser Asp Val Asp Phe Val Phe
 210 215 220
 Ser Ser Trp Thr Thr Gly Arg Glu Val Glu Leu Ala Thr Leu Met Lys
 225 230 235 240
 Pro Gln Ser His Leu Val Leu Ile Asp Asp Pro Val Asp Pro Asn Leu
 245 250 255
 Gly Ala Phe Lys Gln Lys Ala Ile Ala Leu His Trp Glu Phe Met Phe
 260 265 270
 Thr Arg Ala Met Phe Asn Thr Pro Asp Met Gly Glu Gln Gly Lys Ile
 275 280 285
 Leu Asn Lys Ile Ala Asp Met Val Asp Arg Gly Gln Phe Glu Ser Val
 290 295 300
 Thr Ala Thr Val Leu Asp Gly Leu Asn Ala Ala Asn Ile Met Glu Gly
 305 310 315 320
 His Arg Leu Val Glu Gln Gly Lys Thr Ser Gly Lys Ile Val Val Arg
 325 330 335
 Val

<210> 705
 <211> 1089
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1066)
 <223> RXA02741

<400> 705
 actgggtcacc tggtttggtc tgcactctga ctccctcaa aagggcaciaa tttggtcaat 60
 ttcccaacct tgtctttcag tcatgggttag tgtgggaacc atg aag gca atc tta 115
 Met Lys Ala Ile Leu
 1 5

gtt tcc cgc acc ggc gga cca gag gtg ttg gag ttc acc gac act gac 163
 Val Ser Arg Thr Gly Gly Pro Glu Val Leu Glu Phe Thr Asp Thr Asp
 10 15 20

gcc cca aag ccc act gat gat cag gtt tta gtt gaa gtt gat atg gct	211
Ala Pro Lys Pro Thr Asp Asp Gln Val Leu Val Glu Val Asp Met Ala	
25 30 35	
ggc gtc aac ttt att gat act tac tat cgc cag ggt gaa tat cac gct	259
Gly Val Asn Phe Ile Asp Thr Tyr Tyr Arg Gln Gly Glu Tyr His Ala	
40 45 50	
cgc ctg ccg ttt atc cca ggt ttt gaa ggc act ggt cgg gtg ttg gag	307
Arg Leu Pro Phe Ile Pro Gly Phe Glu Gly Thr Gly Arg Val Leu Glu	
55 60 65	
gat ccg cag ggg ttg att gcg gcg ggt acc aag gtg gcg tgg tgt gat	355
Asp Pro Gln Gly Leu Ile Ala Ala Gly Thr Lys Val Ala Trp Cys Asp	
70 75 80 85	
gcc atg ggt tcg tat gct cag cag gtg tgt gtg ccg cgg gat cgc ttg	403
Ala Met Gly Ser Tyr Ala Gln Gln Val Cys Val Pro Arg Asp Arg Leu	
90 95 100	
gtg gcg gtt ccc gag ggc gtg agt tcg gaa gtg gct gcg tcg atg ttg	451
Val Ala Val Pro Glu Gly Val Ser Ser Glu Val Ala Ala Ser Met Leu	
105 110 115	
atg cag gga atc act gcg cat tat cta acc aat ggt gtg tat gag ctt	499
Met Gln Gly Ile Thr Ala His Tyr Leu Thr Asn Gly Val Tyr Glu Leu	
120 125 130	
gaa gag ggc gat tct tgc ctc atc act gct ggc gcg ggt ggt gtt gga	547
Glu Glu Gly Asp Ser Cys Leu Ile Thr Ala Gly Ala Gly Gly Val Gly	
135 140 145	
ttg ttg gct acg cag atg gcg gcg gcc aag gga gtg cgc gtg tac agc	595
Leu Leu Ala Thr Gln Met Ala Ala Ala Lys Gly Val Arg Val Tyr Ser	
150 155 160 165	
gtg gtg tcc acg gat gaa aaa gct gag ctt gct ttg gat gcc ggt gct	643
Val Val Ser Thr Asp Glu Lys Ala Glu Leu Ala Leu Asp Ala Gly Ala	
170 175 180	
tat gag gtg ttt cgt tat tcc gat aat ttg gcg gag cag gtt cgt cgg	691
Tyr Glu Val Phe Arg Tyr Ser Asp Asn Leu Ala Glu Gln Val Arg Arg	
185 190 195	
cac aac ggg ggt cgc gga gtt gat gtg gtg tat gac ggt gtc ggc cag	739
His Asn Gly Gly Arg Gly Val Asp Val Val Tyr Asp Gly Val Gly Gln	
200 205 210	
tcc acg ttc aat gag tcc tta gag gct gtt cgt ccg cgc ggc act gtg	787
Ser Thr Phe Asn Glu Ser Leu Glu Ala Val Arg Pro Arg Gly Thr Val	
215 220 225	
tgt ttg ttt ggt gcg gcg tcg ggt cct gtg gag cct ttt gat ccg cag	835
Cys Leu Phe Gly Ala Ala Ser Gly Pro Val Glu Glu Pro Phe Asp Pro Gln	
230 235 240 245	
ctg ttg aac act cac ggt tcg atc ttc ttg acc cgc cca agc att ggc	883
Leu Leu Asn Thr His Gly Ser Ile Phe Leu Thr Arg Pro Ser Ile Gly	
250 255 260	

gcg tgg acg tct gag gag ggc gaa ttt gcc aag cgt gca cag gcg gtc 931
 Ala Trp Thr Ser Glu Glu Gly Glu Phe Ala Lys Arg Ala Gln Ala Val
 265 270 275

acg cag gcc atc gtc gaa ggc acc ttg cgg gtt cgc gtt act ggc aca 979
 Thr Gln Ala Ile Val Glu Gly Thr Leu Arg Val Arg Val Thr Gly Thr
 280 285 290

tat tcg ctt gcc gac gcc tac atc gcc cac cgc gac ctt cag gcg cgt 1027
 Tyr Ser Leu Ala Asp Ala Tyr Ile Ala His Arg Asp Leu Gln Ala Arg
 295 300 305

agc acg agc ggt tct ttg gtc ttg gaa atc ccg aag gac taaacacgca 1076
 Ser Thr Ser Gly Ser Leu Val Leu Glu Ile Pro Lys Asp
 310 315 320

taaaaagatc ctg 1089

<210> 706

<211> 322

<212> PRT

<213> Corynebacterium glutamicum

<400> 706

Met Lys Ala Ile Leu Val Ser Arg Thr Gly Gly Pro Glu Val Leu Glu
 1 5 10 15

Phe Thr Asp Thr Asp Ala Pro Lys Pro Thr Asp Asp Gln Val Leu Val
 20 25 30

Glu Val Asp Met Ala Gly Val Asn Phe Ile Asp Thr Tyr Tyr Arg Gln
 35 40 45

Gly Glu Tyr His Ala Arg Leu Pro Phe Ile Pro Gly Phe Glu Gly Thr
 50 55 60

Gly Arg Val Leu Glu Asp Pro Gln Gly Leu Ile Ala Ala Gly Thr Lys
 65 70 75 80

Val Ala Trp Cys Asp Ala Met Gly Ser Tyr Ala Gln Gln Val Cys Val
 85 90 95

Pro Arg Asp Arg Leu Val Ala Val Pro Glu Gly Val Ser Ser Glu Val
 100 105 110

Ala Ala Ser Met Leu Met Gln Gly Ile Thr Ala His Tyr Leu Thr Asn
 115 120 125

Gly Val Tyr Glu Leu Glu Glu Gly Asp Ser Cys Leu Ile Thr Ala Gly
 130 135 140

Ala Gly Gly Val Gly Leu Leu Ala Thr Gln Met Ala Ala Ala Lys Gly
 145 150 155 160

Val Arg Val Tyr Ser Val Val Ser Thr Asp Glu Lys Ala Glu Leu Ala
 165 170 175

Leu Asp Ala Gly Ala Tyr Glu Val Phe Arg Tyr Ser Asp Asn Leu Ala
 180 185 190

Glu Gln Val Arg Arg His Asn Gly Gly Arg Gly Val Asp Val Val Tyr
 195 200 205
 Asp Gly Val Gly Gln Ser Thr Phe Asn Glu Ser Leu Glu Ala Val Arg
 210 215 220
 Pro Arg Gly Thr Val Cys Leu Phe Gly Ala Ala Ser Gly Pro Val Glu
 225 230 235 240
 Pro Phe Asp Pro Gln Leu Leu Asn Thr His Gly Ser Ile Phe Leu Thr
 245 250 255
 Arg Pro Ser Ile Gly Ala Trp Thr Ser Glu Glu Gly Glu Phe Ala Lys
 260 265 270
 Arg Ala Gln Ala Val Thr Gln Ala Ile Val Glu Gly Thr Leu Arg Val
 275 280 285
 Arg Val Thr Gly Thr Tyr Ser Leu Ala Asp Ala Tyr Ile Ala His Arg
 290 295 300
 Asp Leu Gln Ala Arg Ser Thr Ser Gly Ser Leu Val Leu Glu Ile Pro
 305 310 315 320
 Lys Asp

<210> 707
 <211> 990
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(967)
 <223> RXN02560

<400> 707
 ttggggcaag ccagctaacg catttcttgt ggaaaccgca gacattgagg ccgcccacgc 60
 ggaacttcta agagcagtggt aatgaaataa tccggtgctg atg cag ggc aac tcg 115
 Met Gln Gly Asn Ser
 1 5
 ctt aat ctg gca gac aac agc gag aga aag aag ccc atg ccg tca cca 163
 Leu Asn Leu Ala Asp Asn Ser Glu Arg Lys Lys Pro Met Pro Ser Pro
 10 15 20
 gga gaa ctt tta gcc gcc cgc tac gga caa cct gca acc tgg acg cca 211
 Gly Glu Leu Leu Ala Ala Arg Tyr Gly Gln Pro Ala Thr Trp Thr Pro
 25 30 35
 ccg cag tgg aat gag acg ctt gat gtc att cac cag cat cga tca gtt 259
 Pro Gln Trp Asn Glu Thr Leu Asp Val Ile His Gln His Arg Ser Val
 40 45 50
 cgc agg tgg ttg gat aaa ccg gtt gat gat gac acc atc cgc acc att 307
 Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp Thr Ile Arg Thr Ile
 55 60 65

att tcc gcc gca caa tcg gct gga acc tct tcc aat aag cag gtc att	355
Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser Asn Lys Gln Val Ile	
70 75 80 85	
tct gtc atc gtg gtt aaa gat cct gag ctg agg aaa ggc ctc gcg ggg	403
Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg Lys Gly Leu Ala Gly	
90 95 100	
atc act cgc cag atg ttt ccg cac ctt gag cag gtt ccc gcg gtg ctg	451
Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln Val Pro Ala Val Leu	
105 110 115	
att tgg ttg att gat tat tcc cga atc agt gcg gtg gca gcc aga gaa	499
Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala Val Ala Ala Arg Glu	
120 125 130	
gat ctc cca aca ggg gct ctt gat tat ctc gat gag gcc gcg tgg ggg	547
Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp Glu Ala Ala Trp Gly	
135 140 145	
ttc ctc gac gcc gga atc gca gct caa aac gct gca att gct gcg gag	595
Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala Ala Ile Ala Ala Glu	
150 155 160 165	
tca ctt gga ttg gga acg ctc tat ttg ggt tcg gtg cgc aac gat gcg	643
Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser Val Arg Asn Asp Ala	
170 175 180	
gaa gcc gtg cac aaa ttg ctt ggc ctt cca cct gag atc gtg cct gtc	691
Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro Glu Ile Val Pro Val	
185 190 195	
gtg ggc ttg gaa atg ggg cat gcg gat ccg cct gaa cct gcc gga att	739
Val Gly Leu Glu Met Gly His Ala Asp Pro Pro Glu Pro Ala Gly Ile	
200 205 210	
aaa cct ccc ctg cca caa gaa gcc att gtt cac tgg gat acc tac acc	787
Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His Trp Asp Thr Tyr Thr	
215 220 225	
gag aaa aac ctc gaa ctt atc gat tcc tac gac cgc gcc ctc gac act	835
Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp Arg Ala Leu Asp Thr	
230 235 240 245	
tac tat tct cgc tac ggc cag cac cag ctc tgg tcg aag cag acg gcg	883
Tyr Tyr Ser Arg Tyr Gly Gln His Gln Leu Trp Ser Lys Gln Thr Ala	
250 255 260	
cat agg gcg gcg tcg aaa agc ttt tca aaa acc aac agg cag ttc ctt	931
His Arg Ala Ala Ser Lys Ser Phe Ser Lys Thr Asn Arg Gln Phe Leu	
265 270 275	
agg ggc gtg ttt gag cgc gcc ggg ttt ggg ctg aga taaaagcatg	977
Arg Gly Val Phe Glu Arg Ala Gly Phe Gly Leu Arg	
280 285	
attatggacg cct	990

<210> 708

<211> 289

Ala Met Ile Gly Ser Val Thr Asp Ala Val Val Val Gly Gly Gly Phe
 145 150 155 160

Ile Gly Leu Glu Ala Ala Cys Ser Leu His Asp Leu Gly Lys Asn Val
 165 170 175

Thr Val Leu Glu Tyr Gly Pro Arg Leu Ile Gly Arg Ala Val Gly Glu
 180 185 190

Glu Thr Ala Ala Phe Phe Leu Glu Gln His Arg Ser Arg Gly Val Asn
 195 200 205

Ile Val Leu Asp Ala Arg Met Lys Gln Phe Val Gly Lys Asp Gly Lys
 210 215 220

Leu Ser Gly Ile Glu Leu Glu Asp Gly Thr Val Ile Pro Ala Gln Leu
 225 230 235 240

Val Ile Val Gly Ile Gly Val Ile Pro Asn Thr Glu Leu Ala Ala Val
 245 250 255

Leu Gly Leu Asp Ile Asn Asn Gly Ile Val Val Asp Lys His Ala Val
 260 265 270

Ala Ser Asp Gly Thr Thr Ile Ala Ile Gly Asp Val Ala Asn Ile Pro
 275 280 285

Asn Pro Ile Pro Gly Ser Pro Ala Asp Glu Arg Ile Arg Leu Glu Ser
 290 295 300

Val Asn Asn Ala Ile Glu His Ala Lys Ile Ala Ala Tyr Ser Leu Val
 305 310 315 320

Gly Gln Pro Glu Ala Tyr Ala Gly Ile Pro Trp Phe Trp Ser Asn Gln
 325 330 335

Gly Asp Leu Lys Leu Gln Ile Ala Gly Leu Thr Leu Gly Tyr Asp Ser
 340 345 350

Thr Val Ile Arg Gln Asp Pro Glu Lys Lys Lys Phe Ser Val Leu Tyr
 355 360 365

Tyr Arg Gly Asp Asn Ile Ile Ala Ala Asp Cys Val Asn Ala Pro Leu
 370 375 380

Asp Phe Met Ala Val Arg Ser Ala Leu Ser Arg Asn Gln Asn Ile Pro
 385 390 395 400

Ala Asp Leu Ala Ala Asp Ile Ser Gln Pro Leu Lys Lys Leu Ala Val
 405 410 415

Asp Leu Glu Val Thr Arg
 420

<210> 679

<211> 1074

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1051)

<223> RXA00224

<400> 679

```

gtgatgtcat tgggtgcatcg ggtgctgctg aaaagattgc tgagtacctc gcttcagaga 60

acctcatcta gccactatct tcacaaagga gaacatttaa atg tct att tct tat 115
                               Met Ser Ile Ser Tyr
                               1       5

gtg ctg gtt gag cag cta gat ggc cgc cca gaa cca gtt acc ctt gaa 163
Val Leu Val Glu Gln Leu Asp Gly Arg Pro Glu Pro Val Thr Leu Glu
          10              15              20

ttg atc act gct gct cgc gca ctc ggt gac gtc gtt gcc gtt gtc gtt 211
Leu Ile Thr Ala Ala Arg Ala Leu Gly Asp Val Val Ala Val Val Val
          25              30              35

ggc gag cca ggt gcc ggc gta aac ctt gct gct gag ctc ggc aat tgg 259
Gly Glu Pro Gly Ala Gly Val Asn Leu Ala Ala Glu Leu Gly Asn Trp
          40              45              50

ggt gca gca cag gtt gtt tcc gct gaa atc tct ggc gct tcc aac cgt 307
Gly Ala Ala Gln Val Val Ser Ala Glu Ile Ser Gly Ala Ser Asn Arg
          55              60              65

ttg atc ttg cct gct gtt gat gcg ctg cac att ttg gct gcg aac aac 355
Leu Ile Leu Pro Ala Val Asp Ala Leu His Ile Leu Ala Ala Asn Asn
          70              75              80              85

cca ggt cca att gtt atc gct gca act gca agc ggt aat gag atc gct 403
Pro Gly Pro Ile Val Ile Ala Ala Thr Ala Ser Gly Asn Glu Ile Ala
          90              95              100

ggt cgt ttg gct gcc cgt ttg gct tct ggt gtg ctc acc gat gtc gtc 451
Gly Arg Leu Ala Ala Arg Leu Ala Ser Gly Val Leu Thr Asp Val Val
          105              110              115

gga atc aat gcc gac cgc acc gca cag cag tcc att ttc ggc gac acc 499
Gly Ile Asn Ala Asp Arg Thr Ala Gln Gln Ser Ile Phe Gly Asp Thr
          120              125              130

att cag gtg tcc gct gca gtt ggt ggc gct tca ccg ctg tac acc ctg 547
Ile Gln Val Ser Ala Ala Val Gly Gly Ala Ser Pro Leu Tyr Thr Leu
          135              140              145

cgt cca ggt gcc ctt gat ggc gtg gcc gtt cct gca acc ggt gaa ttg 595
Arg Pro Gly Ala Leu Asp Gly Val Ala Val Pro Ala Thr Gly Glu Leu
          150              155              160              165

gca acc att gag atc cca ggc gca acc gcc aag gat gtc acc atc acc 643
Ala Thr Ile Glu Ile Pro Gly Ala Thr Ala Lys Asp Val Thr Ile Thr
          170              175              180

tcc ttc acg cca agc acc cag agc gat cgc cct gag ctg cca cag gca 691
Ser Phe Thr Pro Ser Thr Gln Ser Asp Arg Pro Glu Leu Pro Gln Ala
          185              190              195

aag gtc gtt atc gca ggt gga cgt ggt gtc gga agc gaa gaa aac ttc 739

```

Lys Val Val Ile Ala Gly Gly Arg Gly Val Gly Ser Glu Glu Asn Phe
 200 205 210
 cgc agc atc gtt gaa cca ctg gca gat gca ttg ggc ggt gcc gtt ggc 787
 Arg Ser Ile Val Glu Pro Leu Ala Asp Ala Leu Gly Gly Ala Val Gly
 215 220 225
 gca acc cgc gac gcc gtt gat ctg ggc tac tac cca ggc gag tac cag 835
 Ala Thr Arg Asp Ala Val Asp Leu Gly Tyr Tyr Pro Gly Glu Tyr Gln
 230 235 240 245
 gtt ggt cag acc ggt gtc acc gtg tcc cca gac ctc tac atc ggc ctc 883
 Val Gly Gln Thr Gly Val Thr Val Ser Pro Asp Leu Tyr Ile Gly Leu
 250 255 260
 ggc att tcc ggt gca att cag cac act tct ggt atg cag acc gca aag 931
 Gly Ile Ser Gly Ala Ile Gln His Thr Ser Gly Met Gln Thr Ala Lys
 265 270 275
 aag gtt att gtg atc aac aac gat gag gac gcg ccg atc ttc cag att 979
 Lys Val Ile Val Ile Asn Asn Asp Glu Asp Ala Pro Ile Phe Gln Ile
 280 285 290
 gcg gac ctc ggt gtc gtt ggc gac ctc ttt gac atc gcc cct gcg ctc 1027
 Ala Asp Leu Gly Val Val Gly Asp Leu Phe Asp Ile Ala Pro Ala Leu
 295 300 305
 atc gaa gag atc aac aag cgc aag taggagtttt gaacactttt tat 1074
 Ile Glu Glu Ile Asn Lys Arg Lys
 310 315

<210> 680

<211> 317

<212> PRT

<213> Corynebacterium glutamicum

<400> 680

Met Ser Ile Ser Tyr Val Leu Val Glu Gln Leu Asp Gly Arg Pro Glu
 1 5 10 15
 Pro Val Thr Leu Glu Leu Ile Thr Ala Ala Arg Ala Leu Gly Asp Val
 20 25 30
 Val Ala Val Val Val Gly Glu Pro Gly Ala Gly Val Asn Leu Ala Ala
 35 40 45
 Glu Leu Gly Asn Trp Gly Ala Ala Gln Val Val Ser Ala Glu Ile Ser
 50 55 60
 Gly Ala Ser Asn Arg Leu Ile Leu Pro Ala Val Asp Ala Leu His Ile
 65 70 75 80
 Leu Ala Ala Asn Asn Pro Gly Pro Ile Val Ile Ala Ala Thr Ala Ser
 85 90 95
 Gly Asn Glu Ile Ala Gly Arg Leu Ala Ala Arg Leu Ala Ser Gly Val
 100 105 110
 Leu Thr Asp Val Val Gly Ile Asn Ala Asp Arg Thr Ala Gln Gln Ser
 115 120 125

Ile Phe Gly Asp Thr Ile Gln Val Ser Ala Ala Val Gly Gly Ala Ser
 130 135 140
 Pro Leu Tyr Thr Leu Arg Pro Gly Ala Leu Asp Gly Val Ala Val Pro
 145 150 155 160
 Ala Thr Gly Glu Leu Ala Thr Ile Glu Ile Pro Gly Ala Thr Ala Lys
 165 170 175
 Asp Val Thr Ile Thr Ser Phe Thr Pro Ser Thr Gln Ser Asp Arg Pro
 180 185 190
 Glu Leu Pro Gln Ala Lys Val Val Ile Ala Gly Gly Arg Gly Val Gly
 195 200 205
 Ser Glu Glu Asn Phe Arg Ser Ile Val Glu Pro Leu Ala Asp Ala Leu
 210 215 220
 Gly Gly Ala Val Gly Ala Thr Arg Asp Ala Val Asp Leu Gly Tyr Tyr
 225 230 235 240
 Pro Gly Glu Tyr Gln Val Gly Gln Thr Gly Val Thr Val Ser Pro Asp
 245 250 255
 Leu Tyr Ile Gly Leu Gly Ile Ser Gly Ala Ile Gln His Thr Ser Gly
 260 265 270
 Met Gln Thr Ala Lys Lys Val Ile Val Ile Asn Asn Asp Glu Asp Ala
 275 280 285
 Pro Ile Phe Gln Ile Ala Asp Leu Gly Val Val Gly Asp Leu Phe Asp
 290 295 300
 Ile Ala Pro Ala Leu Ile Glu Glu Ile Asn Lys Arg Lys
 305 310 315

<210> 681

<211> 909

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(886)

<223> RXA00225

<400> 681

gtaggcgctcg aaaagcaatg ggcgaagccc gcgtagtatg ggcgggcaac gctaaaagcg 60

ccaaaaacgc caaaaatcgt gaattgaaag gtgagtgtgg atg tcc aca atc gtg 115
 Met Ser Thr Ile Val
 1 5

gtt ctg gtt aaa aat gtt cca gac acc tgg tct aag agg act ctg gaa 163
 Val Leu Val Lys Asn Val Pro Asp Thr Trp Ser Lys Arg Thr Leu Glu
 10 15 20

gct gat ttc acc ctt gac cgt gag ggt gta gat cga gtc ttg gat gag 211
 Ala Asp Phe Thr Leu Asp Arg Glu Gly Val Asp Arg Val Leu Asp Glu

25	30	35	
atc aat gag ttt gct ctg gag cag gca ctg cgc ttg cgg gag tcc aac Ile Asn Glu Phe Ala Leu Glu Gln Ala Leu Arg Leu Arg Glu Ser Asn 40 45 50			259
ccg gat gct ggt tac cgc gtt gtt gcg ctg agc gcc ggc cct gcc ggt Pro Asp Ala Gly Tyr Arg Val Val Ala Leu Ser Ala Gly Pro Ala Gly 55 60 65			307
ggg gaa gag gcg ctg cgt aag gcg ctg tcc atg ggt gct gat gaa gca Gly Glu Glu Ala Leu Arg Lys Ala Leu Ser Met Gly Ala Asp Glu Ala 70 75 80 85			355
atc cag ctc agt gat gat gcc ttg gct ggt tct gat ctt ttg gga acc Ile Gln Leu Ser Asp Asp Ala Leu Ala Gly Ser Asp Leu Leu Gly Thr 90 95 100			403
gct tgg gcg ctg aac aac gct atc aac acc atc gcg ggt gtt gct ctc Ala Trp Ala Leu Asn Asn Ala Ile Asn Thr Ile Ala Gly Val Ala Leu 105 110 115			451
atc gtg acg ggt tcg gct tct tcc gat ggt tcc atg ggt gcg ctt cct Ile Val Thr Gly Ser Ala Ser Ser Asp Gly Ser Met Gly Ala Leu Pro 120 125 130			499
ggc gtg tta gct gag tac cgc cag gtc cca gcg ttg act aac ttg tct Gly Val Leu Ala Glu Tyr Arg Gln Val Pro Ala Leu Thr Asn Leu Ser 135 140 145			547
gcg ctg aag gtc gag ggt gca tct att act gcc act cgc att gat aac Ala Leu Lys Val Glu Gly Ala Ser Ile Thr Ala Thr Arg Ile Asp Asn 150 155 160 165			595
cac ggc acc tat gag ttg cag gct gca ctt cct gcg gtt gtg tcg att His Gly Thr Tyr Glu Leu Gln Ala Ala Leu Pro Ala Val Val Ser Ile 170 175 180			643
tcc gat aag gct gac aag cca cgt ttc cct aac ttc aag ggc atc atg Ser Asp Lys Ala Asp Lys Pro Arg Phe Pro Asn Phe Lys Gly Ile Met 185 190 195			691
gct gct aag aag gct gag atc aag aag ctt tcc ttg gct gaa atc ggc Ala Ala Lys Lys Ala Glu Ile Lys Lys Leu Ser Leu Ala Glu Ile Gly 200 205 210			739
gtg gct cca gag cag gtt ggt ctg tct cac gcg gca act gct gtt act Val Ala Pro Glu Gln Val Gly Leu Ser His Ala Ala Thr Ala Val Thr 215 220 225			787
gct gca gct gat cgt cct gag cgc tcc caa ggt gat gtc att ggt gca Ala Ala Ala Asp Arg Pro Glu Arg Ser Gln Gly Asp Val Ile Gly Ala 230 235 240 245			835
tcg ggt gct gct gaa aag att gct gag tac ctc gct tca gag aac ctc Ser Gly Ala Ala Glu Lys Ile Ala Glu Tyr Leu Ala Ser Glu Asn Leu 250 255 260			883
atc tagccactat cttcacaag gag Ile			909

<210> 682
 <211> 262
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 682

```

Met Ser Thr Ile Val Val Leu Val Lys Asn Val Pro Asp Thr Trp Ser
 1             5             10             15

Lys Arg Thr Leu Glu Ala Asp Phe Thr Leu Asp Arg Glu Gly Val Asp
          20             25             30

Arg Val Leu Asp Glu Ile Asn Glu Phe Ala Leu Glu Gln Ala Leu Arg
      35             40             45

Leu Arg Glu Ser Asn Pro Asp Ala Gly Tyr Arg Val Val Ala Leu Ser
      50             55             60

Ala Gly Pro Ala Gly Gly Glu Glu Ala Leu Arg Lys Ala Leu Ser Met
 65             70             75             80

Gly Ala Asp Glu Ala Ile Gln Leu Ser Asp Asp Ala Leu Ala Gly Ser
          85             90             95

Asp Leu Leu Gly Thr Ala Trp Ala Leu Asn Asn Ala Ile Asn Thr Ile
      100             105             110

Ala Gly Val Ala Leu Ile Val Thr Gly Ser Ala Ser Ser Asp Gly Ser
      115             120             125

Met Gly Ala Leu Pro Gly Val Leu Ala Glu Tyr Arg Gln Val Pro Ala
      130             135             140

Leu Thr Asn Leu Ser Ala Leu Lys Val Glu Gly Ala Ser Ile Thr Ala
      145             150             155             160

Thr Arg Ile Asp Asn His Gly Thr Tyr Glu Leu Gln Ala Ala Leu Pro
          165             170             175

Ala Val Val Ser Ile Ser Asp Lys Ala Asp Lys Pro Arg Phe Pro Asn
      180             185             190

Phe Lys Gly Ile Met Ala Ala Lys Lys Ala Glu Ile Lys Lys Leu Ser
      195             200             205

Leu Ala Glu Ile Gly Val Ala Pro Glu Gln Val Gly Leu Ser His Ala
      210             215             220

Ala Thr Ala Val Thr Ala Ala Ala Asp Arg Pro Glu Arg Ser Gln Gly
      225             230             235             240

Asp Val Ile Gly Ala Ser Gly Ala Ala Glu Lys Ile Ala Glu Tyr Leu
          245             250             255

Ala Ser Glu Asn Leu Ile
          260

```

<210> 683

<211> 2378
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (82)..(2355)
 <223> RXN00606

<400> 683

```
tgcggtggcg attgctgcga cccaagctgg caccaccagc ctogatggta ttttgcactc 60

tgatttctgg cggagaagcc agtg ctc acg ggt gtt att gcg gtg ctg att 111
                Val Leu Thr Gly Val Ile Ala Val Leu Ile
                1                      5                      10

gca atg tcc gcg ttc act aag tcc gca cag ttc ccg ttc cac ttc tgg 159
Ala Met Ser Ala Phe Thr Lys Ser Ala Gln Phe Pro Phe His Phe Trp
                15                      20                      25

ctg cct gag gcg atg gct gcg gcc acc cca gtg tcg gcg ttc ctg cac 207
Leu Pro Glu Ala Met Ala Ala Ala Thr Pro Val Ser Ala Phe Leu His
                30                      35                      40

gct gcg gcc gtg gtc aag gcg ggt att tac ctg ttg ctg cgc ttt agc 255
Ala Ala Ala Val Val Lys Ala Gly Ile Tyr Leu Leu Leu Arg Phe Ser
                45                      50                      55

att gtg ttc cat gat gtt gcg gtc tgg aat tgg ttg ctg att atc gtc 303
Ile Val Phe His Asp Val Ala Val Trp Asn Trp Leu Leu Ile Ile Val
                60                      65                      70

ggc atg ggt acg gcc atc atg tcg gcg tat ttc gcg gtg cag aag acc 351
Gly Met Gly Thr Ala Ile Met Ser Ala Tyr Phe Ala Val Gln Lys Thr
                75                      80                      85                      90

gat ctg aag aag ctc acg gca tat tcc acg gtg tcg cat ttg ggt tgg 399
Asp Leu Lys Lys Leu Thr Ala Tyr Ser Thr Val Ser His Leu Gly Trp
                95                      100                      105

atc gta gcg acc atc ggc gtg ggc act cct ttc gcg ctc ggc gct gcc 447
Ile Val Ala Thr Ile Gly Val Gly Thr Pro Phe Ala Leu Gly Ala Ala
                110                      115                      120

att gtg cac acg ctc agc cac gcg ctg ttt aag tcc tcg ttg ttc atg 495
Ile Val His Thr Leu Ser His Ala Leu Phe Lys Ser Ser Leu Phe Met
                125                      130                      135

ctc att ggc gtg att gat cac cag act ggc acg cgc gat att cgt cgc 543
Leu Ile Gly Val Ile Asp His Gln Thr Gly Thr Arg Asp Ile Arg Arg
                140                      145                      150

ctc ggt ttc ctg gtc aag aag atg ccg ttc acg ttt gtg tct gta tta 591
Leu Gly Phe Leu Val Lys Lys Met Pro Phe Thr Phe Val Ser Val Leu
                155                      160                      165                      170

ata ggt gcg ttg tcg atg gca tcg gtt ccg ccg ttg ctc ggc ttc gtg 639
Ile Gly Ala Leu Ser Met Ala Ser Val Pro Pro Leu Leu Gly Phe Val
                175                      180                      185

tcc aaa gaa ggc atg atc aca gcg ttc atg gac gcc ccc atc ggc aac 687
```

Ser	Lys	Glu	Gly	Met	Ile	Thr	Ala	Phe	Met	Asp	Ala	Pro	Ile	Gly	Asn	
			190					195					200			
tcc	tat	gtt	gta	tta	ctg	ctg	gtc	ggc	gca	gca	atc	ggc	gcg	gtc	cta	735
Ser	Tyr	Val	Val	Leu	Leu	Leu	Val	Gly	Ala	Ala	Ile	Gly	Ala	Val	Leu	
		205					210					215				
acc	ttc	aca	tac	tcc	gcg	aaa	ctc	gtg	ctc	ggc	gca	ttc	gtc	gac	ggc	783
Thr	Phe	Thr	Tyr	Ser	Ala	Lys	Leu	Val	Leu	Gly	Ala	Phe	Val	Asp	Gly	
	220					225					230					
cca	cgc	gac	atg	tca	cac	gtc	aag	gaa	gcc	ccc	gtc	tcc	ctc	tgg	ctt	831
Pro	Arg	Asp	Met	Ser	His	Val	Lys	Glu	Ala	Pro	Val	Ser	Leu	Trp	Leu	
235					240					245					250	
ccg	gcc	gcc	ctg	cct	gga	ctt	atg	tct	ctg	cca	cta	gtc	cta	gta	ctt	879
Pro	Ala	Ala	Leu	Pro	Gly	Leu	Met	Ser	Leu	Pro	Leu	Val	Leu	Val	Leu	
				255					260					265		
tcg	ctt	ttc	gac	gcc	ccc	gtc	tcc	gcc	gca	gcc	acc	tcc	gcc	gcg	ggg	927
Ser	Leu	Phe	Asp	Ala	Pro	Val	Ser	Ala	Ala	Ala	Thr	Ser	Ala	Ala	Gly	
			270					275					280			
gaa	gcg	gcg	cac	atg	cac	ctg	gca	ttg	tgg	cac	ggc	atc	aac	acc	cca	975
Glu	Ala	Ala	His	Met	His	Leu	Ala	Leu	Trp	His	Gly	Ile	Asn	Thr	Pro	
		285					290					295				
ctg	ttg	att	tcc	ttg	ggt	gtg	ctg	gtg	gcc	gga	atc	ctt	ggt	gtg	ctg	1023
Leu	Leu	Ile	Ser	Leu	Gly	Val	Leu	Val	Ala	Gly	Ile	Leu	Gly	Val	Leu	
	300					305					310					
ttc	cgc	aaa	gag	ctg	tgg	aaa	atc	gcc	gag	acc	agc	cct	ttc	ccc	atc	1071
Phe	Arg	Lys	Glu	Leu	Trp	Lys	Ile	Ala	Glu	Thr	Ser	Pro	Phe	Pro	Ile	
315					320					325					330	
gcc	aca	ggc	aac	gac	atc	cta	tcg	atg	ctg	gtt	tac	cga	gcc	aac	ttg	1119
Ala	Thr	Gly	Asn	Asp	Ile	Leu	Ser	Met	Leu	Val	Tyr	Arg	Ala	Asn	Leu	
				335					340					345		
ctg	ggt	aaa	ttc	ttc	ggt	cgc	atg	gct	gat	tcg	atg	agc	cca	cgc	agg	1167
Leu	Gly	Lys	Phe	Phe	Gly	Arg	Met	Ala	Asp	Ser	Met	Ser	Pro	Arg	Arg	
			350					355					360			
cac	ttg	gtc	agc	ctc	atc	gtg	ctg	ctc	tgg	gcg	ctg	gct	gct	ttt	gcc	1215
His	Leu	Val	Ser	Leu	Ile	Val	Leu	Leu	Trp	Ala	Leu	Ala	Ala	Phe	Ala	
		365					370					375				
acc	att	cac	ccc	tcg	gtt	cag	ctt	gca	cca	aag	caa	ccg	gga	att	gat	1263
Thr	Ile	His	Pro	Ser	Val	Gln	Leu	Ala	Pro	Lys	Gln	Pro	Gly	Ile	Asp	
	380					385					390					
cgt	tgg	atc	gac	ctc	att	ccg	ctt	gcc	atc	atc	gcg	cta	tct	gtc	ttc	1311
Arg	Trp	Ile	Asp	Leu	Ile	Pro	Leu	Ala	Ile	Ile	Ala	Leu	Ser	Val	Phe	
395					400					405					410	
ggc	ctg	ctc	acc	acc	cga	aac	cgc	ctc	agc	gca	gcc	gtg	ctt	gtg	ggt	1359
Gly	Leu	Leu	Thr	Thr	Arg	Asn	Arg	Leu	Ser	Ala	Ala	Val	Leu	Val	Gly	
				415					420					425		
acc	gtt	ggt	gtg	ggt	gtt	tcc	ttc	cag	atg	cta	ctt	ctg	ggc	gct	ccc	1407
Thr	Val	Gly	Val	Gly	Val	Ser	Phe	Gln	Met	Leu	Leu	Leu	Gly	Ala	Pro	

430										435										440									
gat	gtt	gca	ctt	acc	cag	ttc	ctg	gta	gaa	ggc	ctc	gtc	gtg	gta	atc														
Asp	Val	Ala	Leu	Thr	Gln	Phe	Leu	Val	Glu	Gly	Leu	Val	Val	Val	Ile														
		445																											
atc	atg	atg	gtt	gtc	cgg	cac	cag	cct	gcc	aac	ttc	aag	cgc	atc	aag														
Ile	Met	Met	Val	Val	Arg	His	Gln	Pro	Ala	Asn	Phe	Lys	Arg	Ile	Lys														
		460																											
ccc	agc	aga	agg	cgc	agc	acc	gtt	ctt	gtc	gcc	gtc	ctt	gct	gcc	ttc														
Pro	Ser	Arg	Arg	Arg	Ser	Thr	Val	Leu	Val	Ala	Val	Leu	Ala	Ala	Phe														
		475																											
gcc	gca	ttc	atg	gcg	gtg	tgg	gga	ttg	ctt	ggc	cgt	cac	gaa	cgt	tct														
Ala	Ala	Phe	Met	Ala	Val	Trp	Gly	Leu	Leu	Gly	Arg	His	Glu	Arg	Ser														
gag	ctg	gcc	atg	tgg	tac	ctc	aac	caa	ggg	cca	gag	atc	acc	tct	ggc														
Glu	Leu	Ala	Met	Trp	Tyr	Leu	Asn	Gln	Gly	Pro	Glu	Ile	Thr	Ser	Gly														
gcc	aac	gtg	gtg	aac	acc	atc	ctc	gtg	gaa	ttc	cgt	gca	ctg	gat	acg														
Ala	Asn	Val	Val	Asn	Thr	Ile	Leu	Val	Glu	Phe	Arg	Ala	Leu	Asp	Thr														
ttg	ggc	gag	ctc	tcc	gtg	ctt	ggc	atg	gca	gct	gtc	gtc	atc	ggg	gcg														
Leu	Gly	Glu	Leu	Ser	Val	Leu	Gly	Met	Ala	Ala	Val	Val	Ile	Gly	Ala														
atg	gtg	gct	tcc	atg	cct	cgt	cat	ccg	ttt	gcc	aag	ggc	acc	cac	cct														
Met	Val	Ala	Ser	Met	Pro	Arg	His	Pro	Phe	Ala	Lys	Gly	Thr	His	Pro														
cgc	ccc	ttt	ggc	caa	tca	cag	ttg	aac	tcc	att	ccg	ctg	cgc	atg	ctg														
Arg	Pro	Phe	Gly	Gln	Ser	Gln	Leu	Asn	Ser	Ile	Pro	Leu	Arg	Met	Leu														
ctt	aag	gtg	ctg	gtt	cca	gcg	cta	tgc	ttc	ttg	agc	ttc	atg	gtg	ttc														
Leu	Lys	Val	Leu	Val	Pro	Ala	Leu	Cys	Phe	Leu	Ser	Phe	Met	Val	Phe														
atg	cgt	gga	cac	aat	gat	ccg	gga	ggc	ggg	ttc	atc	gca	gcc	cta	att														
Met	Arg	Gly	His	Asn	Asp	Pro	Gly	Gly	Gly	Phe	Ile	Ala	Ala	Leu	Ile														
gcc	ggg	ggc	gcg	ctg	atg	ctc	ctg	tac	ctg	tcc	aag	gcc	aaa	gat	ggc														
Ala	Gly	Gly	Ala	Leu	Met	Leu	Leu	Tyr	Leu	Ser	Lys	Ala	Lys	Asp	Gly														
cgc	att	ttc	cgc	ccg	aat	gtt	cct	ttc	att	ctc	act	ggg	gcg	ggc	atc														
Arg	Ile	Phe	Arg	Pro	Asn	Val	Pro	Phe	Ile	Leu	Thr	Gly	Ala	Gly	Ile														
ttg	atg	gca	gtg	ttc	tcg	ggc	gta	ctg	gga	ctc	acc	cac	ggg	tct	ttc														
Leu	Met	Ala	Val	Phe	Ser	Gly	Val	Leu	Gly	Leu	Thr	His	Gly	Ser	Phe														
ctg	tac	gcc	atc	cac	ttc	aac	ttc	gta	ggc	cag	cac	tgg	acc	acc	tcg														
Leu	Tyr	Ala	Ile	His	Phe	Asn	Phe	Val	Gly	Gln	His	Trp	Thr	Thr	Ser														

atg atc ttc gac ctc ggc gtg tac ctg gcc gtg ttg ggc atg gtg tcc 2175
 Met Ile Phe Asp Leu Gly Val Tyr Leu Ala Val Leu Gly Met Val Ser
 685 690 695

atg gca atc aac ggc ctg ggc gga tac ctg cgc cca ggt acc gac aat 2223
 Met Ala Ile Asn Gly Leu Gly Gly Tyr Leu Arg Pro Gly Thr Asp Asn
 700 705 710

gca gat ctg gac tac gcc cgc cga agt ggc cca ctg cca gca acg cca 2271
 Ala Asp Leu Asp Tyr Ala Arg Arg Ser Gly Pro Leu Pro Ala Thr Pro
 715 720 725 730

acg gtt gaa ccc gaa cca gaa ggc gat gaa gac tgg ccc gaa ccc atc 2319
 Thr Val Glu Pro Glu Pro Glu Gly Asp Glu Asp Trp Pro Glu Pro Ile
 735 740 745

aac ccc gca ggc gat aac aaa gag gag gca aac cga tgattctcgc 2365
 Asn Pro Ala Gly Asp Asn Lys Glu Glu Ala Asn Arg
 750 755

actgacagtc gcg 2378

<210> 684

<211> 758

<212> PRT

<213> Corynebacterium glutamicum

<400> 684

Val Leu Thr Gly Val Ile Ala Val Leu Ile Ala Met Ser Ala Phe Thr
 1 5 10 15

Lys Ser Ala Gln Phe Pro Phe His Phe Trp Leu Pro Glu Ala Met Ala
 20 25 30

Ala Ala Thr Pro Val Ser Ala Phe Leu His Ala Ala Ala Val Val Lys
 35 40 45

Ala Gly Ile Tyr Leu Leu Leu Arg Phe Ser Ile Val Phe His Asp Val
 50 55 60

Ala Val Trp Asn Trp Leu Leu Ile Ile Val Gly Met Gly Thr Ala Ile
 65 70 75 80

Met Ser Ala Tyr Phe Ala Val Gln Lys Thr Asp Leu Lys Lys Leu Thr
 85 90 95

Ala Tyr Ser Thr Val Ser His Leu Gly Trp Ile Val Ala Thr Ile Gly
 100 105 110

Val Gly Thr Pro Phe Ala Leu Gly Ala Ala Ile Val His Thr Leu Ser
 115 120 125

His Ala Leu Phe Lys Ser Ser Leu Phe Met Leu Ile Gly Val Ile Asp
 130 135 140

His Gln Thr Gly Thr Arg Asp Ile Arg Arg Leu Gly Phe Leu Val Lys
 145 150 155 160

Lys Met Pro Phe Thr Phe Val Ser Val Leu Ile Gly Ala Leu Ser Met

165					170					175					
Ala	Ser	Val	Pro	Pro	Leu	Leu	Gly	Phe	Val	Ser	Lys	Glu	Gly	Met	Ile
			180					185					190		
Thr	Ala	Phe	Met	Asp	Ala	Pro	Ile	Gly	Asn	Ser	Tyr	Val	Val	Leu	Leu
			195				200					205			
Leu	Val	Gly	Ala	Ala	Ile	Gly	Ala	Val	Leu	Thr	Phe	Thr	Tyr	Ser	Ala
	210					215					220				
Lys	Leu	Val	Leu	Gly	Ala	Phe	Val	Asp	Gly	Pro	Arg	Asp	Met	Ser	His
225					230					235					240
Val	Lys	Glu	Ala	Pro	Val	Ser	Leu	Trp	Leu	Pro	Ala	Ala	Leu	Pro	Gly
				245					250					255	
Leu	Met	Ser	Leu	Pro	Leu	Val	Leu	Val	Leu	Ser	Leu	Phe	Asp	Ala	Pro
			260					265					270		
Val	Ser	Ala	Ala	Ala	Thr	Ser	Ala	Ala	Gly	Glu	Ala	Ala	His	Met	His
			275				280					285			
Leu	Ala	Leu	Trp	His	Gly	Ile	Asn	Thr	Pro	Leu	Leu	Ile	Ser	Leu	Gly
	290					295					300				
Val	Leu	Val	Ala	Gly	Ile	Leu	Gly	Val	Leu	Phe	Arg	Lys	Glu	Leu	Trp
305					310					315					320
Lys	Ile	Ala	Glu	Thr	Ser	Pro	Phe	Pro	Ile	Ala	Thr	Gly	Asn	Asp	Ile
				325					330					335	
Leu	Ser	Met	Leu	Val	Tyr	Arg	Ala	Asn	Leu	Leu	Gly	Lys	Phe	Phe	Gly
			340					345					350		
Arg	Met	Ala	Asp	Ser	Met	Ser	Pro	Arg	Arg	His	Leu	Val	Ser	Leu	Ile
			355				360					365			
Val	Leu	Leu	Trp	Ala	Leu	Ala	Ala	Phe	Ala	Thr	Ile	His	Pro	Ser	Val
	370					375					380				
Gln	Leu	Ala	Pro	Lys	Gln	Pro	Gly	Ile	Asp	Arg	Trp	Ile	Asp	Leu	Ile
385					390					395					400
Pro	Leu	Ala	Ile	Ile	Ala	Leu	Ser	Val	Phe	Gly	Leu	Leu	Thr	Thr	Arg
				405					410					415	
Asn	Arg	Leu	Ser	Ala	Ala	Val	Leu	Val	Gly	Thr	Val	Gly	Val	Gly	Val
			420					425					430		
Ser	Phe	Gln	Met	Leu	Leu	Leu	Gly	Ala	Pro	Asp	Val	Ala	Leu	Thr	Gln
			435				440					445			
Phe	Leu	Val	Glu	Gly	Leu	Val	Val	Val	Ile	Ile	Met	Met	Val	Val	Arg
	450					455					460				
His	Gln	Pro	Ala	Asn	Phe	Lys	Arg	Ile	Lys	Pro	Ser	Arg	Arg	Arg	Ser
465					470					475					480
Thr	Val	Leu	Val	Ala	Val	Leu	Ala	Ala	Phe	Ala	Ala	Phe	Met	Ala	Val
				485				490					495		

Trp Gly Leu Leu Gly Arg His Glu Arg Ser Glu Leu Ala Met Trp Tyr
 500 505 510
 Leu Asn Gln Gly Pro Glu Ile Thr Ser Gly Ala Asn Val Val Asn Thr
 515 520 525
 Ile Leu Val Glu Phe Arg Ala Leu Asp Thr Leu Gly Glu Leu Ser Val
 530 535 540
 Leu Gly Met Ala Ala Val Val Ile Gly Ala Met Val Ala Ser Met Pro
 545 550 555 560
 Arg His Pro Phe Ala Lys Gly Thr His Pro Arg Pro Phe Gly Gln Ser
 565 570 575
 Gln Leu Asn Ser Ile Pro Leu Arg Met Leu Leu Lys Val Leu Val Pro
 580 585 590
 Ala Leu Cys Phe Leu Ser Phe Met Val Phe Met Arg Gly His Asn Asp
 595 600 605
 Pro Gly Gly Gly Phe Ile Ala Ala Leu Ile Ala Gly Gly Ala Leu Met
 610 615 620
 Leu Leu Tyr Leu Ser Lys Ala Lys Asp Gly Arg Ile Phe Arg Pro Asn
 625 630 635 640
 Val Pro Phe Ile Leu Thr Gly Ala Gly Ile Leu Met Ala Val Phe Ser
 645 650 655
 Gly Val Leu Gly Leu Thr His Gly Ser Phe Leu Tyr Ala Ile His Phe
 660 665 670
 Asn Phe Val Gly Gln His Trp Thr Thr Ser Met Ile Phe Asp Leu Gly
 675 680 685
 Val Tyr Leu Ala Val Leu Gly Met Val Ser Met Ala Ile Asn Gly Leu
 690 695 700
 Gly Gly Tyr Leu Arg Pro Gly Thr Asp Asn Ala Asp Leu Asp Tyr Ala
 705 710 715 720
 Arg Arg Ser Gly Pro Leu Pro Ala Thr Pro Thr Val Glu Pro Glu Pro
 725 730 735
 Glu Gly Asp Glu Asp Trp Pro Glu Pro Ile Asn Pro Ala Gly Asp Asn
 740 745 750
 Lys Glu Glu Ala Asn Arg
 755

<210> 685
 <211> 1872
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1849)

<223> FRXA00606

<400> 685

```

atggataacc agactggcac gcgcgatatt cgtcgcctcg gtttcctggt caagaaaaat 60
gccgttcacg tttgtgtctg tattaatagg tgcgttgtcg atg gca tcg gtt ccg 115
                                         Met Ala Ser Val Pro
                                         1           5

ccg ttg ctc ggc ttc gtg tcc aaa gaa ggc atg atc aca gcg ttc atg 163
Pro Leu Leu Gly Phe Val Ser Lys Glu Gly Met Ile Thr Ala Phe Met
          10           15           20

gac gcc ccc atc ggc aac tcc tat gtt gta tta ctg ctg gtc ggc gca 211
Asp Ala Pro Ile Gly Asn Ser Tyr Val Val Leu Leu Leu Val Gly Ala
          25           30           35

gca atc ggc gcg gtc cta acc ttc aca tac tcc gcg aaa ctc gtg ctc 259
Ala Ile Gly Ala Val Leu Thr Phe Thr Tyr Ser Ala Lys Leu Val Leu
          40           45           50

ggc gca ttc gtc gac ggc cca cgc gac atg tca cac gtc aag gaa gcc 307
Gly Ala Phe Val Asp Gly Pro Arg Asp Met Ser His Val Lys Glu Ala
          55           60           65

ccc gtc tcc ctc tgg ctt ccg gcc gcc ctg cct gga ctt atg tct ctg 355
Pro Val Ser Leu Trp Leu Pro Ala Ala Leu Pro Gly Leu Met Ser Leu
          70           75           80           85

cca cta gtc cta gta ctt tcg ctt ttc gac gcc ccc gtc tcc gcc gca 403
Pro Leu Val Leu Val Leu Ser Leu Phe Asp Ala Pro Val Ser Ala Ala
          90           95           100

gcc acc tcc gcc gcg ggg gaa gcg gcg cac atg cac ctg gca ttg tgg 451
Ala Thr Ser Ala Ala Gly Glu Ala Ala His Met His Leu Ala Leu Trp
          105           110           115

cac ggc atc aac acc cca ctg ttg att tcc ttg ggt gtg ctg gtg gcc 499
His Gly Ile Asn Thr Pro Leu Leu Ile Ser Leu Gly Val Leu Val Ala
          120           125           130

gga atc ctt ggt gtg ctg ttc cgc aaa gag ctg tgg aaa atc gcc gag 547
Gly Ile Leu Gly Val Leu Phe Arg Lys Glu Leu Trp Lys Ile Ala Glu
          135           140           145

acc agc cct ttc ccc atc gcc aca ggc aac gac atc cta tcg atg ctg 595
Thr Ser Pro Phe Pro Ile Ala Thr Gly Asn Asp Ile Leu Ser Met Leu
          150           155           160           165

gtt tac cga gcc aac ttg ctg ggt aaa ttc ttc ggt cgc atg gct gat 643
Val Tyr Arg Ala Asn Leu Leu Gly Lys Phe Phe Gly Arg Met Ala Asp
          170           175           180

tcg atg agc cca cgc agg cac ttg gtc agc ctc atc gtg ctg ctc tgg 691
Ser Met Ser Pro Arg Arg His Leu Val Ser Leu Ile Val Leu Leu Trp
          185           190           195

gcg ctg gct gct ttt gcc acc att cac ccc tcg gtt cag ctt gca cca 739
Ala Leu Ala Ala Phe Ala Thr Ile His Pro Ser Val Gln Leu Ala Pro
          200           205           210

```

aag	caa	ccg	gga	att	gat	cgt	tgg	atc	gac	ctc	att	ccg	ctt	gcc	atc	787
Lys	Gln	Pro	Gly	Ile	Asp	Arg	Trp	Ile	Asp	Leu	Ile	Pro	Leu	Ala	Ile	
	215					220					225					
atc	gcg	cta	tct	gtc	ttc	ggc	ctg	ctc	acc	acc	cga	aac	cgc	ctc	agc	835
Ile	Ala	Leu	Ser	Val	Phe	Gly	Leu	Leu	Thr	Thr	Arg	Asn	Arg	Leu	Ser	
230					235					240					245	
gca	gcc	gtg	ctt	gtg	ggg	acc	gtt	ggg	gtg	ggg	gtt	tcc	ttc	cag	atg	883
Ala	Ala	Val	Leu	Val	Gly	Thr	Val	Gly	Val	Gly	Val	Ser	Phe	Gln	Met	
				250					255					260		
cta	ctt	ctg	ggc	gct	ccc	gat	gtt	gca	ctt	acc	cag	ttc	ctg	gta	gaa	931
Leu	Leu	Leu	Gly	Ala	Pro	Asp	Val	Ala	Leu	Thr	Gln	Phe	Leu	Val	Glu	
			265					270					275			
ggc	ctc	gtc	gtg	gta	atc	atc	atg	atg	gtt	gtc	cgg	cac	cag	cct	gcc	979
Gly	Leu	Val	Val	Val	Ile	Ile	Met	Met	Val	Val	Arg	His	Gln	Pro	Ala	
		280					285					290				
aac	ttc	aag	cgc	atc	aag	ccc	agc	aga	agg	cgc	agc	acc	gtt	ctt	gtc	1027
Asn	Phe	Lys	Arg	Ile	Lys	Pro	Ser	Arg	Arg	Arg	Ser	Thr	Val	Leu	Val	
	295					300					305					
gcc	gtc	ctt	gct	gcc	ttc	gcc	gca	ttc	atg	gcg	gtg	tgg	gga	ttg	ctt	1075
Ala	Val	Leu	Ala	Ala	Phe	Ala	Ala	Phe	Met	Ala	Val	Trp	Gly	Leu	Leu	
310					315					320					325	
ggc	cgt	cac	gaa	cgt	tct	gag	ctg	gcc	atg	tgg	tac	ctc	aac	caa	ggg	1123
Gly	Arg	His	Glu	Arg	Ser	Glu	Leu	Ala	Met	Trp	Tyr	Leu	Asn	Gln	Gly	
				330					335					340		
cca	gag	atc	acc	tct	ggc	gcc	aac	gtg	gtg	aac	acc	atc	ctc	gtg	gaa	1171
Pro	Glu	Ile	Thr	Ser	Gly	Ala	Asn	Val	Val	Asn	Thr	Ile	Leu	Val	Glu	
			345					350					355			
ttc	cgt	gca	ctg	gat	acg	ttg	ggc	gag	ctc	tcc	gtg	ctt	ggc	atg	gca	1219
Phe	Arg	Ala	Leu	Asp	Thr	Leu	Gly	Glu	Leu	Ser	Val	Leu	Gly	Met	Ala	
		360					365					370				
gct	gtc	gtc	atc	ggg	gcg	atg	gtg	gct	tcc	atg	cct	cgt	cat	ccg	ttt	1267
Ala	Val	Val	Ile	Gly	Ala	Met	Val	Ala	Ser	Met	Pro	Arg	His	Pro	Phe	
	375					380					385					
gcc	aag	ggc	acc	cac	cct	cgc	ccc	ttt	ggc	caa	tca	cag	ttg	aac	tcc	1315
Ala	Lys	Gly	Thr	His	Pro	Arg	Pro	Phe	Gly	Gln	Ser	Gln	Leu	Asn	Ser	
390					395					400					405	
att	ccg	ctg	cgc	atg	ctg	ctt	aag	gtg	ctg	gtt	cca	gcg	cta	tgc	ttc	1363
Ile	Pro	Leu	Arg	Met	Leu	Leu	Lys	Val	Leu	Val	Pro	Ala	Leu	Cys	Phe	
				410					415					420		
ttg	agc	ttc	atg	gtg	ttc	atg	cgt	gga	cac	aat	gat	ccg	gga	ggc	ggg	1411
Leu	Ser	Phe	Met	Val	Phe	Met	Arg	Gly	His	Asn	Asp	Pro	Gly	Gly	Gly	
			425					430					435			
ttc	atc	gca	gcc	cta	att	gcc	ggg	ggc	gcg	ctg	atg	ctc	ctg	tac	ctg	1459
Phe	Ile	Ala	Ala	Leu	Ile	Ala	Gly	Gly	Ala	Leu	Met	Leu	Leu	Tyr	Leu	
		440					445					450				
tcc	aag	gcc	aaa	gat	ggc	cgc	att	ttc	cgc	ccg	aat	gtt	cct	ttc	att	1507

Ser Lys Ala Lys Asp Gly Arg Ile Phe Arg Pro Asn Val Pro Phe Ile
 455 460 465

ctc act ggt gcg ggc atc ttg atg gca gtg ttc tcg ggc gta ctg gga 1555
 Leu Thr Gly Ala Gly Ile Leu Met Ala Val Phe Ser Gly Val Leu Gly
 470 475 480 485

ctc acc cac ggt tct ttc ctg tac gcc atc cac ttc aac ttc gta ggc 1603
 Leu Thr His Gly Ser Phe Leu Tyr Ala Ile His Phe Asn Phe Val Gly
 490 495 500

cag cac tgg acc acc tcg atg atc ttc gac ctc ggc gtg tac ctg gcc 1651
 Gln His Trp Thr Thr Ser Met Ile Phe Asp Leu Gly Val Tyr Leu Ala
 505 510 515

gtg ttg ggc atg gtg tcc atg gca atc aac ggc ctg ggc gga tac ctg 1699
 Val Leu Gly Met Val Ser Met Ala Ile Asn Gly Leu Gly Gly Tyr Leu
 520 525 530

cgc cca ggt acc gac aat gca gat ctg gac tac gcc cgc cga agt ggc 1747
 Arg Pro Gly Thr Asp Asn Ala Asp Leu Asp Tyr Ala Arg Arg Ser Gly
 535 540 545

cca ctg cca gca acg cca acg gtt gaa ccc gaa cca gaa ggc gat gaa 1795
 Pro Leu Pro Ala Thr Pro Thr Val Glu Pro Glu Pro Glu Gly Asp Glu
 550 555 560 565

gac tgg ccc gaa ccc atc aac ccc gca ggc gat aac aaa gag gag gca 1843
 Asp Trp Pro Glu Pro Ile Asn Pro Ala Gly Asp Asn Lys Glu Glu Ala
 570 575 580

aac cga tgattctcgc actgacagtc gcg 1872
 Asn Arg

<210> 686

<211> 583

<212> PRT

<213> Corynebacterium glutamicum

<400> 686

Met Ala Ser Val Pro Pro Leu Leu Gly Phe Val Ser Lys Glu Gly Met
 1 5 10 15

Ile Thr Ala Phe Met Asp Ala Pro Ile Gly Asn Ser Tyr Val Val Leu
 20 25 30

Leu Leu Val Gly Ala Ala Ile Gly Ala Val Leu Thr Phe Thr Tyr Ser
 35 40 45

Ala Lys Leu Val Leu Gly Ala Phe Val Asp Gly Pro Arg Asp Met Ser
 50 55 60

His Val Lys Glu Ala Pro Val Ser Leu Trp Leu Pro Ala Ala Leu Pro
 65 70 75 80

Gly Leu Met Ser Leu Pro Leu Val Leu Val Leu Ser Leu Phe Asp Ala
 85 90 95

Pro Val Ser Ala Ala Ala Thr Ser Ala Ala Gly Glu Ala Ala His Met

100					105					110					
His	Leu	Ala	Leu	Trp	His	Gly	Ile	Asn	Thr	Pro	Leu	Leu	Ile	Ser	Leu
	115						120					125			
Gly	Val	Leu	Val	Ala	Gly	Ile	Leu	Gly	Val	Leu	Phe	Arg	Lys	Glu	Leu
	130					135					140				
Trp	Lys	Ile	Ala	Glu	Thr	Ser	Pro	Phe	Pro	Ile	Ala	Thr	Gly	Asn	Asp
	145					150					155				160
Ile	Leu	Ser	Met	Leu	Val	Tyr	Arg	Ala	Asn	Leu	Leu	Gly	Lys	Phe	Phe
			165						170					175	
Gly	Arg	Met	Ala	Asp	Ser	Met	Ser	Pro	Arg	Arg	His	Leu	Val	Ser	Leu
		180						185					190		
Ile	Val	Leu	Leu	Trp	Ala	Leu	Ala	Ala	Phe	Ala	Thr	Ile	His	Pro	Ser
	195						200					205			
Val	Gln	Leu	Ala	Pro	Lys	Gln	Pro	Gly	Ile	Asp	Arg	Trp	Ile	Asp	Leu
	210					215					220				
Ile	Pro	Leu	Ala	Ile	Ile	Ala	Leu	Ser	Val	Phe	Gly	Leu	Leu	Thr	Thr
	225					230					235				240
Arg	Asn	Arg	Leu	Ser	Ala	Ala	Val	Leu	Val	Gly	Thr	Val	Gly	Val	Gly
			245						250					255	
Val	Ser	Phe	Gln	Met	Leu	Leu	Leu	Gly	Ala	Pro	Asp	Val	Ala	Leu	Thr
		260						265					270		
Gln	Phe	Leu	Val	Glu	Gly	Leu	Val	Val	Val	Ile	Ile	Met	Met	Val	Val
	275						280					285			
Arg	His	Gln	Pro	Ala	Asn	Phe	Lys	Arg	Ile	Lys	Pro	Ser	Arg	Arg	Arg
	290					295					300				
Ser	Thr	Val	Leu	Val	Ala	Val	Leu	Ala	Ala	Phe	Ala	Ala	Phe	Met	Ala
	305					310					315				320
Val	Trp	Gly	Leu	Leu	Gly	Arg	His	Glu	Arg	Ser	Glu	Leu	Ala	Met	Trp
			325						330					335	
Tyr	Leu	Asn	Gln	Gly	Pro	Glu	Ile	Thr	Ser	Gly	Ala	Asn	Val	Val	Asn
		340						345					350		
Thr	Ile	Leu	Val	Glu	Phe	Arg	Ala	Leu	Asp	Thr	Leu	Gly	Glu	Leu	Ser
	355						360					365			
Val	Leu	Gly	Met	Ala	Ala	Val	Val	Ile	Gly	Ala	Met	Val	Ala	Ser	Met
	370					375					380				
Pro	Arg	His	Pro	Phe	Ala	Lys	Gly	Thr	His	Pro	Arg	Pro	Phe	Gly	Gln
	385					390					395				400
Ser	Gln	Leu	Asn	Ser	Ile	Pro	Leu	Arg	Met	Leu	Leu	Lys	Val	Leu	Val
			405						410					415	
Pro	Ala	Leu	Cys	Phe	Leu	Ser	Phe	Met	Val	Phe	Met	Arg	Gly	His	Asn
		420						425					430		

Asp Pro Gly Gly Gly Phe Ile Ala Ala Leu Ile Ala Gly Gly Ala Leu
 435 440 445

Met Leu Leu Tyr Leu Ser Lys Ala Lys Asp Gly Arg Ile Phe Arg Pro
 450 455 460

Asn Val Pro Phe Ile Leu Thr Gly Ala Gly Ile Leu Met Ala Val Phe
 465 470 475 480

Ser Gly Val Leu Gly Leu Thr His Gly Ser Phe Leu Tyr Ala Ile His
 485 490 495

Phe Asn Phe Val Gly Gln His Trp Thr Thr Ser Met Ile Phe Asp Leu
 500 505 510

Gly Val Tyr Leu Ala Val Leu Gly Met Val Ser Met Ala Ile Asn Gly
 515 520 525

Leu Gly Gly Tyr Leu Arg Pro Gly Thr Asp Asn Ala Asp Leu Asp Tyr
 530 535 540

Ala Arg Arg Ser Gly Pro Leu Pro Ala Thr Pro Thr Val Glu Pro Glu
 545 550 555 560

Pro Glu Gly Asp Glu Asp Trp Pro Glu Pro Ile Asn Pro Ala Gly Asp
 565 570 575

Asn Lys Glu Glu Ala Asn Arg
 580

<210> 687
 <211> 1653
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1630)
 <223> RXN00595

<400> 687
 cgacgacacc cgggtccatcg aaccagatga cgatcaatcg cctttgacta ctagecgtcg 60

ttcagtcacc aacccaacag atcaggagga taaagcttaa atg gcc atg gat gtt 115
 Met Ala Met Asp Val
 1 5

ctc ctt cct att ttc gtt gca gtt ccc ctt gct gcc tct gcc att gcg 163
 Leu Leu Pro Ile Phe Val Ala Val Pro Leu Ala Ala Ser Ala Ile Ala
 10 15 20

gtg ctt ctg ccg tgg cgt ctc atc cgc gat att ttg cac atc atc gtg 211
 Val Leu Leu Pro Trp Arg Leu Ile Arg Asp Ile Leu His Ile Ile Val
 25 30 35

cct ttc gcg ggt att ttt gct ggc atc tgg ttg ttt gca cac acc gct 259
 Pro Phe Ala Gly Ile Phe Ala Gly Ile Trp Leu Phe Ala His Thr Ala
 40 45 50

gaa cac ggc ccg att gct cac aac gtg ggc ctt tat gtc ggt ggc gtg	307
Glu His Gly Pro Ile Ala His Asn Val Gly Leu Tyr Val Gly Gly Val	
55 60 65	
gca atc ccc ttt gct gcc gat acg ttc agc gcc atc atg ttg atc acc	355
Ala Ile Pro Phe Ala Ala Asp Thr Phe Ser Ala Ile Met Leu Ile Thr	
70 75 80 85	
acc tcg atc gtt gcg gtg gct gcc aac tgg ttt gcc acc atc gtc ggt	403
Thr Ser Ile Val Ala Val Ala Ala Asn Trp Phe Ala Thr Ile Val Gly	
90 95 100	
gaa acc cgc gcg cgt ttc tat cca gcg ctc aca ttg atg ctg atc acg	451
Glu Thr Arg Ala Arg Phe Tyr Pro Ala Leu Thr Leu Met Leu Ile Thr	
105 110 115	
ggc gtc aac ggt gct ctg ctg act gcc gat ctg ttc aac ttc ttt gtg	499
Gly Val Asn Gly Ala Leu Leu Thr Ala Asp Leu Phe Asn Phe Phe Val	
120 125 130	
ttc atc gaa gtg atg ctg ctg cct tcc tat ggt ttg atc gcc atg acc	547
Phe Ile Glu Val Met Leu Leu Pro Ser Tyr Gly Leu Ile Ala Met Thr	
135 140 145	
gga acg tgg gcg cgc cta gcc tct gga cga atc ttc gta cta gtc aat	595
Gly Thr Trp Ala Arg Leu Ala Ser Gly Arg Ile Phe Val Leu Val Asn	
150 155 160 165	
ctc tct gcc tcc aca ttg ctg gtt gca ggt gtg gga atc gtc tac ggt	643
Leu Ser Ala Ser Thr Leu Leu Val Ala Gly Val Gly Ile Val Tyr Gly	
170 175 180	
gtc ata ggc tca gtc aac atc gca gct ctg caa gat gtc gta gag ggc	691
Val Ile Gly Ser Val Asn Ile Ala Ala Leu Gln Asp Val Val Glu Gly	
185 190 195	
aac ccc ctg gtt gcc agc gca atg ggc atc gtg gtt att gcc atc gcg	739
Asn Pro Leu Val Ala Ser Ala Met Gly Ile Val Val Ile Ala Ile Ala	
200 205 210	
gtt aaa gcc ggt gta ttc cca gtg cac aca tgg ctg cca cgc acc tat	787
Val Lys Ala Gly Val Phe Pro Val His Thr Trp Leu Pro Arg Thr Tyr	
215 220 225	
cct ggt aca tca gca gct gtg atg ggg ttg ttc tcc ggt ttg cac acc	835
Pro Gly Thr Ser Ala Ala Val Met Gly Leu Phe Ser Gly Leu His Thr	
230 235 240 245	
aaa gtc gcg gta tac atg ctc tat cgc att tgg gtc cac att ttt aac	883
Lys Val Ala Val Tyr Met Leu Tyr Arg Ile Trp Val His Ile Phe Asn	
250 255 260	
atg gat ccc acg tgg aat tgg ctg att gtc gca ttc atg gtg ata tcc	931
Met Asp Pro Thr Trp Asn Trp Leu Ile Val Ala Phe Met Val Ile Ser	
265 270 275	
atg ctg gtc ggt ggc ttc gct gga ctt gct gaa aac tcc atc cgt cgc	979
Met Leu Val Gly Gly Phe Ala Gly Leu Ala Glu Asn Ser Ile Arg Arg	
280 285 290	
gtc ctt gcc tac caa atg gtc aac ggc atg cca ttt att ctc atc atg	1027

Val	Leu	Ala	Tyr	Gln	Met	Val	Asn	Gly	Met	Pro	Phe	Ile	Leu	Ile	Met		
295						300					305						
atg	gcg	ttt	acc	tct	gac	gat	cca	cag	cg	gca	ctt	gcc	gct	ggt	ctg	1075	
Met	Ala	Phe	Thr	Ser	Asp	Asp	Pro	Gln	Arg	Ala	Leu	Ala	Ala	Gly	Leu		
310					315					320					325		
ttg	tac	acc	ctg	cac	cac	atg	atc	acc	atc	gcc	gca	ttg	gtg	ctc	act	1123	
Leu	Tyr	Thr	Leu	His	His	Met	Ile	Thr	Ile	Ala	Ala	Leu	Val	Leu	Thr		
				330						335					340		
tcc	ggc	gca	atc	gaa	gaa	acc	tac	ggc	acc	ggt	atg	ttg	tcc	aag	ctg	1171	
Ser	Gly	Ala	Ile	Glu	Glu	Thr	Tyr	Gly	Thr	Gly	Met	Leu	Ser	Lys	Leu		
			345					350					355				
tct	ggc	ctt	gca	cgc	cgc	gaa	ccc	gtc	gtc	gca	gca	gtg	ttc	gct	gca	1219	
Ser	Gly	Leu	Ala	Arg	Arg	Glu	Pro	Val	Val	Ala	Ala	Val	Phe	Ala	Ala		
		360					365						370				
ggt	gcc	ttc	tct	gtt	gtc	ggt	ttc	cca	ccg	ttt	tcc	ggt	atg	tgg	ggc	1267	
Gly	Ala	Phe	Ser	Val	Val	Gly	Phe	Pro	Pro	Phe	Ser	Gly	Met	Trp	Gly		
	375					380					385						
aaa	gcg	ctc	atc	ctg	ctc	gag	atc	gcc	cgc	gtc	ggc	aat	att	gca	gca	1315	
Lys	Ala	Leu	Ile	Leu	Leu	Glu	Ile	Ala	Arg	Val	Gly	Asn	Ile	Ala	Ala		
390					395					400					405		
tgg	atc	gca	atc	gcc	gcc	atc	atc	atc	gcc	agc	ctg	ggc	gca	ctg	ctc	1363	
Trp	Ile	Ala	Ile	Ala	Ala	Ile	Ile	Ile	Ala	Ser	Leu	Gly	Ala	Leu	Leu		
				410					415					420			
tcg	atg	atc	cgc	gtg	tgg	cgt	gaa	gtc	ttc	tgg	ggt	ggc	gca	atg	cac	1411	
Ser	Met	Ile	Arg	Val	Trp	Arg	Glu	Val	Phe	Trp	Gly	Gly	Ala	Met	His		
			425					430					435				
cag	cgc	ggc	gtc	tcg	ccg	cag	ctg	cgc	atc	agc	cca	gca	aaa	atc	gcc	1459	
Gln	Arg	Gly	Val	Ser	Pro	Gln	Leu	Arg	Ile	Ser	Pro	Ala	Lys	Ile	Ala		
		440					445					450					
cca	gcg	ctc	agc	ctg	atc	att	tta	tcg	gta	ggc	atg	ttc	atc	ttc	gcg	1507	
Pro	Ala	Leu	Ser	Leu	Ile	Ile	Leu	Ser	Val	Gly	Met	Phe	Ile	Phe	Ala		
		455				460					465						
ggc	ccg	ctt	atc	gac	gcg	acc	ctc	acc	gcc	acc	gac	ggc	ctc	ttg	aac	1555	
Gly	Pro	Leu	Ile	Asp	Ala	Thr	Leu	Thr	Ala	Thr	Asp	Gly	Leu	Leu	Asn		
470					475				480						485		
acc	gat	gca	tac	caa	cag	gct	gtg	ctc	ggt	gaa	aat	gcc	atc	gga	gtg	1603	
Thr	Asp	Ala	Tyr	Gln	Gln	Ala	Val	Leu	Gly	Glu	Asn	Ala	Ile	Gly	Val		
				490					495					500			
cca	agc	cct	agc	tac	cag	gga	gga	aac	taatgcttaa	cgccctgaaa						1650	
Pro	Ser	Pro	Ser	Tyr	Gln	Gly	Gly	Asn									
			505				510										
ttc																1653	

<210> 688
 <211> 510
 <212> PRT

<213> Corynebacterium glutamicum

<400> 688

Met Ala Met Asp Val Leu Leu Pro Ile Phe Val Ala Val Pro Leu Ala
 1 5 10 15
 Ala Ser Ala Ile Ala Val Leu Leu Pro Trp Arg Leu Ile Arg Asp Ile
 20 25 30
 Leu His Ile Ile Val Pro Phe Ala Gly Ile Phe Ala Gly Ile Trp Leu
 35 40 45
 Phe Ala His Thr Ala Glu His Gly Pro Ile Ala His Asn Val Gly Leu
 50 55 60
 Tyr Val Gly Gly Val Ala Ile Pro Phe Ala Ala Asp Thr Phe Ser Ala
 65 70 75 80
 Ile Met Leu Ile Thr Thr Ser Ile Val Ala Val Ala Ala Asn Trp Phe
 85 90 95
 Ala Thr Ile Val Gly Glu Thr Arg Ala Arg Phe Tyr Pro Ala Leu Thr
 100 105 110
 Leu Met Leu Ile Thr Gly Val Asn Gly Ala Leu Leu Thr Ala Asp Leu
 115 120 125
 Phe Asn Phe Phe Val Phe Ile Glu Val Met Leu Leu Pro Ser Tyr Gly
 130 135 140
 Leu Ile Ala Met Thr Gly Thr Trp Ala Arg Leu Ala Ser Gly Arg Ile
 145 150 155 160
 Phe Val Leu Val Asn Leu Ser Ala Ser Thr Leu Leu Val Ala Gly Val
 165 170 175
 Gly Ile Val Tyr Gly Val Ile Gly Ser Val Asn Ile Ala Ala Leu Gln
 180 185 190
 Asp Val Val Glu Gly Asn Pro Leu Val Ala Ser Ala Met Gly Ile Val
 195 200 205
 Val Ile Ala Ile Ala Val Lys Ala Gly Val Phe Pro Val His Thr Trp
 210 215 220
 Leu Pro Arg Thr Tyr Pro Gly Thr Ser Ala Ala Val Met Gly Leu Phe
 225 230 235 240
 Ser Gly Leu His Thr Lys Val Ala Val Tyr Met Leu Tyr Arg Ile Trp
 245 250 255
 Val His Ile Phe Asn Met Asp Pro Thr Trp Asn Trp Leu Ile Val Ala
 260 265 270
 Phe Met Val Ile Ser Met Leu Val Gly Gly Phe Ala Gly Leu Ala Glu
 275 280 285
 Asn Ser Ile Arg Arg Val Leu Ala Tyr Gln Met Val Asn Gly Met Pro
 290 295 300
 Phe Ile Leu Ile Met Met Ala Phe Thr Ser Asp Asp Pro Gln Arg Ala

305	310	315	320
Leu Ala Ala Gly	Leu Leu Tyr Thr	Leu His His Met	Ile Thr Ile Ala
	325	330	335
Ala Leu Val Leu	Thr Ser Gly Ala	Ile Glu Glu Thr	Tyr Gly Thr Gly
	340	345	350
Met Leu Ser Lys	Leu Ser Gly Leu	Ala Arg Arg Glu	Pro Val Val Ala
	355	360	365
Ala Val Phe Ala	Ala Gly Ala Phe	Ser Val Val Gly	Phe Pro Pro Phe
	370	375	380
Ser Gly Met Trp	Gly Lys Ala Leu	Ile Leu Leu Glu	Ile Ala Arg Val
385	390	395	400
Gly Asn Ile Ala	Ala Trp Ile Ala	Ile Ala Ala Ile	Ile Ile Ala Ser
	405	410	415
Leu Gly Ala Leu	Leu Ser Met Ile	Arg Val Trp Arg	Glu Val Phe Trp
	420	425	430
Gly Gly Ala Met	His Gln Arg Gly	Val Ser Pro Gln	Leu Arg Ile Ser
	435	440	445
Pro Ala Lys Ile	Ala Pro Ala Leu	Ser Leu Ile Ile	Leu Ser Val Gly
	450	455	460
Met Phe Ile Phe	Ala Gly Pro Leu	Ile Asp Ala Thr	Leu Thr Ala Thr
465	470	475	480
Asp Gly Leu Leu	Asn Thr Asp Ala	Tyr Gln Gln Ala	Val Leu Gly Glu
	485	490	495
Asn Ala Ile Gly	Val Pro Ser Pro	Ser Tyr Gln Gly	Gly Asn
	500	505	510

<210> 689

<211> 865

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(865)

<223> FRXA00608

<400> 689

```

cgacgacacc cgggtccatcg aaccagatga cgatcaatcg cctttgacta ctagcgctcg 60
ttcagtcacc aacccaacag atcaggagga taaagcttaa atg gcc atg gat gtt 115
                                     Met Ala Met Asp Val
                                     1 5
ctc ctt cct att ttc gtt gca gtt ccc ctt gct gcc tot gcc att gcg 163
Leu Leu Pro Ile Phe Val Ala Val Pro Leu Ala Ala Ser Ala Ile Ala
                10                15                20
gtg ctt ctg cgg tgg cgt ctc atc cgc gat att ttg cac atc atc gtg 211

```

Val	Leu	Leu	Pro	Trp	Arg	Leu	Ile	Arg	Asp	Ile	Leu	His	Ile	Ile	Val		
			25					30					35				
cct	ttc	gcg	ggg	att	ttt	gct	ggc	atc	tgg	ttg	ttt	gca	cac	acc	gct	259	
Pro	Phe	Ala	Gly	Ile	Phe	Ala	Gly	Ile	Trp	Leu	Phe	Ala	His	Thr	Ala		
		40					45					50					
gaa	cac	ggc	ccg	att	gct	cac	aac	gtg	ggc	ctt	tat	gtc	ggg	ggc	gtg	307	
Glu	His	Gly	Pro	Ile	Ala	His	Asn	Val	Gly	Leu	Tyr	Val	Gly	Gly	Val		
	55					60				65							
gca	atc	ccc	ttt	gct	gcc	gat	acg	ttc	agc	gcc	atc	atg	ttg	atc	acc	355	
Ala	Ile	Pro	Phe	Ala	Ala	Asp	Thr	Phe	Ser	Ala	Ile	Met	Leu	Ile	Thr		
	70				75				80						85		
acc	tgc	atc	gtt	gcg	gtg	gct	gcc	aac	tgg	ttt	gcc	acc	atc	gtc	ggg	403	
Thr	Ser	Ile	Val	Ala	Val	Ala	Ala	Asn	Trp	Phe	Ala	Thr	Ile	Val	Gly		
			90					95						100			
gaa	acc	cgc	gcg	cgt	ttc	tat	cca	gcg	ctc	aca	ttg	atg	ctg	atc	acg	451	
Glu	Thr	Arg	Ala	Arg	Phe	Tyr	Pro	Ala	Leu	Thr	Leu	Met	Leu	Ile	Thr		
		105						110					115				
ggc	gtc	aac	ggg	gct	ctg	ctg	act	gcc	gat	ctg	ttc	aac	ttc	ttt	gtg	499	
Gly	Val	Asn	Gly	Ala	Leu	Leu	Thr	Ala	Asp	Leu	Phe	Asn	Phe	Phe	Val		
		120					125					130					
ttc	atc	gaa	gtg	atg	ctg	ctg	cct	tcc	tat	ggg	ttg	atc	gcc	atg	acc	547	
Phe	Ile	Glu	Val	Met	Leu	Leu	Pro	Ser	Tyr	Gly	Leu	Ile	Ala	Met	Thr		
	135					140					145						
gga	acg	tgg	gcg	cgc	cta	gcc	tct	gga	cga	atc	ttc	gta	cta	gtc	aat	595	
Gly	Thr	Trp	Ala	Arg	Leu	Ala	Ser	Gly	Arg	Ile	Phe	Val	Leu	Val	Asn		
	150				155				160						165		
ctc	tct	gcc	tcc	aca	ttg	ctg	gtt	gca	ggg	gtg	gga	atc	gtc	tac	ggg	643	
Leu	Ser	Ala	Ser	Thr	Leu	Leu	Val	Ala	Gly	Val	Gly	Ile	Val	Tyr	Gly		
			170					175						180			
gtc	ata	ggc	tca	gtc	aac	atc	gca	gct	ctg	caa	gat	gtc	gta	gag	ggc	691	
Val	Ile	Gly	Ser	Val	Asn	Ile	Ala	Ala	Leu	Gln	Asp	Val	Val	Glu	Gly		
			185				190						195				
aac	ccc	ctg	gtt	gcc	agc	gca	atg	ggc	atc	gtg	gtt	att	gcc	atc	gcg	739	
Asn	Pro	Leu	Val	Ala	Ser	Ala	Met	Gly	Ile	Val	Val	Ile	Ala	Ile	Ala		
		200					205					210					
gtt	aaa	gcc	ggg	gta	ttc	cca	gtg	cac	aca	tgg	ctg	cca	cgc	acc	tat	787	
Val	Lys	Ala	Gly	Val	Phe	Pro	Val	His	Thr	Trp	Leu	Pro	Arg	Thr	Tyr		
	215					220					225						
cct	ggg	aca	tca	gca	gct	gtg	atg	ggg	ttg	ttc	tcc	ggg	ttg	cac	acc	835	
Pro	Gly	Thr	Ser	Ala	Ala	Val	Met	Gly	Leu	Phe	Ser	Gly	Leu	His	Thr		
	230				235				240						245		
aaa	gtc	gcg	gta	tac	atg	ctc	tat	cgc	att							865	
Lys	Val	Ala	Val	Tyr	Met	Leu	Tyr	Arg	Ile								
			250					255									

<210> 690

<211> 255
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 690

```

Met Ala Met Asp Val Leu Leu Pro Ile Phe Val Ala Val Pro Leu Ala
 1             5             10             15

Ala Ser Ala Ile Ala Val Leu Leu Pro Trp Arg Leu Ile Arg Asp Ile
          20             25             30

Leu His Ile Ile Val Pro Phe Ala Gly Ile Phe Ala Gly Ile Trp Leu
      35             40             45

Phe Ala His Thr Ala Glu His Gly Pro Ile Ala His Asn Val Gly Leu
  50             55             60

Tyr Val Gly Gly Val Ala Ile Pro Phe Ala Ala Asp Thr Phe Ser Ala
 65             70             75             80

Ile Met Leu Ile Thr Thr Ser Ile Val Ala Val Ala Ala Asn Trp Phe
          85             90             95

Ala Thr Ile Val Gly Glu Thr Arg Ala Arg Phe Tyr Pro Ala Leu Thr
      100             105             110

Leu Met Leu Ile Thr Gly Val Asn Gly Ala Leu Leu Thr Ala Asp Leu
  115             120             125

Phe Asn Phe Phe Val Phe Ile Glu Val Met Leu Leu Pro Ser Tyr Gly
  130             135             140

Leu Ile Ala Met Thr Gly Thr Trp Ala Arg Leu Ala Ser Gly Arg Ile
 145             150             155             160

Phe Val Leu Val Asn Leu Ser Ala Ser Thr Leu Leu Val Ala Gly Val
          165             170             175

Gly Ile Val Tyr Gly Val Ile Gly Ser Val Asn Ile Ala Ala Leu Gln
      180             185             190

Asp Val Val Glu Gly Asn Pro Leu Val Ala Ser Ala Met Gly Ile Val
  195             200             205

Val Ile Ala Ile Ala Val Lys Ala Gly Val Phe Pro Val His Thr Trp
  210             215             220

Leu Pro Arg Thr Tyr Pro Gly Thr Ser Ala Ala Val Met Gly Leu Phe
 225             230             235             240

Ser Gly Leu His Thr Lys Val Ala Val Tyr Met Leu Tyr Arg Ile
      245             250             255

```

<210> 691
 <211> 2118
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS

<222> (1)..(2118)

<223> RXA00913

<400> 691

```

att att tcc gtg gtg ggc att ggt acc cgc gaa gct ttg ctg gca ggt 48
Ile Ile Ser Val Val Gly Ile Gly Thr Arg Glu Ala Leu Leu Ala Gly
  1             5             10             15

ctt gca ctg acc gtt gcg cac tcc ttg ttt aag gca aca ttg ttc atg 96
Leu Ala Leu Thr Val Ala His Ser Leu Phe Lys Ala Thr Leu Phe Met
             20             25             30

aca gtt ggt gcc att gac cac acc acc gga act cgt gat att cgt aaa 144
Thr Val Gly Ala Ile Asp His Thr Thr Gly Thr Arg Asp Ile Arg Lys
             35             40             45

ctc tcc ggt ctg tgg cgt aaa caa ccg atc ctg ttc gcc gtt gct gct 192
Leu Ser Gly Leu Trp Arg Lys Gln Pro Ile Leu Phe Ala Val Ala Ala
             50             55             60

gtt tcg gcg gcg tcc atg gct ggt att ccg cca ctg ttt ggt ttt atc 240
Val Ser Ala Ala Ser Met Ala Gly Ile Pro Pro Leu Phe Gly Phe Ile
             65             70             75             80

gcc aag gaa aca gcg ctg gat acc gtg ttg aat gag cag atg ttg cat 288
Ala Lys Glu Thr Ala Leu Asp Thr Val Leu Asn Glu Gln Met Leu His
             85             90             95

ggc atg cca ggt cga ttg atg ctg gct ggc atc gtt ttg ggt tcc atc 336
Gly Met Pro Gly Arg Leu Met Leu Ala Gly Ile Val Leu Gly Ser Ile
             100             105             110

ttc acc atg gca tat tcc tgc tac ttc ctg tac gaa gcc ttt gcc acg 384
Phe Thr Met Ala Tyr Ser Cys Tyr Phe Leu Tyr Glu Ala Phe Ala Thr
             115             120             125

aag cac tcc aaa ttc cca gag gcc aac ggt gtc tca cct gca gtg gag 432
Lys His Ser Lys Phe Pro Glu Ala Asn Gly Val Ser Pro Ala Val Glu
             130             135             140

gca atg cat ccg gtg aag ttt aag ctg tgg atc gca cct gtc atc ctg 480
Ala Met His Pro Val Lys Phe Lys Leu Trp Ile Ala Pro Val Ile Leu
             145             150             155             160

gct att ttg acc gta gtg ttt ggt gtt ttc ccc aag cca gtg tcg gaa 528
Ala Ile Leu Thr Val Val Phe Gly Val Phe Pro Lys Pro Val Ser Glu
             165             170             175

gca att gtc acg cat ctt gat aac gtc acg cca tcg ctt gat gat gtc 576
Ala Ile Val Thr His Leu Asp Asn Val Thr Pro Ser Leu Asp Asp Val
             180             185             190

cac acc aaa ctg gcc ttg tgg cat ggt ctg aat cta ccg ctg ctg ctg 624
His Thr Lys Leu Ala Leu Trp His Gly Leu Asn Leu Pro Leu Leu Leu
             195             200             205

tct gtg gtg atc atc att tcc gga ttc atc atc ttc tgg gag cga gac 672
Ser Val Val Ile Ile Ile Ser Gly Phe Ile Ile Phe Trp Glu Arg Asp
             210             215             220

acc gtc gaa cgt ttg cgc cct aac acc gca gcg ttt ggc agt gcc gat 720

```

Thr 225	Val	Glu	Arg	Leu	Arg 230	Pro	Asn	Thr	Ala	Ala 235	Phe	Gly	Ser	Ala	Asp 240	
acc	gcc	tac	gac	gcc	att	ctt	gat	gca	ctg	cgt	gtg	ctc	tcc	cac	cgc	768
Thr	Ala	Tyr	Asp	Ala	Ile	Leu	Asp	Ala	Leu	Arg	Val	Leu	Ser	His	Arg	
				245					250					255		
ctg	act	gca	tcc	acc	cag	cgt	ggg	tct	ttg	acc	ctg	aac	gtc	ggg	gtg	816
Leu	Thr	Ala	Ser	Thr	Gln	Arg	Gly	Ser	Leu	Thr	Leu	Asn	Val	Gly	Val	
			260					265					270			
atc	ttc	ttc	gtc	ctc	acg	att	gtt	ccg	ctg	atc	gct	ttg	atc	act	ggc	864
Ile	Phe	Phe	Val	Leu	Thr	Ile	Val	Pro	Leu	Ile	Ala	Leu	Ile	Thr	Gly	
		275					280					285				
gaa	caa	agc	gat	gtc	cgc	atg	gag	ctg	tgg	gat	agc	cct	att	cag	ggc	912
Glu	Gln	Ser	Asp	Val	Arg	Met	Glu	Leu	Trp	Asp	Ser	Pro	Ile	Gln	Gly	
	290					295					300					
ttc	atc	gcg	gcc	atc	att	atc	gtc	gtt	gcg	att	gtg	gca	acc	acc	atg	960
Phe	Ile	Ala	Ala	Ile	Ile	Ile	Val	Val	Ala	Ile	Val	Ala	Thr	Thr	Met	
305					310				315						320	
gat	aac	cgt	ttg	tct	gcg	ctg	att	ttg	gtg	ggg	gtg	aca	ggg	tat	ggc	1008
Asp	Asn	Arg	Leu	Ser	Ala	Leu	Ile	Leu	Val	Gly	Val	Thr	Gly	Tyr	Gly	
				325					330					335		
att	gcc	gtt	atc	ttc	gcg	cta	cat	ggc	gca	ccg	gac	ttg	gcg	cta	acc	1056
Ile	Ala	Val	Ile	Phe	Ala	Leu	His	Gly	Ala	Pro	Asp	Leu	Ala	Leu	Thr	
			340					345					350			
cag	gtg	ctg	gtg	gag	acc	atc	gtc	atg	gtg	gta	ttc	atg	ctg	gtg	ctg	1104
Gln	Val	Leu	Val	Glu	Thr	Ile	Val	Met	Val	Val	Phe	Met	Leu	Val	Leu	
		355					360					365				
cgt	aaa	atg	ccg	aca	gaa	gtt	gcg	tgg	aag	gca	gaa	cct	aaa	cag	tct	1152
Arg	Lys	Met	Pro	Thr	Glu	Val	Ala	Trp	Lys	Ala	Glu	Pro	Lys	Gln	Ser	
	370					375					380					
cgc	gtg	cga	gcg	tgg	ctt	gct	ggc	gcc	acc	gga	ttg	tcc	gtt	gtt	att	1200
Arg	Val	Arg	Ala	Trp	Leu	Ala	Gly	Ala	Thr	Gly	Leu	Ser	Val	Val	Ile	
385					390					395					400	
gtc	acc	att	ttt	gcc	atg	aat	gct	cgc	acc	act	gaa	ccg	atc	tct	gta	1248
Val	Thr	Ile	Phe	Ala	Met	Asn	Ala	Arg	Thr	Thr	Glu	Pro	Ile	Ser	Val	
				405				410						415		
tac	atg	cag	gat	ctg	gcc	tat	gag	atc	gga	cat	ggc	gca	aac	acc	gtc	1296
Tyr	Met	Gln	Asp	Leu	Ala	Tyr	Glu	Ile	Gly	His	Gly	Ala	Asn	Thr	Val	
			420					425					430			
aac	gta	ctg	ctc	gta	gac	ctg	cgt	ggg	ttt	gat	acc	ttc	ggg	gaa	att	1344
Asn	Val	Leu	Leu	Val	Asp	Leu	Arg	Gly	Phe	Asp	Thr	Phe	Gly	Glu	Ile	
		435					440					445				
tcc	gtc	ctt	gtg	atc	gcg	gca	acc	ggg	atc	gcc	tcc	ctg	gtc	tac	cga	1392
Ser	Val	Leu	Val	Ile	Ala	Ala	Thr	Gly	Ile	Ala	Ser	Leu	Val	Tyr	Arg	
		450				455					460					
aac	cgc	agc	ttc	cgc	aag	gat	tct	cgc	aga	cca	acc	ctg	gct	acc	act	1440
Asn	Arg	Ser	Phe	Arg	Lys	Asp	Ser	Arg	Arg	Pro	Thr	Leu	Ala	Thr	Thr	

465	470	475	480
ggt cgc cgt tgg ttg gct gct gct gtt gat acc gaa agg gcg cag aac 1488 Gly Arg Arg Trp Leu Ala Ala Ala Val Asp Thr Glu Arg Ala Gln Asn 485 490 495			
cgc tcg ctg atg gtt gat gtg gca acg cgc atc ctc ttc cct gcc atg 1536 Arg Ser Leu Met Val Asp Val Ala Thr Arg Ile Leu Phe Pro Ala Met 500 505 510			
atc atg ttg tct gtg tac ttc ttc ttc gcc gga cac aac gcg ccg ggc 1584 Ile Met Leu Ser Val Tyr Phe Phe Phe Ala Gly His Asn Ala Pro Gly 515 520 525			
ggc gga ttc gcc ggc ggc ctt gtt gcc tcc ttg gcg ttc gcc ttg cgc 1632 Gly Gly Phe Ala Gly Gly Leu Val Ala Ser Leu Ala Phe Ala Leu Arg 530 535 540			
tac ctt gcc ggt gga cgt gaa gaa ctt gaa gaa gcg ttg cct atc gac 1680 Tyr Leu Ala Gly Gly Arg Glu Glu Leu Glu Glu Ala Leu Pro Ile Asp 545 550 555 560			
gcc ggc cgt atc ttg gga act gga cta ttt gtt tct gca act gca gtg 1728 Ala Gly Arg Ile Leu Gly Thr Gly Leu Phe Val Ser Ala Thr Ala Val 565 570 575			
ctg tgg ccc atg gtt ctt ctt ggt gaa cca ccg ctg acc tcc cat att 1776 Leu Trp Pro Met Val Leu Leu Gly Glu Pro Pro Leu Thr Ser His Ile 580 585 590			
tgg gat ctc aca ctg cca ctt atc ggt gag att cac att gca tcc gcg 1824 Trp Asp Leu Thr Leu Pro Leu Ile Gly Glu Ile His Ile Ala Ser Ala 595 600 605			
ctg ctc ttt gac ctt ggt gtc tac ctg atc gtc atc ggt ttg acc atg 1872 Leu Leu Phe Asp Leu Gly Val Tyr Leu Ile Val Ile Gly Leu Thr Met 610 615 620			
cac att ctc aac agt ttg ggc ggc cag ctc gac cgc gat gag gaa atg 1920 His Ile Leu Asn Ser Leu Gly Gly Gln Leu Asp Arg Asp Glu Glu Met 625 630 635 640			
cgt aag cag cgt gcg cgc gac cga gct cga cgc ttg gcg cgc aac cag 1968 Arg Lys Gln Arg Ala Arg Asp Arg Ala Arg Arg Leu Ala Arg Asn Gln 645 650 655			
cgt cga gaa gca gca acc gtc ggc gca cgc agg tcg aac gag aaa tcg 2016 Arg Arg Glu Ala Ala Thr Val Gly Ala Arg Arg Ser Asn Glu Lys Ser 660 665 670			
aca cgc caa atg ccg acg att cgg cct cca ggg gca gac aca gaa tcg 2064 Thr Arg Gln Met Pro Thr Ile Arg Pro Pro Gly Ala Asp Thr Glu Ser 675 680 685			
gtg gag cag aac ggt gag aac cag acg tcg ata agc aca aag cgt tta 2112 Val Glu Gln Asn Gly Glu Asn Gln Thr Ser Ile Ser Thr Lys Arg Leu 690 695 700			
aag cag Lys Gln 705			2118

<210> 692
 <211> 706
 <212> PRT
 <213> *Corynebacterium glutamicum*

 <400> 692
 Ile Ile Ser Val Val Gly Ile Gly Thr Arg Glu Ala Leu Leu Ala Gly
 1 5 10 15
 Leu Ala Leu Thr Val Ala His Ser Leu Phe Lys Ala Thr Leu Phe Met
 20 25 30
 Thr Val Gly Ala Ile Asp His Thr Thr Gly Thr Arg Asp Ile Arg Lys
 35 40 45
 Leu Ser Gly Leu Trp Arg Lys Gln Pro Ile Leu Phe Ala Val Ala Ala
 50 55 60
 Val Ser Ala Ala Ser Met Ala Gly Ile Pro Pro Leu Phe Gly Phe Ile
 65 70 75 80
 Ala Lys Glu Thr Ala Leu Asp Thr Val Leu Asn Glu Gln Met Leu His
 85 90 95
 Gly Met Pro Gly Arg Leu Met Leu Ala Gly Ile Val Leu Gly Ser Ile
 100 105 110
 Phe Thr Met Ala Tyr Ser Cys Tyr Phe Leu Tyr Glu Ala Phe Ala Thr
 115 120 125
 Lys His Ser Lys Phe Pro Glu Ala Asn Gly Val Ser Pro Ala Val Glu
 130 135 140
 Ala Met His Pro Val Lys Phe Lys Leu Trp Ile Ala Pro Val Ile Leu
 145 150 155 160
 Ala Ile Leu Thr Val Val Phe Gly Val Phe Pro Lys Pro Val Ser Glu
 165 170 175
 Ala Ile Val Thr His Leu Asp Asn Val Thr Pro Ser Leu Asp Asp Val
 180 185 190
 His Thr Lys Leu Ala Leu Trp His Gly Leu Asn Leu Pro Leu Leu Leu
 195 200 205
 Ser Val Val Ile Ile Ile Ser Gly Phe Ile Ile Phe Trp Glu Arg Asp
 210 215 220
 Thr Val Glu Arg Leu Arg Pro Asn Thr Ala Ala Phe Gly Ser Ala Asp
 225 230 235 240
 Thr Ala Tyr Asp Ala Ile Leu Asp Ala Leu Arg Val Leu Ser His Arg
 245 250 255
 Leu Thr Ala Ser Thr Gln Arg Gly Ser Leu Thr Leu Asn Val Gly Val
 260 265 270
 Ile Phe Phe Val Leu Thr Ile Val Pro Leu Ile Ala Leu Ile Thr Gly
 275 280 285

Glu Gln Ser Asp Val Arg Met Glu Leu Trp Asp Ser Pro Ile Gln Gly
 290 295 300
 Phe Ile Ala Ala Ile Ile Ile Val Val Ala Ile Val Ala Thr Thr Met
 305 310 315 320
 Asp Asn Arg Leu Ser Ala Leu Ile Leu Val Gly Val Thr Gly Tyr Gly
 325 330 335
 Ile Ala Val Ile Phe Ala Leu His Gly Ala Pro Asp Leu Ala Leu Thr
 340 345 350
 Gln Val Leu Val Glu Thr Ile Val Met Val Val Phe Met Leu Val Leu
 355 360 365
 Arg Lys Met Pro Thr Glu Val Ala Trp Lys Ala Glu Pro Lys Gln Ser
 370 375 380
 Arg Val Arg Ala Trp Leu Ala Gly Ala Thr Gly Leu Ser Val Val Ile
 385 390 395 400
 Val Thr Ile Phe Ala Met Asn Ala Arg Thr Thr Glu Pro Ile Ser Val
 405 410 415
 Tyr Met Gln Asp Leu Ala Tyr Glu Ile Gly His Gly Ala Asn Thr Val
 420 425 430
 Asn Val Leu Leu Val Asp Leu Arg Gly Phe Asp Thr Phe Gly Glu Ile
 435 440 445
 Ser Val Leu Val Ile Ala Ala Thr Gly Ile Ala Ser Leu Val Tyr Arg
 450 455 460
 Asn Arg Ser Phe Arg Lys Asp Ser Arg Arg Pro Thr Leu Ala Thr Thr
 465 470 475 480
 Gly Arg Arg Trp Leu Ala Ala Ala Val Asp Thr Glu Arg Ala Gln Asn
 485 490 495
 Arg Ser Leu Met Val Asp Val Ala Thr Arg Ile Leu Phe Pro Ala Met
 500 505 510
 Ile Met Leu Ser Val Tyr Phe Phe Phe Ala Gly His Asn Ala Pro Gly
 515 520 525
 Gly Gly Phe Ala Gly Gly Leu Val Ala Ser Leu Ala Phe Ala Leu Arg
 530 535 540
 Tyr Leu Ala Gly Gly Arg Glu Glu Leu Glu Glu Ala Leu Pro Ile Asp
 545 550 555 560
 Ala Gly Arg Ile Leu Gly Thr Gly Leu Phe Val Ser Ala Thr Ala Val
 565 570 575
 Leu Trp Pro Met Val Leu Leu Gly Glu Pro Pro Leu Thr Ser His Ile
 580 585 590
 Trp Asp Leu Thr Leu Pro Leu Ile Gly Glu Ile His Ile Ala Ser Ala
 595 600 605

Leu Leu Phe Asp Leu Gly Val Tyr Leu Ile Val Ile Gly Leu Thr Met
 610 615 620
 His Ile Leu Asn Ser Leu Gly Gly Gln Leu Asp Arg Asp Glu Glu Met
 625 630 635 640
 Arg Lys Gln Arg Ala Arg Asp Arg Ala Arg Arg Leu Ala Arg Asn Gln
 645 650 655
 Arg Arg Glu Ala Ala Thr Val Gly Ala Arg Arg Ser Asn Glu Lys Ser
 660 665 670
 Thr Arg Gln Met Pro Thr Ile Arg Pro Pro Gly Ala Asp Thr Glu Ser
 675 680 685
 Val Glu Gln Asn Gly Glu Asn Gln Thr Ser Ile Ser Thr Lys Arg Leu
 690 695 700
 Lys Gln
 705

<210> 693
 <211> 955
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(955)
 <223> RXA00909

<400> 693
 tcgatgtgtg ttgctaactg ggggtggcac gcacgttggc gttgttgttt ggtgtggctc 60
 cagagtaatc cacaacgcgc aaaggggaac tggagaacac gtg ctc att ctt ttt 115
 Val Leu Ile Leu Phe
 1 5
 ctc gcg ctc act gca gcc gca gta gtc gcc ccc atc ctg atc cga act 163
 Leu Ala Leu Thr Ala Ala Val Val Ala Pro Ile Leu Ile Arg Thr
 10 15 20
 ctc ggt cga cca gct ttt ggt ctg ctg gcg ctt gta cct ggc att ggt 211
 Leu Gly Arg Pro Ala Phe Gly Leu Leu Ala Leu Val Pro Gly Ile Gly
 25 30 35
 ttt ttc tgg gtg ctt tcg gag ttc atc aaa ggc act ttc aag gat gga 259
 Phe Phe Trp Val Leu Ser Glu Phe Ile Lys Gly Thr Phe Lys Asp Gly
 40 45 50
 ggt gaa ctc ctc ctc cac tat gcc tgg atg cct tcg gct cac ctc aat 307
 Gly Glu Leu Leu Leu His Tyr Ala Trp Met Pro Ser Ala His Leu Asn
 55 60 65
 atc gat ttc cgt atg gat tcc ctc gcg gcg ctg ttc tca ctc atc gtc 355
 Ile Asp Phe Arg Met Asp Ser Leu Ala Ala Leu Phe Ser Leu Ile Val
 70 75 80 85
 tta ggc gtg ggc gcc cta gtg ctg ctg tac tgc tgg gga tat ttt gat 403
 Leu Gly Val Gly Ala Leu Val Leu Leu Tyr Cys Trp Gly Tyr Phe Asp

	90	95	100	
tcc aac gcg ggt cgc ctc agt gcc ttt ggt gct gaa ctg gtg gcc ttc				451
Ser Asn Ala Gly Arg Leu Ser Ala Phe Gly Ala Glu Leu Val Ala Phe				
	105	110	115	
gcc atg gcg atg ttt ggt ctt gtc att tca gac aac atc ctg ctg atg				499
Ala Met Ala Met Phe Gly Leu Val Ile Ser Asp Asn Ile Leu Leu Met				
	120	125	130	
tac gtc ttc tgg gaa atc acc tcc gtt tta tcc ttc ctc ctg gtt ggt				547
Tyr Val Phe Trp Glu Ile Thr Ser Val Leu Ser Phe Leu Leu Val Gly				
	135	140	145	
tat tac ggc gaa cgc gca tct tca cgt cgc tct gca ggt caa gcc ttg				595
Tyr Tyr Gly Glu Arg Ala Ser Ser Arg Arg Ser Ala Gly Gln Ala Leu				
	150	155	160	165
atg gtg acc acc ctg ggt gga ttg gcc atg ctg gtg ggc atc att ttg				643
Met Val Thr Thr Leu Gly Gly Leu Ala Met Leu Val Gly Ile Ile Leu				
	170	175	180	
atg ggt acc caa act ggc gtg tgg cga ttc tct gag atc cct gcc tac				691
Met Gly Thr Gln Thr Gly Val Trp Arg Phe Ser Glu Ile Pro Ala Tyr				
	185	190	195	
tca agc tcc tgg gca gat gtg ccg tat att tcc gct gct gct gcc ctt				739
Ser Ser Ser Trp Ala Asp Val Pro Tyr Ile Ser Ala Ala Ala Ala Leu				
	200	205	210	
atc ttg gct ggc gca cta tcc aaa tcg gct atc gca cca acc cac ttc				787
Ile Leu Ala Gly Ala Leu Ser Lys Ser Ala Ile Ala Pro Thr His Phe				
	215	220	225	
tgg ctt ccc ggc gcg atg gcc gca cca acg ccg gtg tct gct tac ctg				835
Trp Leu Pro Gly Ala Met Ala Ala Pro Thr Pro Val Ser Ala Tyr Leu				
	230	235	240	245
cac tcc gca gcg atg gtg aag gcg ggt att tac ctt gtg gct cgc ctc				883
His Ser Ala Ala Met Val Lys Ala Gly Ile Tyr Leu Val Ala Arg Leu				
	250	255	260	
tct cca gac ctc aac gta gtt ggt tcg tgg tac ctg atc atc atc ccg				931
Ser Pro Asp Leu Asn Val Val Gly Ser Trp Tyr Leu Ile Ile Ile Pro				
	265	270	275	
ttg ggc atg ttg acc atg ctc atg				955
Leu Gly Met Leu Thr Met Leu Met				
	280	285		

<210> 694

<211> 285

<212> PRT

<213> Corynebacterium glutamicum

<400> 694

Val	Leu	Ile	Leu	Phe	Leu	Ala	Leu	Thr	Ala	Ala	Ala	Val	Val	Ala	Pro
1				5				10						15	

Ile Leu Ile Arg Thr Leu Gly Arg Pro Ala Phe Gly Leu Leu Ala Leu

20					25					30									
Val	Pro	Gly	Ile	Gly	Phe	Phe	Trp	Val	Leu	Ser	Glu	Phe	Ile	Lys	Gly				
35					40					45									
Thr	Phe	Lys	Asp	Gly	Gly	Glu	Leu	Leu	Leu	His	Tyr	Ala	Trp	Met	Pro				
50					55					60									
Ser	Ala	His	Leu	Asn	Ile	Asp	Phe	Arg	Met	Asp	Ser	Leu	Ala	Ala	Leu				
65					70					75					80				
Phe	Ser	Leu	Ile	Val	Leu	Gly	Val	Gly	Ala	Leu	Val	Leu	Leu	Tyr	Cys				
85					90					95									
Trp	Gly	Tyr	Phe	Asp	Ser	Asn	Ala	Gly	Arg	Leu	Ser	Ala	Phe	Gly	Ala				
100					105					110									
Glu	Leu	Val	Ala	Phe	Ala	Met	Ala	Met	Phe	Gly	Leu	Val	Ile	Ser	Asp				
115					120					125									
Asn	Ile	Leu	Leu	Met	Tyr	Val	Phe	Trp	Glu	Ile	Thr	Ser	Val	Leu	Ser				
130					135					140									
Phe	Leu	Leu	Val	Gly	Tyr	Tyr	Gly	Glu	Arg	Ala	Ser	Ser	Arg	Arg	Ser				
145					150					155					160				
Ala	Gly	Gln	Ala	Leu	Met	Val	Thr	Thr	Leu	Gly	Gly	Leu	Ala	Met	Leu				
165					170					175									
Val	Gly	Ile	Ile	Leu	Met	Gly	Thr	Gln	Thr	Gly	Val	Trp	Arg	Phe	Ser				
180					185					190									
Glu	Ile	Pro	Ala	Tyr	Ser	Ser	Ser	Trp	Ala	Asp	Val	Pro	Tyr	Ile	Ser				
195					200					205									
Ala	Ala	Ala	Ala	Leu	Ile	Leu	Ala	Gly	Ala	Leu	Ser	Lys	Ser	Ala	Ile				
210					215					220									
Ala	Pro	Thr	His	Phe	Trp	Leu	Pro	Gly	Ala	Met	Ala	Ala	Pro	Thr	Pro				
225					230					235					240				
Val	Ser	Ala	Tyr	Leu	His	Ser	Ala	Ala	Met	Val	Lys	Ala	Gly	Ile	Tyr				
245					250					255									
Leu	Val	Ala	Arg	Leu	Ser	Pro	Asp	Leu	Asn	Val	Val	Gly	Ser	Trp	Tyr				
260					265					270									
Leu	Ile	Ile	Ile	Pro	Leu	Gly	Met	Leu	Thr	Met	Leu	Met							
275					280					285									

<210> 695

<211> 927

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(904)

<223> RXA00700

<400> 695

acgccccaca agtcgcaaaa atcaccgccg gcatccaaga ggaatcacac tggctcacag 60

tctcgggccgt gaaagctgcg ctagggcatg gtgaaatctc atg atc aac gcc atc 115
 Met Ile Asn Ala Ile
 1 5

aca ctc aag ccc aaa acc ttc ctc acc tta agc ttc ctt gcg gtt ttg 163
 Thr Leu Lys Pro Lys Thr Phe Leu Thr Leu Ser Phe Leu Ala Val Leu
 10 15 20

agc atc gtg att ttc ttc tgg ccg ctg atc gtc aac ccg gaa tcc ttc 211
 Ser Ile Val Ile Phe Phe Trp Pro Leu Ile Val Asn Pro Glu Ser Phe
 25 30 35

ctg tcc gac aaa gcc caa gcg ccc ctc tac atc gcg atc gtc att ccc 259
 Leu Ser Asp Lys Ala Gln Ala Pro Leu Tyr Ile Ala Ile Val Ile Pro
 40 45 50

ctc gtg ctg gcc gct gtc atc gcc gaa atc agt gaa aac gga ttc gac 307
 Leu Val Leu Ala Ala Val Ile Ala Glu Ile Ser Glu Asn Gly Phe Asp
 55 60 65

gtt aaa gcc gta gcc atg ctc ggc gtc ctc acc gcc atg gtt gcc gta 355
 Val Lys Ala Val Ala Met Leu Gly Val Leu Thr Ala Met Val Ala Val
 70 75 80 85

gtc cga cca ttc ggt gcc ggc gca gca ggc ttt gaa gca gtc ttc ttt 403
 Val Arg Pro Phe Gly Ala Gly Ala Ala Gly Phe Glu Ala Val Phe Phe
 90 95 100

gtc ctc atc ctc ggc gga cga gcc ttc gga ccc ggc ttc gga ttc atc 451
 Val Leu Ile Leu Gly Gly Arg Ala Phe Gly Pro Gly Phe Gly Phe Ile
 105 110 115

ctc ggc aac acc gga ctg ttc gca tcc gcg ctg ctc acc gca gga atc 499
 Leu Gly Asn Thr Gly Leu Phe Ala Ser Ala Leu Leu Thr Ala Gly Ile
 120 125 130

gga ccg tgg ctc ccc tac caa atg ctc gca gcc gcc tgg gtc agc ttc 547
 Gly Pro Trp Leu Pro Tyr Gln Met Leu Ala Ala Trp Val Ser Phe
 135 140 145

ggc gcc ggc cta ctc ccc caa gta cgc ggc aaa aag gaa atg ctc atc 595
 Gly Ala Gly Leu Leu Pro Gln Val Arg Gly Lys Lys Glu Met Leu Ile
 150 155 160 165

atc gtc cta tac gcc atc gtc tct tca ctc ggc tac gga acc atg atg 643
 Ile Val Leu Tyr Ala Ile Val Ser Ser Leu Gly Tyr Gly Thr Met Met
 170 175 180

aac atg agc ttc tgg ccc tac gcc atc ggt gtc acc agc ggg ctt tcc 691
 Asn Met Ser Phe Trp Pro Tyr Ala Ile Gly Val Thr Ser Gly Leu Ser
 185 190 195

ttc aca ccc ggc gcg ccc gtc ctg gaa aac ctc cac acc ttc atg ctg 739
 Phe Thr Pro Gly Ala Pro Val Leu Glu Asn Leu His Thr Phe Met Leu
 200 205 210

ttc tgc ctc acc aca tcc atg ggt tgg gat ctc ggc cgc gcc ttc ttc 787
 Phe Cys Leu Thr Thr Ser Met Gly Trp Asp Leu Gly Arg Ala Phe Phe

215 220 225

acc tca gtg cta tta ctg ctc aca gcc aaa ccc gtt tta ggt gct tta 835
 Thr Ser Val Leu Leu Leu Leu Thr Ala Lys Pro Val Leu Gly Ala Leu
 230 235 240 245

cga cgc gcc agc cgc cgc gcc gct ttc ggc gtc gag cgt gac ttc ggg 883
 Arg Arg Ala Ser Arg Arg Ala Ala Phe Gly Val Glu Arg Asp Phe Gly
 250 255 260

gag gcc ggg gtg cct cgg gtc taaagatttt gttggcttgc ttc 927
 Glu Ala Gly Val Pro Arg Val
 265

<210> 696

<211> 268

<212> PRT

<213> Corynebacterium glutamicum

<400> 696

Met Ile Asn Ala Ile Thr Leu Lys Pro Lys Thr Phe Leu Thr Leu Ser
 1 5 10 15

Phe Leu Ala Val Leu Ser Ile Val Ile Phe Phe Trp Pro Leu Ile Val
 20 25 30

Asn Pro Glu Ser Phe Leu Ser Asp Lys Ala Gln Ala Pro Leu Tyr Ile
 35 40 45

Ala Ile Val Ile Pro Leu Val Leu Ala Ala Val Ile Ala Glu Ile Ser
 50 55 60

Glu Asn Gly Phe Asp Val Lys Ala Val Ala Met Leu Gly Val Leu Thr
 65 70 75 80

Ala Met Val Ala Val Val Arg Pro Phe Gly Ala Gly Ala Ala Gly Phe
 85 90 95

Glu Ala Val Phe Phe Val Leu Ile Leu Gly Gly Arg Ala Phe Gly Pro
 100 105 110

Gly Phe Gly Phe Ile Leu Gly Asn Thr Gly Leu Phe Ala Ser Ala Leu
 115 120 125

Leu Thr Ala Gly Ile Gly Pro Trp Leu Pro Tyr Gln Met Leu Ala Ala
 130 135 140

Ala Trp Val Ser Phe Gly Ala Gly Leu Leu Pro Gln Val Arg Gly Lys
 145 150 155 160

Lys Glu Met Leu Ile Ile Val Leu Tyr Ala Ile Val Ser Ser Leu Gly
 165 170 175

Tyr Gly Thr Met Met Asn Met Ser Phe Trp Pro Tyr Ala Ile Gly Val
 180 185 190

Thr Ser Gly Leu Ser Phe Thr Pro Gly Ala Pro Val Leu Glu Asn Leu
 195 200 205

His Thr Phe Met Leu Phe Cys Leu Thr Thr Ser Met Gly Trp Asp Leu

210				215				220							
Gly	Arg	Ala	Phe	Phe	Thr	Ser	Val	Leu	Leu	Leu	Leu	Thr	Ala	Lys	Pro
225					230					235					240
Val	Leu	Gly	Ala	Leu	Arg	Arg	Ala	Ser	Arg	Arg	Ala	Ala	Phe	Gly	Val
				245					250					255	
Glu	Arg	Asp	Phe	Gly	Glu	Ala	Gly	Val	Pro	Arg	Val				
			260					265							

```
<210> 697
<211> 1587
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(1564)  
<223> RXN00483
```

<400> 697															
agaccaaga gtaaaatccc aggatttgcg tatacttgcg ctcatggata atcaacttcg 60															
tcccactttg cattatcaag ctcaaaaccc gcaccggcga gtg ctg gtc acc ggt 115															
Val Leu Val Thr Gly 5															
gcg aca ggc tac att ggc ggc agg ttg att act gag tta ctt gct gcc 163															
Ala Thr Gly Tyr Ile Gly Gly Arg Leu Ile Thr Glu Leu Leu Ala Ala 20															
ggt ttc caa gtt cgg gcc acc tcg agg aaa aaa aca agt ctt cag cgc 211															
Gly Phe Gln Val Arg Ala Thr Ser Arg Lys Lys Thr Ser Leu Gln Arg 35															
ttt gac tgg tac gag gac gtc gag gca gtg gaa gcg gat ctg act gac 259															
Phe Asp Trp Tyr Glu Asp Val Glu Ala Val Glu Ala Asp Leu Thr Asp 50															
gcg act gag tta gat acg tta ttt aag gat gta gac gtt gtt tac tat 307															
Ala Thr Glu Leu Asp Thr Leu Phe Lys Asp Val Asp Val Val Tyr Tyr 65															
cta gtg cat tcc atg gga ggt aag aat gtt gat ttt gaa gag caa gag 355															
Leu Val His Ser Met Gly Gly Lys Asn Val Asp Phe Glu Glu Gln Glu 85															
caa cgc act gct gaa aat gta att caa gct gct gat caa gcc ggg ata 403															
Gln Arg Thr Ala Glu Asn Val Ile Gln Ala Ala Asp Gln Ala Gly Ile 100															
aaa cag att gtc tac ctt tcc ggc tta cac ccg cgt aat cga aaa ata 451															
Lys Gln Ile Val Tyr Leu Ser Gly Leu His Pro Arg Asn Arg Lys Ile 115															
gaa gaa cta tct aag cac atg cgc tca cgg gaa aag gtc gcc cag att 499															
Glu Glu Leu Ser Lys His Met Arg Ser Arg Glu Lys Val Ala Gln Ile 120															
125 130															

ttg ctg gca ggc cag aca cca gct tta att tta agg gct gcc aca att	547
Leu Leu Ala Gly Gln Thr Pro Ala Leu Ile Leu Arg Ala Ala Thr Ile	
135 140 145	
att ggt tcc ggc tct gca tca ttt gaa ata atc cgt cat ctc acg gag	595
Ile Gly Ser Gly Ser Ala Ser Phe Glu Ile Ile Arg His Leu Thr Glu	
150 155 160 165	
cgt ttg cct aga atg ata gcg cct cag tgg att act aat cag att gag	643
Arg Leu Pro Arg Met Ile Ala Pro Gln Trp Ile Thr Asn Gln Ile Glu	
170 175 180	
cct tta gca ata cgg gat gtt ttg cat tac cta atc tcg gcg gct gat	691
Pro Leu Ala Ile Arg Asp Val Leu His Tyr Leu Ile Ser Ala Ala Asp	
185 190 195	
tta aag gat cca gtc aac cgc tcc tgc gat att ggg tgt gga aag tcg	739
Leu Lys Asp Pro Val Asn Arg Ser Cys Asp Ile Gly Cys Gly Lys Ser	
200 205 210	
tat gaa ttt gcg gat cta ttg cgt atc tat gcc gat gtt cgg gga ctg	787
Tyr Glu Phe Ala Asp Leu Leu Arg Ile Tyr Ala Asp Val Arg Gly Leu	
215 220 225	
aaa cgt cat gta aat tcc gta cct ctc aat ttg ccc atg gac aag cta	835
Lys Arg His Val Asn Ser Val Pro Leu Asn Leu Pro Met Asp Lys Leu	
230 235 240 245	
tcc ggt ctt tgg att agt cta gtg aca cct gtt cca ttt caa ttg tct	883
Ser Gly Leu Trp Ile Ser Leu Val Thr Pro Val Pro Phe Gln Leu Ser	
250 255 260	
ttc cct tta gct caa tca atg gct gag gat gcc gtc act gaa gag cac	931
Phe Pro Leu Ala Gln Ser Met Ala Glu Asp Ala Val Thr Glu Glu His	
265 270 275	
agc att aaa gat att att tca gat cca ccc gat ggt ttt att gag tat	979
Ser Ile Lys Asp Ile Ile Ser Asp Pro Pro Asp Gly Phe Ile Glu Tyr	
280 285 290	
cgg gaa gca gtg gag ctg gca tta gct gca gaa ttt gat cgt gga gtt	1027
Arg Glu Ala Val Glu Leu Ala Leu Ala Ala Glu Phe Asp Arg Gly Val	
295 300 305	
cca acg tca tgg gat cga agc tgg act gta caa caa ccg tgg gct ggc	1075
Pro Thr Ser Trp Asp Arg Ser Trp Thr Val Gln Gln Pro Trp Ala Gly	
310 315 320 325	
cag cct acc gat cca gag tgg gcg ggc aaa gct gta tat gaa gac gtc	1123
Gln Pro Thr Asp Pro Glu Trp Ala Gly Lys Ala Val Tyr Glu Asp Val	
330 335 340	
cgc aca gaa gat act gat ctc cga gca gcg cag gtc tgg ccg atc att	1171
Arg Thr Glu Asp Thr Asp Leu Arg Ala Ala Gln Val Trp Pro Ile Ile	
345 350 355	
gaa ggt ttg ggt ggc gtg aac ggc tgg tat tct gca cca ctg cta tgg	1219
Glu Gly Leu Gly Gly Val Asn Gly Trp Tyr Ser Ala Pro Leu Leu Trp	
360 365 370	
cga ttg cgg ggt atc gct gac aga ctc atc ggc ggt cca ggt ttg ggc	1267

Arg Leu Arg Gly Ile Ala Asp Arg Leu Ile Gly Gly Pro Gly Leu Gly
 375 380 385
 gga cgg cgg gat ccc cgt cat ttg aaa ctt ggg gat cgc att gat tgg 1315
 Gly Arg Arg Asp Pro Arg His Leu Lys Leu Gly Asp Arg Ile Asp Trp
 390 395 400 405
 tgg cgg gtt act gag atc gat cca cca cat aga tta gtg ctc acc gca 1363
 Trp Arg Val Thr Glu Ile Asp Pro Pro His Arg Leu Val Leu Thr Ala
 410 415 420
 gag atg aaa gta gat ggt ggc gct tgg ctg atc ctg gaa gtt gcg gac 1411
 Glu Met Lys Val Asp Gly Gly Ala Trp Leu Ile Leu Glu Val Ala Asp
 425 430 435
 aag gaa aat ggc gga tgt act tat acc cag cgc gca ata ttt gag ccg 1459
 Lys Glu Asn Gly Gly Cys Thr Tyr Thr Gln Arg Ala Ile Phe Glu Pro
 440 445 450
 aag ggt ttg ccc ggt tat ctc tat tgg tgg gtt gtt tca ccg ttc cat 1507
 Lys Gly Leu Pro Gly Tyr Leu Tyr Trp Trp Val Val Ser Pro Phe His
 455 460 465
 gcg att att ttt cct tat atg cgt tcg aat att tta aaa gct gcg cgt 1555
 Ala Ile Ile Phe Pro Tyr Met Arg Ser Asn Ile Leu Lys Ala Ala Arg
 470 475 480 485
 aaa ctc act taatcgcaga gtaggcgtct aaa 1587
 Lys Leu Thr

<210> 698

<211> 488

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 698

Val Leu Val Thr Gly Ala Thr Gly Tyr Ile Gly Gly Arg Leu Ile Thr
 1 5 10 15
 Glu Leu Leu Ala Ala Gly Phe Gln Val Arg Ala Thr Ser Arg Lys Lys
 20 25 30
 Thr Ser Leu Gln Arg Phe Asp Trp Tyr Glu Asp Val Glu Ala Val Glu
 35 40 45
 Ala Asp Leu Thr Asp Ala Thr Glu Leu Asp Thr Leu Phe Lys Asp Val
 50 55 60
 Asp Val Val Tyr Tyr Leu Val His Ser Met Gly Gly Lys Asn Val Asp
 65 70 75 80
 Phe Glu Glu Gln Glu Gln Arg Thr Ala Glu Asn Val Ile Gln Ala Ala
 85 90 95
 Asp Gln Ala Gly Ile Lys Gln Ile Val Tyr Leu Ser Gly Leu His Pro
 100 105 110
 Arg Asn Arg Lys Ile Glu Glu Leu Ser Lys His Met Arg Ser Arg Glu
 115 120 125

Lys Val Ala Gln Ile Leu Leu Ala Gly Gln Thr Pro Ala Leu Ile Leu
 130 135 140
 Arg Ala Ala Thr Ile Ile Gly Ser Gly Ser Ala Ser Phe Glu Ile Ile
 145 150 155 160
 Arg His Leu Thr Glu Arg Leu Pro Arg Met Ile Ala Pro Gln Trp Ile
 165 170 175
 Thr Asn Gln Ile Glu Pro Leu Ala Ile Arg Asp Val Leu His Tyr Leu
 180 185 190
 Ile Ser Ala Ala Asp Leu Lys Asp Pro Val Asn Arg Ser Cys Asp Ile
 195 200 205
 Gly Cys Gly Lys Ser Tyr Glu Phe Ala Asp Leu Leu Arg Ile Tyr Ala
 210 215 220
 Asp Val Arg Gly Leu Lys Arg His Val Asn Ser Val Pro Leu Asn Leu
 225 230 235 240
 Pro Met Asp Lys Leu Ser Gly Leu Trp Ile Ser Leu Val Thr Pro Val
 245 250 255
 Pro Phe Gln Leu Ser Phe Pro Leu Ala Gln Ser Met Ala Glu Asp Ala
 260 265 270
 Val Thr Glu Glu His Ser Ile Lys Asp Ile Ile Ser Asp Pro Pro Asp
 275 280 285
 Gly Phe Ile Glu Tyr Arg Glu Ala Val Glu Leu Ala Leu Ala Ala Glu
 290 295 300
 Phe Asp Arg Gly Val Pro Thr Ser Trp Asp Arg Ser Trp Thr Val Gln
 305 310 315 320
 Gln Pro Trp Ala Gly Gln Pro Thr Asp Pro Glu Trp Ala Gly Lys Ala
 325 330 335
 Val Tyr Glu Asp Val Arg Thr Glu Asp Thr Asp Leu Arg Ala Ala Gln
 340 345 350
 Val Trp Pro Ile Ile Glu Gly Leu Gly Gly Val Asn Gly Trp Tyr Ser
 355 360 365
 Ala Pro Leu Leu Trp Arg Leu Arg Gly Ile Ala Asp Arg Leu Ile Gly
 370 375 380
 Gly Pro Gly Leu Gly Gly Arg Arg Asp Pro Arg His Leu Lys Leu Gly
 385 390 395 400
 Asp Arg Ile Asp Trp Trp Arg Val Thr Glu Ile Asp Pro Pro His Arg
 405 410 415
 Leu Val Leu Thr Ala Glu Met Lys Val Asp Gly Gly Ala Trp Leu Ile
 420 425 430
 Leu Glu Val Ala Asp Lys Glu Asn Gly Gly Cys Thr Tyr Thr Gln Arg
 435 440 445

Ala Ile Phe Glu Pro Lys Gly Leu Pro Gly Tyr Leu Tyr Trp Trp Val
 450 455 460

Val Ser Pro Phe His Ala Ile Ile Phe Pro Tyr Met Arg Ser Asn Ile
 465 470 475 480

Leu Lys Ala Ala Arg Lys Leu Thr
 485

<210> 699
 <211> 1587
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1564)
 <223> FRXA00483

<400> 699
 agacccaaga gtaaaatccc aggatttgct tatacttgcg ctcatggata atcaacttcg 60

tcccactttg cattatcaag ctcaaaaccc gcaccggcga gtg ctg gtc acc ggt 115
 Val Leu Val Thr Gly
 1 5

gcg aca ggc tac att ggc ggc agg ttg att act gag tta ctt gct gcc 163
 Ala Thr Gly Tyr Ile Gly Gly Arg Leu Ile Thr Glu Leu Leu Ala Ala
 10 15 20

ggt ttc caa gtt cgg gcc acc tcg agg aaa aaa aca agt ctt cag cgc 211
 Gly Phe Gln Val Arg Ala Thr Ser Arg Lys Lys Thr Ser Leu Gln Arg
 25 30 35

ttt gac tgg tac gag gac gtc gag gca gtg gaa gcg gat ctg act gac 259
 Phe Asp Trp Tyr Glu Asp Val Glu Ala Val Glu Ala Asp Leu Thr Asp
 40 45 50

gcg act gag tta gat acg tta ttt aag gat gta gac gtt gtt tac tat 307
 Ala Thr Glu Leu Asp Thr Leu Phe Lys Asp Val Asp Val Val Tyr Tyr
 55 60 65

cta gtg cat tcc atg gga ggt aag aat gtt gat ttt gaa gag caa gag 355
 Leu Val His Ser Met Gly Gly Lys Asn Val Asp Phe Glu Glu Gln Glu
 70 75 80 85

caa cgc act gct gaa aat gta att caa gct gct gat caa gcc ggg ata 403
 Gln Arg Thr Ala Glu Asn Val Ile Gln Ala Ala Asp Gln Ala Gly Ile
 90 95 100

aaa cag att gtc tac ctt tcc ggc tta cac ccg cgt aat cga aaa ata 451
 Lys Gln Ile Val Tyr Leu Ser Gly Leu His Pro Arg Asn Arg Lys Ile
 105 110 115

gaa gaa cta tct aag cac atg cgc tca cgg gaa aag gtc gcc cag att 499
 Glu Glu Leu Ser Lys His Met Arg Ser Arg Glu Lys Val Ala Gln Ile
 120 125 130

ttg ctg gca ggc cag aca cca gct tta att tta agg gct gcc aca att 547
 Leu Leu Ala Gly Gln Thr Pro Ala Leu Ile Leu Arg Ala Ala Thr Ile

135	140	145	
att ggt tcc ggc tct gca tca ttt gaa ata atc cgt cat ctc acg gag Ile Gly Ser Gly Ser Ala Ser Phe Glu Ile Ile Arg His Leu Thr Glu 150 155 160 165			595
cgt ttg cct aga atg ata gcg cct cag tgg att act aat cag att gag Arg Leu Pro Arg Met Ile Ala Pro Gln Trp Ile Thr Asn Gln Ile Glu 170 175 180			643
cct tta gca ata cgg gat gtt ttg cat tac cta atc tcg gcg gct gat Pro Leu Ala Ile Arg Asp Val Leu His Tyr Leu Ile Ser Ala Ala Asp 185 190 195			691
tta aag gat cca gtc aac cgc tcc tgc gat att ggg tgt gga aag tcg Leu Lys Asp Pro Val Asn Arg Ser Cys Asp Ile Gly Cys Gly Lys Ser 200 205 210			739
tat gaa ttt gcg gat cta ttg cgt atc tat gcc gat gtt cgg gga ctg Tyr Glu Phe Ala Asp Leu Leu Arg Ile Tyr Ala Asp Val Arg Gly Leu 215 220 225			787
aaa cgt cat gta aat tcc gta cct ctc aat ttg ccc atg gac aag cta Lys Arg His Val Asn Ser Val Pro Leu Asn Leu Pro Met Asp Lys Leu 230 235 240 245			835
tcc ggt ctt tgg att agt cta gtg aca cct gtt cca ttt caa ttg tct Ser Gly Leu Trp Ile Ser Leu Val Thr Pro Val Pro Phe Gln Leu Ser 250 255 260			883
ttc cct tta gct caa tca atg gct gag gat gcc gtc act gaa gag cac Phe Pro Leu Ala Gln Ser Met Ala Glu Asp Ala Val Thr Glu Glu His 265 270 275			931
agc att aaa gat att att tca gat cca ccc gat ggt ttt att gag tat Ser Ile Lys Asp Ile Ile Ser Asp Pro Pro Asp Gly Phe Ile Glu Tyr 280 285 290			979
cgg gaa gca gtg gag ctg gca tta gct gca gaa ttt gat cgt gga gtt Arg Glu Ala Val Glu Leu Ala Leu Ala Ala Glu Phe Asp Arg Gly Val 295 300 305			1027
cca acg tca tgg gat cga agc tgg act gta caa caa ccg tgg gct ggc Pro Thr Ser Trp Asp Arg Ser Trp Thr Val Gln Gln Pro Trp Ala Gly 310 315 320 325			1075
cag cct acc gat cca gag tgg gcg ggc aaa gct gta tat gaa gac gtc Gln Pro Thr Asp Pro Glu Trp Ala Gly Lys Ala Val Tyr Glu Asp Val 330 335 340			1123
cgc aca gaa gat act gat ctc cga gca gcg cag gtc tgg ccg atc att Arg Thr Glu Asp Thr Asp Leu Arg Ala Ala Gln Val Trp Pro Ile Ile 345 350 355			1171
gaa ggt ttg ggt ggc gtg aac ggc tgg tat tct gca cca ctg cta tgg Glu Gly Leu Gly Gly Val Asn Gly Trp Tyr Ser Ala Pro Leu Leu Trp 360 365 370			1219
cga ttg cgg ggt atc gct gac aga ctc atc ggc ggt cca ggt ttg ggc Arg Leu Arg Gly Ile Ala Asp Arg Leu Ile Gly Gly Pro Gly Leu Gly 375 380 385			1267

gga cgg cgg gat ccc cgt cat ttg aaa ctt ggg gat cgc att gat tgg 1315
 Gly Arg Arg Asp Pro Arg His Leu Lys Leu Gly Asp Arg Ile Asp Trp
 390 395 400 405

tgg cgg gtt act gag atc gat cca cca cat aga tta gtg ctc acc gca 1363
 Trp Arg Val Thr Glu Ile Asp Pro Pro His Arg Leu Val Leu Thr Ala
 410 415 420

gag atg aaa gta gat ggt ggc gct tgg ctg atc ctg gaa gtt gcg gac 1411
 Glu Met Lys Val Asp Gly Gly Ala Trp Leu Ile Leu Glu Val Ala Asp
 425 430 435

aag gaa aat ggc gga tgt act tat acc cag cgc gca ata ttt gag ccg 1459
 Lys Glu Asn Gly Gly Cys Thr Tyr Thr Gln Arg Ala Ile Phe Glu Pro
 440 445 450

aag ggt ttg ccc ggt tat ctc tat tgg tgg gtt gtt tca ccg ttc cat 1507
 Lys Gly Leu Pro Gly Tyr Leu Tyr Trp Trp Val Val Ser Pro Phe His
 455 460 465

gcg att att ttt cct tat atg cgt tcg aat att tta aaa gct gcg cgt 1555
 Ala Ile Ile Phe Pro Tyr Met Arg Ser Asn Ile Leu Lys Ala Ala Arg
 470 475 480 485

aaa ctc act taatcgcaga gtaggcgtct aaa 1587
 Lys Leu Thr

<210> 700

<211> 488

<212> PRT

<213> Corynebacterium glutamicum

<400> 700

Val Leu Val Thr Gly Ala Thr Gly Tyr Ile Gly Gly Arg Leu Ile Thr
 1 5 10 15

Glu Leu Leu Ala Ala Gly Phe Gln Val Arg Ala Thr Ser Arg Lys Lys
 20 25 30

Thr Ser Leu Gln Arg Phe Asp Trp Tyr Glu Asp Val Glu Ala Val Glu
 35 40 45

Ala Asp Leu Thr Asp Ala Thr Glu Leu Asp Thr Leu Phe Lys Asp Val
 50 55 60

Asp Val Val Tyr Tyr Leu Val His Ser Met Gly Gly Lys Asn Val Asp
 65 70 75 80

Phe Glu Glu Gln Glu Gln Arg Thr Ala Glu Asn Val Ile Gln Ala Ala
 85 90 95

Asp Gln Ala Gly Ile Lys Gln Ile Val Tyr Leu Ser Gly Leu His Pro
 100 105 110

Arg Asn Arg Lys Ile Glu Glu Leu Ser Lys His Met Arg Ser Arg Glu
 115 120 125

Lys Val Ala Gln Ile Leu Leu Ala Gly Gln Thr Pro Ala Leu Ile Leu

130	135	140
Arg Ala Ala Thr Ile Ile Gly Ser Gly Ser Ala Ser Phe Glu Ile Ile 145 150 155 160		
Arg His Leu Thr Glu Arg Leu Pro Arg Met Ile Ala Pro Gln Trp Ile 165 170 175		
Thr Asn Gln Ile Glu Pro Leu Ala Ile Arg Asp Val Leu His Tyr Leu 180 185 190		
Ile Ser Ala Ala Asp Leu Lys Asp Pro Val Asn Arg Ser Cys Asp Ile 195 200 205		
Gly Cys Gly Lys Ser Tyr Glu Phe Ala Asp Leu Leu Arg Ile Tyr Ala 210 215 220		
Asp Val Arg Gly Leu Lys Arg His Val Asn Ser Val Pro Leu Asn Leu 225 230 235 240		
Pro Met Asp Lys Leu Ser Gly Leu Trp Ile Ser Leu Val Thr Pro Val 245 250 255		
Pro Phe Gln Leu Ser Phe Pro Leu Ala Gln Ser Met Ala Glu Asp Ala 260 265 270		
Val Thr Glu Glu His Ser Ile Lys Asp Ile Ile Ser Asp Pro Pro Asp 275 280 285		
Gly Phe Ile Glu Tyr Arg Glu Ala Val Glu Leu Ala Leu Ala Ala Glu 290 295 300		
Phe Asp Arg Gly Val Pro Thr Ser Trp Asp Arg Ser Trp Thr Val Gln 305 310 315 320		
Gln Pro Trp Ala Gly Gln Pro Thr Asp Pro Glu Trp Ala Gly Lys Ala 325 330 335		
Val Tyr Glu Asp Val Arg Thr Glu Asp Thr Asp Leu Arg Ala Ala Gln 340 345 350		
Val Trp Pro Ile Ile Glu Gly Leu Gly Gly Val Asn Gly Trp Tyr Ser 355 360 365		
Ala Pro Leu Leu Trp Arg Leu Arg Gly Ile Ala Asp Arg Leu Ile Gly 370 375 380		
Gly Pro Gly Leu Gly Gly Arg Arg Asp Pro Arg His Leu Lys Leu Gly 385 390 395 400		
Asp Arg Ile Asp Trp Trp Arg Val Thr Glu Ile Asp Pro Pro His Arg 405 410 415		
Leu Val Leu Thr Ala Glu Met Lys Val Asp Gly Gly Ala Trp Leu Ile 420 425 430		
Leu Glu Val Ala Asp Lys Glu Asn Gly Gly Cys Thr Tyr Thr Gln Arg 435 440 445		
Ala Ile Phe Glu Pro Lys Gly Leu Pro Gly Tyr Leu Tyr Trp Trp Val 450 455 460		

Val Ser Pro Phe His Ala Ile Ile Phe Pro Tyr Met Arg Ser Asn Ile
 465 470 475 480

Leu Lys Ala Ala Arg Lys Leu Thr
 485

<210> 701

<211> 612

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(589)

<223> RXA01534

<400> 701

attgctctca tcggttcgat atagactgaa ttgtctaggt taatatccaa tatggaagaa 60

aaactagaca gttaagtaga ctgaatggcc tactaggtgc atg act tca gca atc 115
 Met Thr Ser Ala Ile
 1 5

acc acc gca act gat ctt cgc tcc gta ctg cga aac gta cca acc cca 163
 Thr Thr Ala Thr Asp Leu Arg Ser Val Leu Arg Asn Val Pro Thr Pro
 10 15 20

att agc ttc att gca acc cac acc gat cag cct ctg ggc atg atc gtt 211
 Ile Ser Phe Ile Ala Thr His Thr Asp Gln Pro Leu Gly Met Ile Val
 25 30 35

ggg tca ttc gtc agc att agc gcc gaa cca cca ttg gta ggc atc ttc 259
 Gly Ser Phe Val Ser Ile Ser Ala Glu Pro Pro Leu Val Gly Ile Phe
 40 45 50

ttg cag aag agc tct tct tca tgg cca gct atc gag cag gca tta gtt 307
 Leu Gln Lys Ser Ser Ser Ser Trp Pro Ala Ile Glu Gln Ala Leu Val
 55 60 65

acc ggc caa gag cta ggc att tct atc ctc ggc ggg gca cac gca gac 355
 Thr Gly Gln Glu Leu Gly Ile Ser Ile Leu Gly Gly Ala His Ala Asp
 70 75 80 85

cat gtg cgt aag ctt tct ggc cca tcc gac cag cgc ttt gaa aac ctt 403
 His Val Arg Lys Leu Ser Gly Pro Ser Asp Gln Arg Phe Glu Asn Leu
 90 95 100

ggg tgg gca tcc acc gaa aac ggt gcg att cac ctt gaa ggc gct gat 451
 Gly Trp Ala Ser Thr Glu Asn Gly Ala Ile His Leu Glu Gly Ala Asp
 105 110 115

gca caa cta acc acg aaa ctt cat gat ctc cag gaa atc ggc gat cac 499
 Ala Gln Leu Thr Thr Lys Leu His Asp Leu Gln Glu Ile Gly Asp His
 120 125 130

ttc ttt gca gtt cta gaa gtt att gac gct tcc gct gac caa gac ttc 547
 Phe Phe Ala Val Leu Glu Val Ile Asp Ala Ser Ala Asp Gln Asp Phe
 135 140 145

agc tca gcg ctg gtg tac cac cgc tca cag gtg tcc tcg ctg 589
 Ser Ser Ala Leu Val Tyr His Arg Ser Gln Val Ser Ser Leu
 150 155 160

taggacacta aattttaaga ggg 612

<210> 702

<211> 163

<212> PRT

<213> Corynebacterium glutamicum

<400> 702

Met Thr Ser Ala Ile Thr Thr Ala Thr Asp Leu Arg Ser Val Leu Arg
 1 5 10 15

Asn Val Pro Thr Pro Ile Ser Phe Ile Ala Thr His Thr Asp Gln Pro
 20 25 30

Leu Gly Met Ile Val Gly Ser Phe Val Ser Ile Ser Ala Glu Pro Pro
 35 40 45

Leu Val Gly Ile Phe Leu Gln Lys Ser Ser Ser Ser Trp Pro Ala Ile
 50 55 60

Glu Gln Ala Leu Val Thr Gly Gln Glu Leu Gly Ile Ser Ile Leu Gly
 65 70 75 80

Gly Ala His Ala Asp His Val Arg Lys Leu Ser Gly Pro Ser Asp Gln
 85 90 95

Arg Phe Glu Asn Leu Gly Trp Ala Ser Thr Glu Asn Gly Ala Ile His
 100 105 110

Leu Glu Gly Ala Asp Ala Gln Leu Thr Thr Lys Leu His Asp Leu Gln
 115 120 125

Glu Ile Gly Asp His Phe Phe Ala Val Leu Glu Val Ile Asp Ala Ser
 130 135 140

Ala Asp Gln Asp Phe Ser Ser Ala Leu Val Tyr His Arg Ser Gln Val
 145 150 155 160

Ser Ser Leu

<210> 703

<211> 1134

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1111)

<223> RXA00288

<400> 703

ggcgtgctaa aaaagcacgt caaatacaga atcggcagat tacatcgctg agcagagaaa 60

acacgggcat gaaacgtacc caagggctaa catcgggggc atg agc gcg caa atg 115

																Met Ser Ala Gln Met	
																1	5
gat acc cct gat ccc act atg tct gct gtt gca atg tta gat tcc atc	163																
Asp Thr Pro Asp Pro Thr Met Ser Ala Val Ala Met Leu Asp Ser Ile																	
				10					15						20		
cct tct gat caa cca gat ttc ctg atc gat gta gaa gta gat cga cca	211																
Pro Ser Asp Gln Pro Asp Phe Leu Ile Asp Val Glu Val Asp Arg Pro																	
			25					30						35			
act ccc gga cca cat gat ctg cta gtc cac att gag gcg gtc tca att	259																
Thr Pro Gly Pro His Asp Leu Leu Val His Ile Glu Ala Val Ser Ile																	
		40					45					50					
aac cct gtt gat acc aag gta cgc atg cgg gcc ggg aag caa aag cat	307																
Asn Pro Val Asp Thr Lys Val Arg Met Arg Ala Gly Lys Gln Lys His																	
	55					60					65						
cct aaa att tta ggt ttt gat gct gca ggt gag gtg gtg gct gtt gga	355																
Pro Lys Ile Leu Gly Phe Asp Ala Ala Gly Glu Val Val Ala Val Gly																	
	70				75				80					85			
tcg cag gtc acg ctc ttc aat gtt ggt gac aaa gtg ttc tac gca gga	403																
Ser Gln Val Thr Leu Phe Asn Val Gly Asp Lys Val Phe Tyr Ala Gly																	
			90					95						100			
tcc aat cag cgt cca gga agt aac gca gag tac cag gtg gtg gat gaa	451																
Ser Asn Gln Arg Pro Gly Ser Asn Ala Glu Tyr Gln Val Val Asp Glu																	
		105					110						115				
cgg ctg gtg ggt cac gca cca caa agc ttg ggg gca cac gac gcc gct	499																
Arg Leu Val Gly His Ala Pro Gln Ser Leu Gly Ala His Asp Ala Ala																	
		120					125					130					
gct ctc cca ctt gtc gcg ctc act gca tgg gag tca ctt ttt gac cga	547																
Ala Leu Pro Leu Val Ala Leu Thr Ala Trp Glu Ser Leu Phe Asp Arg																	
	135					140					145						
ttg gga gta act cag tca act act gga aca ctg ttg gtc ttg ggc ggt	595																
Leu Gly Val Thr Gln Ser Thr Thr Gly Thr Leu Leu Val Leu Gly Gly																	
	150				155				160					165			
tca gga ggt gtg cct tca gct ctt att caa ctt gct cga gct ctc act	643																
Ser Gly Gly Val Pro Ser Ala Leu Ile Gln Leu Ala Arg Ala Leu Thr																	
			170					175					180				
ggt ctg aaa gta gtg gca aca gct tct cgc cct gaa tca caa gaa tgg	691																
Gly Leu Lys Val Val Ala Thr Ala Ser Arg Pro Glu Ser Gln Glu Trp																	
		185					190						195				
gtg aca aag ctc ggt gct cat gag gtg att gat cac tcc aag gat ttg	739																
Val Thr Lys Leu Gly Ala His Glu Val Ile Asp His Ser Lys Asp Leu																	
		200					205					210					
agt gag caa atc tcc gac gtg gat ttt gtt ttc agc tcg tgg act act	787																
Ser Glu Gln Ile Ser Asp Val Asp Phe Val Phe Ser Ser Trp Thr Thr																	
	215					220					225						
ggg cgt gaa gta gag ctc gcc acg ttg atg aaa ccc cag tcc cac cta	835																
Gly Arg Glu Val Glu Leu Ala Thr Leu Met Lys Pro Gln Ser His Leu																	

230	235	240	245	
gtg ctc atc gat gat cca gtg gat ccc aat ttg ggc gct ttt aag caa				883
Val Leu Ile Asp Asp Pro Val Asp Pro Asn Leu Gly Ala Phe Lys Gln	250	255	260	
aaa gcg atc gct ttg cac tgg gag ttc atg ttt acc cgc gct atg ttc				931
Lys Ala Ile Ala Leu His Trp Glu Phe Met Phe Thr Arg Ala Met Phe	265	270	275	
aac act cct gat atg ggt gaa caa ggg aaa att ctg aat aag atc gcc				979
Asn Thr Pro Asp Met Gly Glu Gln Gly Lys Ile Leu Asn Lys Ile Ala	280	285	290	
gac atg gtt gat cgg ggt cag ttt gag tcc gtg aca gca acg gtg ctg				1027
Asp Met Val Asp Arg Gly Gln Phe Glu Ser Val Thr Ala Thr Val Leu	295	300	305	
gat ggg ctc aac gct gca aac atc atg gag ggg cac cgg ctc gtt gag				1075
Asp Gly Leu Asn Ala Ala Asn Ile Met Glu Gly His Arg Leu Val Glu	310	315	320	325
cag ggt aaa acc tca gga aaa att gtt gtg agg gta taaagaggac				1121
Gln Gly Lys Thr Ser Gly Lys Ile Val Val Arg Val	330	335		
ttgaaaaatg cac				1134
<210> 704				
<211> 337				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 704				
Met Ser Ala Gln Met Asp Thr Pro Asp Pro Thr Met Ser Ala Val Ala				
1 5 10 15				
Met Leu Asp Ser Ile Pro Ser Asp Gln Pro Asp Phe Leu Ile Asp Val				
20 25 30				
Glu Val Asp Arg Pro Thr Pro Gly Pro His Asp Leu Leu Val His Ile				
35 40 45				
Glu Ala Val Ser Ile Asn Pro Val Asp Thr Lys Val Arg Met Arg Ala				
50 55 60				
Gly Lys Gln Lys His Pro Lys Ile Leu Gly Phe Asp Ala Ala Gly Glu				
65 70 75 80				
Val Val Ala Val Gly Ser Gln Val Thr Leu Phe Asn Val Gly Asp Lys				
85 90 95				
Val Phe Tyr Ala Gly Ser Asn Gln Arg Pro Gly Ser Asn Ala Glu Tyr				
100 105 110				
Gln Val Val Asp Glu Arg Leu Val Gly His Ala Pro Gln Ser Leu Gly				
115 120 125				
Ala His Asp Ala Ala Ala Leu Pro Leu Val Ala Leu Thr Ala Trp Glu				
130 135 140				

Ser Leu Phe Asp Arg Leu Gly Val Thr Gln Ser Thr Thr Gly Thr Leu
 145 150 155 160
 Leu Val Leu Gly Gly Ser Gly Gly Val Pro Ser Ala Leu Ile Gln Leu
 165 170 175
 Ala Arg Ala Leu Thr Gly Leu Lys Val Val Ala Thr Ala Ser Arg Pro
 180 185 190
 Glu Ser Gln Glu Trp Val Thr Lys Leu Gly Ala His Glu Val Ile Asp
 195 200 205
 His Ser Lys Asp Leu Ser Glu Gln Ile Ser Asp Val Asp Phe Val Phe
 210 215 220
 Ser Ser Trp Thr Thr Gly Arg Glu Val Glu Leu Ala Thr Leu Met Lys
 225 230 235 240
 Pro Gln Ser His Leu Val Leu Ile Asp Asp Pro Val Asp Pro Asn Leu
 245 250 255
 Gly Ala Phe Lys Gln Lys Ala Ile Ala Leu His Trp Glu Phe Met Phe
 260 265 270
 Thr Arg Ala Met Phe Asn Thr Pro Asp Met Gly Glu Gln Gly Lys Ile
 275 280 285
 Leu Asn Lys Ile Ala Asp Met Val Asp Arg Gly Gln Phe Glu Ser Val
 290 295 300
 Thr Ala Thr Val Leu Asp Gly Leu Asn Ala Ala Asn Ile Met Glu Gly
 305 310 315 320
 His Arg Leu Val Glu Gln Gly Lys Thr Ser Gly Lys Ile Val Val Arg
 325 330 335
 Val

<210> 705
 <211> 1089
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1066)
 <223> RXA02741

<400> 705
 actggtcacc tggtttggtc tgcactctga ctccctcaa aagggcacaa tttggtcaat 60
 ttcccaacct tgtotttcag tcatgggttag tgtgggaacc atg aag gca atc tta 115
 Met Lys Ala Ile Leu
 1 5
 gtt tcc cgc acc ggc gga cca gag gtg ttg gag ttc acc gac act gac 163
 Val Ser Arg Thr Gly Gly Pro Glu Val Leu Glu Phe Thr Asp Thr Asp
 10 15 20

```

gcc cca aag ccc act gat gat cag gtt tta gtt gaa gtt gat atg gct 211
Ala Pro Lys Pro Thr Asp Asp Gln Val Leu Val Glu Val Asp Met Ala
      25                      30                      35

ggc gtc aac ttt att gat act tac tat cgc cag ggt gaa tat cac gct 259
Gly Val Asn Phe Ile Asp Thr Tyr Tyr Arg Gln Gly Glu Tyr His Ala
      40                      45                      50

cgc ctg ccg ttt atc cca ggt ttt gaa ggc act ggt cgg gtg ttg gag 307
Arg Leu Pro Phe Ile Pro Gly Phe Glu Gly Thr Gly Arg Val Leu Glu
      55                      60                      65

gat ccg cag ggg ttg att gcg gcg ggt acc aag gtg gcg tgg tgt gat 355
Asp Pro Gln Gly Leu Ile Ala Ala Gly Thr Lys Val Ala Trp Cys Asp
      70                      75                      80                      85

gcc atg ggt tcg tat gct cag cag gtg tgt gtg ccg cgg gat cgc ttg 403
Ala Met Gly Ser Tyr Ala Gln Gln Val Cys Val Pro Arg Asp Arg Leu
      90                      95                      100

gtg gcg gtt ccc gag ggc gtg agt tcg gaa gtg gct gcg tcg atg ttg 451
Val Ala Val Pro Glu Gly Val Ser Ser Glu Val Ala Ala Ser Met Leu
      105                      110                      115

atg cag gga atc act gcg cat tat cta acc aat ggt gtg tat gag ctt 499
Met Gln Gly Ile Thr Ala His Tyr Leu Thr Asn Gly Val Tyr Glu Leu
      120                      125                      130

gaa gag ggc gat tct tgc ctc atc act gct ggc gcg ggt ggt gtt gga 547
Glu Glu Gly Asp Ser Cys Leu Ile Thr Ala Gly Ala Gly Gly Val Gly
      135                      140                      145

ttg ttg gct acg cag atg gcg gcg gcc aag gga gtg cgc gtg tac agc 595
Leu Leu Ala Thr Gln Met Ala Ala Ala Lys Gly Val Arg Val Tyr Ser
      150                      155                      160                      165

gtg gtg tcc acg gat gaa aaa gct gag ctt gct ttg gat gcc ggt gct 643
Val Val Ser Thr Asp Glu Lys Ala Glu Leu Ala Leu Asp Ala Gly Ala
      170                      175                      180

tat gag gtg ttt cgt tat tcc gat aat ttg gcg gag cag gtt cgt cgg 691
Tyr Glu Val Phe Arg Tyr Ser Asp Asn Leu Ala Glu Gln Val Arg Arg
      185                      190                      195

cac aac ggg ggt cgc gga gtt gat gtg gtg tat gac ggt gtc ggc cag 739
His Asn Gly Gly Arg Gly Val Asp Val Val Tyr Asp Gly Val Gly Gln
      200                      205                      210

tcc acg ttc aat gag tcc tta gag gct gtt cgt ccg cgc ggc act gtg 787
Ser Thr Phe Asn Glu Ser Leu Glu Ala Val Arg Pro Arg Gly Thr Val
      215                      220                      225

tgt ttg ttt ggt gcg gcg tcg ggt cct gtg gag cct ttt gat ccg cag 835
Cys Leu Phe Gly Ala Ala Ser Gly Pro Val Glu Pro Phe Asp Pro Gln
      230                      235                      240                      245

ctg ttg aac act cac ggt tcg atc ttc ttg acc cgc cca agc att ggc 883
Leu Leu Asn Thr His Gly Ser Ile Phe Leu Thr Arg Pro Ser Ile Gly
      250                      255                      260

```

gcg tgg acg tct gag gag ggc gaa ttt gcc aag cgt gca cag gcg gtc 931
 Ala Trp Thr Ser Glu Glu Gly Glu Phe Ala Lys Arg Ala Gln Ala Val
 265 270 275

acg cag gcc atc gtc gaa ggc acc ttg cgg gtt cgc gtt act ggc aca 979
 Thr Gln Ala Ile Val Glu Gly Thr Leu Arg Val Arg Val Thr Gly Thr
 280 285 290

tat tcg ctt gcc gac gcc tac atc gcc cac cgc gac ctt cag gcg cgt 1027
 Tyr Ser Leu Ala Asp Ala Tyr Ile Ala His Arg Asp Leu Gln Ala Arg
 295 300 305

agc acg agc ggt tct ttg gtc ttg gaa atc ccg aag gac taaacacgca 1076
 Ser Thr Ser Gly Ser Leu Val Leu Glu Ile Pro Lys Asp
 310 315 320

taaaaagatc ctg 1089

<210> 706
 <211> 322
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 706
 Met Lys Ala Ile Leu Val Ser Arg Thr Gly Gly Pro Glu Val Leu Glu
 1 5 10 15
 Phe Thr Asp Thr Asp Ala Pro Lys Pro Thr Asp Asp Gln Val Leu Val
 20 25 30
 Glu Val Asp Met Ala Gly Val Asn Phe Ile Asp Thr Tyr Tyr Arg Gln
 35 40 45
 Gly Glu Tyr His Ala Arg Leu Pro Phe Ile Pro Gly Phe Glu Gly Thr
 50 55 60
 Gly Arg Val Leu Glu Asp Pro Gln Gly Leu Ile Ala Ala Gly Thr Lys
 65 70 75 80
 Val Ala Trp Cys Asp Ala Met Gly Ser Tyr Ala Gln Gln Val Cys Val
 85 90 95
 Pro Arg Asp Arg Leu Val Ala Val Pro Glu Gly Val Ser Ser Glu Val
 100 105 110
 Ala Ala Ser Met Leu Met Gln Gly Ile Thr Ala His Tyr Leu Thr Asn
 115 120 125
 Gly Val Tyr Glu Leu Glu Glu Gly Asp Ser Cys Leu Ile Thr Ala Gly
 130 135 140
 Ala Gly Gly Val Gly Leu Leu Ala Thr Gln Met Ala Ala Ala Lys Gly
 145 150 155 160
 Val Arg Val Tyr Ser Val Val Ser Thr Asp Glu Lys Ala Glu Leu Ala
 165 170 175
 Leu Asp Ala Gly Ala Tyr Glu Val Phe Arg Tyr Ser Asp Asn Leu Ala
 180 185 190

Glu Gln Val Arg Arg His Asn Gly Gly Arg Gly Val Asp Val Val Tyr
 195 200 205
 Asp Gly Val Gly Gln Ser Thr Phe Asn Glu Ser Leu Glu Ala Val Arg
 210 215 220
 Pro Arg Gly Thr Val Cys Leu Phe Gly Ala Ala Ser Gly Pro Val Glu
 225 230 235 240
 Pro Phe Asp Pro Gln Leu Leu Asn Thr His Gly Ser Ile Phe Leu Thr
 245 250 255
 Arg Pro Ser Ile Gly Ala Trp Thr Ser Glu Glu Gly Glu Phe Ala Lys
 260 265 270
 Arg Ala Gln Ala Val Thr Gln Ala Ile Val Glu Gly Thr Leu Arg Val
 275 280 285
 Arg Val Thr Gly Thr Tyr Ser Leu Ala Asp Ala Tyr Ile Ala His Arg
 290 295 300
 Asp Leu Gln Ala Arg Ser Thr Ser Gly Ser Leu Val Leu Glu Ile Pro
 305 310 315 320
 Lys Asp

<210> 707
 <211> 990
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(967)
 <223> RXN02560

<400> 707
 ttggggcaag ccagctaacg catttcttgt ggaaaccgca gacattgagg ccgcccacgc 60
 ggaacttcta agagcagtggt aatgaaataa tccgggtgctg atg cag ggc aac tcg 115
 Met Gln Gly Asn Ser
 1 5
 ctt aat ctg gca gac aac agc gag aga aag aag ccc atg ccg tca cca 163
 Leu Asn Leu Ala Asp Asn Ser Glu Arg Lys Lys Pro Met Pro Ser Pro
 10 15 20
 gga gaa ctt tta gcc gcc cgc tac gga caa cct gca acc tgg acg cca 211
 Gly Glu Leu Leu Ala Ala Arg Tyr Gly Gln Pro Ala Thr Trp Thr Pro
 25 30 35
 ccg cag tgg aat gag acg ctt gat gtc att cac cag cat cga tca gtt 259
 Pro Gln Trp Asn Glu Thr Leu Asp Val Ile His Gln His Arg Ser Val
 40 45 50
 cgc agg tgg ttg gat aaa ccg gtt gat gat gac acc atc cgc acc att 307
 Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp Thr Ile Arg Thr Ile
 55 60 65

```

att tcc gcc gca caa tcg gct gga acc tct tcc aat aag cag gtc att 355
Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser Asn Lys Gln Val Ile
70 75 80 85

tct gtc atc gtg gtt aaa gat cct gag ctg agg aaa ggc ctc gcg ggg 403
Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg Lys Gly Leu Ala Gly
90 95 100

atc act cgc cag atg ttt ccg cac ctt gag cag gtt ccc gcg gtg ctg 451
Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln Val Pro Ala Val Leu
105 110 115

att tgg ttg att gat tat tcc cga atc agt gcg gtg gca gcc aga gaa 499
Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala Val Ala Ala Arg Glu
120 125 130

gat ctc cca aca ggg gct ctt gat tat ctc gat gag gcc gcg tgg ggg 547
Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp Glu Ala Ala Trp Gly
135 140 145

ttc ctc gac gcc gga atc gca gct caa aac gct gca att gct gcg gag 595
Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala Ala Ile Ala Ala Glu
150 155 160 165

tca ctt gga ttg gga acg ctc tat ttg ggt tcg gtg cgc aac gat gcg 643
Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser Val Arg Asn Asp Ala
170 175 180

gaa gcc gtg cac aaa ttg ctt ggc ctt cca cct gag atc gtg cct gtc 691
Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro Glu Ile Val Pro Val
185 190 195

gtg ggc ttg gaa atg ggg cat gcg gat ccg cct gaa cct gcc gga att 739
Val Gly Leu Glu Met Gly His Ala Asp Pro Pro Glu Pro Ala Gly Ile
200 205 210

aaa cct ccc ctg cca caa gaa gcc att gtt cac tgg gat acc tac acc 787
Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His Trp Asp Thr Tyr Thr
215 220 225

gag aaa aac ctc gaa ctt atc gat tcc tac gac cgc gcc ctc gac act 835
Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp Arg Ala Leu Asp Thr
230 235 240 245

tac tat tct cgc tac ggc cag cac cag ctc tgg tcg aag cag acg gcg 883
Tyr Tyr Ser Arg Tyr Gly Gln His Gln Leu Trp Ser Lys Gln Thr Ala
250 255 260

cat agg gcg gcg tcg aaa agc ttt tca aaa acc aac agg cag ttc ctt 931
His Arg Ala Ala Ser Lys Ser Phe Ser Lys Thr Asn Arg Gln Phe Leu
265 270 275

agg ggc gtg ttt gag cgc gcc ggg ttt ggg ctg aga taaaagcatg 977
Arg Gly Val Phe Glu Arg Ala Gly Phe Gly Leu Arg
280 285

attatggacg cct 990

```

<210> 708

<211> 289

<212> PRT

<213> Corynebacterium glutamicum

<400> 708

```

Met Gln Gly Asn Ser Leu Asn Leu Ala Asp Asn Ser Glu Arg Lys Lys
  1              5              10              15

Pro Met Pro Ser Pro Gly Glu Leu Leu Ala Ala Arg Tyr Gly Gln Pro
          20              25              30

Ala Thr Trp Thr Pro Pro Gln Trp Asn Glu Thr Leu Asp Val Ile His
          35              40              45

Gln His Arg Ser Val Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp
          50              55              60

Thr Ile Arg Thr Ile Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser
          65              70              75              80

Asn Lys Gln Val Ile Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg
          85              90              95

Lys Gly Leu Ala Gly Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln
          100              105              110

Val Pro Ala Val Leu Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala
          115              120              125

Val Ala Ala Arg Glu Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp
          130              135              140

Glu Ala Ala Trp Gly Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala
          145              150              155              160

Ala Ile Ala Ala Glu Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser
          165              170              175

Val Arg Asn Asp Ala Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro
          180              185              190

Glu Ile Val Pro Val Val Gly Leu Glu Met Gly His Ala Asp Pro Pro
          195              200              205

Glu Pro Ala Gly Ile Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His
          210              215              220

Trp Asp Thr Tyr Thr Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp
          225              230              235              240

Arg Ala Leu Asp Thr Tyr Tyr Ser Arg Tyr Gly Gln His Gln Leu Trp
          245              250              255

Ser Lys Gln Thr Ala His Arg Ala Ala Ser Lys Ser Phe Ser Lys Thr
          260              265              270

Asn Arg Gln Phe Leu Arg Gly Val Phe Glu Arg Ala Gly Phe Gly Leu
          275              280              285

```

Arg

gaa gcc gtg cac aaa ttg ctt ggc ctt cca cct gag atc gtg cct gtc 691
 Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro Glu Ile Val Pro Val
 185 190 195

gtg ggc ttg gaa atg ggg cat gcg gat ccg cct gaa cct gcc gga att 739
 Val Gly Leu Glu Met Gly His Ala Asp Pro Pro Glu Pro Ala Gly Ile
 200 205 210

aaa cct ccc ctg cca caa gaa gcc att gtt cac tgg gat acc tac acc 787
 Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His Trp Asp Thr Tyr Thr
 215 220 225

gag aaa aac ctc gaa ctt atc gat tcc tac gac cgc gcc ctc gac act 835
 Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp Arg Ala Leu Asp Thr
 230 235 240 245

tac tat tct cgc tac ggc cag cac cag ctc tgg tcg aag cag acg gcg 883
 Tyr Tyr Ser Arg Tyr Gly Gln His Gln Leu Trp Ser Lys Gln Thr Ala
 250 255 260

cat agg gcg gcg tct aaa cgc tgt tac aag aac caa gaa 922
 His Arg Ala Ala Ser Lys Arg Cys Tyr Lys Asn Gln Glu
 265 270

<210> 710

<211> 274

<212> PRT

<213> Corynebacterium glutamicum

<400> 710

Met Gln Gly Asn Ser Leu Asn Leu Ala Asp Asn Ser Glu Arg Lys Lys
 1 5 10 15

Pro Met Pro Ser Pro Gly Glu Leu Leu Ala Ala Arg Tyr Gly Gln Pro
 20 25 30

Ala Thr Trp Thr Pro Pro Gln Trp Asn Glu Thr Leu Asp Val Ile His
 35 40 45

Gln His Arg Ser Val Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp
 50 55 60

Thr Ile Arg Thr Ile Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser
 65 70 75 80

Asn Lys Gln Val Ile Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg
 85 90 95

Lys Gly Leu Ala Gly Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln
 100 105 110

Val Pro Ala Val Leu Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala
 115 120 125

Val Ala Ala Arg Glu Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp
 130 135 140

Glu Ala Ala Trp Gly Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala
 145 150 155 160

Ala Ile Ala Ala Glu Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser
 165 170 175

Val Arg Asn Asp Ala Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro
 180 185 190

Glu Ile Val Pro Val Val Gly Leu Glu Met Gly His Ala Asp Pro Pro
 195 200 205

Glu Pro Ala Gly Ile Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His
 210 215 220

Trp Asp Thr Tyr Thr Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp
 225 230 235 240

Arg Ala Leu Asp Thr Tyr Tyr Ser Arg Tyr Gly Gln His Gln Leu Trp
 245 250 255

Ser Lys Gln Thr Ala His Arg Ala Ala Ser Lys Arg Cys Tyr Lys Asn
 260 265 270

Gln Glu

<210> 711
 <211> 870
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(847)
 <223> RXA01311

<400> 711
 tcgtctccgc atgggaacca ggcgagaatg gaaccttcgt ctgccacgca gaaccactgt 60

tcttcgaatc tgtcccactg cagacaagga actacaagta atg aaa ctt aca ctt 115
 Met Lys Leu Thr Leu
 1 5

gag atc tgg cgt caa gca ggc cca act gcg gaa ggc aag ttc gaa acc 163
 Glu Ile Trp Arg Gln Ala Gly Pro Thr Ala Glu Gly Lys Phe Glu Thr
 10 15 20

gtc cag gtt gac gac gcc gtc gcg cag atg tcc atc ctg gag ctg ctt 211
 Val Gln Val Asp Asp Ala Val Ala Gln Met Ser Ile Leu Glu Leu Leu
 25 30 35

gac cac gta aac aac aag ttc atc gaa gaa ggc aaa gaa cca ttc gcg 259
 Asp His Val Asn Asn Lys Phe Ile Glu Glu Gly Lys Glu Pro Phe Ala
 40 45 50

ttc gcc tct gac tgc cgc gaa ggc att tgt ggt acc tgt ggt ctc ctc 307
 Phe Ala Ser Asp Cys Arg Glu Gly Ile Cys Gly Thr Cys Gly Leu Leu
 55 60 65

gtg aac ggt cgc cct cac ggc gcc gac cag aac aag cct gcc tgt gcg 355
 Val Asn Gly Arg Pro His Gly Ala Asp Gln Asn Lys Pro Ala Cys Ala

70	75	80	85	
cag cgc ctg gtc agc tac aag gaa ggc gac acc ctc aag atc gaa cca				403
Gln Arg Leu Val Ser Tyr Lys Glu Gly Asp Thr Leu Lys Ile Glu Pro				
	90	95	100	
ctg cgt tcc gcc gca tac cca gtg atc aag gac atg gtc gtc gac cgc				451
Leu Arg Ser Ala Ala Tyr Pro Val Ile Lys Asp Met Val Val Asp Arg				
	105	110	115	
tcc gca ctg gac cgt gtc atg gaa cag ggt ggc tac gtg acc atc aac				499
Ser Ala Leu Asp Arg Val Met Glu Gln Gly Gly Tyr Val Thr Ile Asn				
	120	125	130	
gca ggt acc gca cct gac gct gat acc ctc cac gtc aac cac gaa acc				547
Ala Gly Thr Ala Pro Asp Ala Asp Thr Leu His Val Asn His Glu Thr				
	135	140	145	
gca gaa ctc gca ctt gac cac gca gcc tgc atc ggc tgt ggc gca tgt				595
Ala Glu Leu Ala Leu Asp His Ala Ala Cys Ile Gly Cys Gly Ala Cys				
	150	155	160	165
gtt gct gcc tgc cct aac ggc gca gca cac ctg ttc acc ggc gca aag				643
Val Ala Ala Cys Pro Asn Gly Ala Ala His Leu Phe Thr Gly Ala Lys				
	170	175	180	
ctt gtt cac ctc tcc ctc ctc cca ctg ggt aag gaa gag cgc gga ctg				691
Leu Val His Leu Ser Leu Leu Pro Leu Gly Lys Glu Glu Arg Gly Leu				
	185	190	195	
cgt gca cgt aag atg gtt gat gaa atg gaa acc aac ttc gga cac tgc				739
Arg Ala Arg Lys Met Val Asp Glu Met Glu Thr Asn Phe Gly His Cys				
	200	205	210	
tcc ctc tac ggc gag tgc gca gat gtc tgc ccc gca ggc atc cca ctg				787
Ser Leu Tyr Gly Glu Cys Ala Asp Val Cys Pro Ala Gly Ile Pro Leu				
	215	220	225	
acc gct gtg gca gct gtc acc aag gaa cgt gcg cgt gca gct ttc cga				835
Thr Ala Val Ala Ala Val Thr Lys Glu Arg Ala Arg Ala Ala Phe Arg				
	230	235	240	245
ggc aaa gac gac tagtctttaa tccaagtaag tac				870
Gly Lys Asp Asp				

<210> 712

<211> 249

<212> PRT

<213> Corynebacterium glutamicum

<400> 712

Met Lys Leu Thr Leu Glu Ile Trp Arg Gln Ala Gly Pro Thr Ala Glu
1 5 10 15

Gly Lys Phe Glu Thr Val Gln Val Asp Asp Ala Val Ala Gln Met Ser
20 25 30

Ile Leu Glu Leu Leu Asp His Val Asn Asn Lys Phe Ile Glu Glu Gly
35 40 45

Lys Glu Pro Phe Ala Phe Ala Ser Asp Cys Arg Glu Gly Ile Cys Gly
 50 55 60
 Thr Cys Gly Leu Leu Val Asn Gly Arg Pro His Gly Ala Asp Gln Asn
 65 70 75 80
 Lys Pro Ala Cys Ala Gln Arg Leu Val Ser Tyr Lys Glu Gly Asp Thr
 85 90 95
 Leu Lys Ile Glu Pro Leu Arg Ser Ala Ala Tyr Pro Val Ile Lys Asp
 100 105 110
 Met Val Val Asp Arg Ser Ala Leu Asp Arg Val Met Glu Gln Gly Gly
 115 120 125
 Tyr Val Thr Ile Asn Ala Gly Thr Ala Pro Asp Ala Asp Thr Leu His
 130 135 140
 Val Asn His Glu Thr Ala Glu Leu Ala Leu Asp His Ala Ala Cys Ile
 145 150 155 160
 Gly Cys Gly Ala Cys Val Ala Ala Cys Pro Asn Gly Ala Ala His Leu
 165 170 175
 Phe Thr Gly Ala Lys Leu Val His Leu Ser Leu Leu Pro Leu Gly Lys
 180 185 190
 Glu Glu Arg Gly Leu Arg Ala Arg Lys Met Val Asp Glu Met Glu Thr
 195 200 205
 Asn Phe Gly His Cys Ser Leu Tyr Gly Glu Cys Ala Asp Val Cys Pro
 210 215 220
 Ala Gly Ile Pro Leu Thr Ala Val Ala Ala Val Thr Lys Glu Arg Ala
 225 230 235 240
 Arg Ala Ala Phe Arg Gly Lys Asp Asp
 245

<210> 713
 <211> 929
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(906)
 <223> RXN03014

<400> 713
 tac gtt ggt ttc gaa gtg ctg ctg gtg gcg tca tac gtg ctg ctc acc 48
 Tyr Val Gly Phe Glu Val Leu Leu Val Ala Ser Tyr Val Leu Leu Thr
 1 5 10 15
 ttg ggt gca tcg ccg gca cgt gta cgt tcc ggc gtg ggt tac gtg atg 96
 Leu Gly Ala Ser Pro Ala Arg Val Arg Ser Gly Val Gly Tyr Val Met
 20 25 30
 gtg tcc atg gcg tca tcg atg gtg ttc ctg ttt gga ctc gca atg gtt 144

Val	Ser	Met	Ala	Ser	Ser	Met	Val	Phe	Leu	Phe	Gly	Leu	Ala	Met	Val	
		35					40					45				
tac	gcc	tca	gtg	ggc	acg	ttg	aac	atg	gct	cac	gtt	ggc	cta	cgc	atg	192
Tyr	Ala	Ser	Val	Gly	Thr	Leu	Asn	Met	Ala	His	Val	Gly	Leu	Arg	Met	
	50					55					60					
gaa	gat	gtt	ccg	tct	gga	act	cgc	tcc	gcg	atc	ttc	gca	gtg	ttg	ctc	240
Glu	Asp	Val	Pro	Ser	Gly	Thr	Arg	Ser	Ala	Ile	Phe	Ala	Val	Leu	Leu	
65					70					75					80	
gtg	gca	ttc	ggg	att	aaa	gct	gcc	gtg	ttc	ccc	cta	gat	tcc	tgg	ctg	288
Val	Ala	Phe	Gly	Ile	Lys	Ala	Ala	Val	Phe	Pro	Leu	Asp	Ser	Trp	Leu	
				85					90					95		
ccg	gac	tcc	tac	ccc	acc	gcg	cca	tcg	ctg	gtc	acc	gcg	gtg	ttc	gca	336
Pro	Asp	Ser	Tyr	Pro	Thr	Ala	Pro	Ser	Leu	Val	Thr	Ala	Val	Phe	Ala	
			100					105					110			
ggg	ctg	ttg	acc	aag	gtg	ggg	gtg	tat	tcc	atc	att	cga	gca	cgc	tcg	384
Gly	Leu	Leu	Thr	Lys	Val	Gly	Val	Tyr	Ser	Ile	Ile	Arg	Ala	Arg	Ser	
	115					120						125				
att	att	ttc	acc	gat	gga	tcc	ctt	gac	acc	atg	ctg	atg	tgg	gtg	gca	432
Ile	Ile	Phe	Thr	Asp	Gly	Ser	Leu	Asp	Thr	Met	Leu	Met	Trp	Val	Ala	
	130					135					140					
ctc	gcc	acc	atg	ctc	att	ggg	att	ttg	ggc	gcg	atg	gcg	caa	aac	gat	480
Leu	Ala	Thr	Met	Leu	Ile	Gly	Ile	Leu	Gly	Ala	Met	Ala	Gln	Asn	Asp	
145					150				155						160	
atc	aaa	cgt	ttg	ttg	tca	ttt	act	ctg	gtc	agc	cac	atc	ggc	tac	atg	528
Ile	Lys	Arg	Leu	Leu	Ser	Phe	Thr	Leu	Val	Ser	His	Ile	Gly	Tyr	Met	
				165				170						175		
atc	ttc	ggc	gta	gcc	ctt	gga	tct	gca	cag	ggg	ttg	tct	ggg	gcg	atc	576
Ile	Phe	Gly	Val	Ala	Leu	Gly	Ser	Ala	Gln	Gly	Leu	Ser	Gly	Ala	Ile	
			180					185					190			
ttc	tac	gca	atc	cac	cac	att	ctg	gtt	cag	act	tcc	ctg	ttc	ctg	gtg	624
Phe	Tyr	Ala	Ile	His	His	Ile	Leu	Val	Gln	Thr	Ser	Leu	Phe	Leu	Val	
		195				200						205				
gtc	ggg	ctg	gtg	gaa	cgc	caa	gcc	gga	tcc	tcc	tcg	ctg	cga	cgc	ctt	672
Val	Gly	Leu	Val	Glu	Arg	Gln	Ala	Gly	Ser	Ser	Ser	Leu	Arg	Arg	Leu	
	210					215					220					
gga	tcc	ctg	gca	tat	atc	tcc	cca	ctt	ctt	gcg	att	ttg	tac	ttc	atc	720
Gly	Ser	Leu	Ala	Tyr	Ile	Ser	Pro	Leu	Leu	Ala	Ile	Leu	Tyr	Phe	Ile	
225					230					235					240	
ccc	gcc	atc	aac	ctg	ggg	ggg	atc	cca	ccg	ttc	tcc	ggc	ttc	ctg	ggc	768
Pro	Ala	Ile	Asn	Leu	Gly	Gly	Ile	Pro	Pro	Phe	Ser	Gly	Phe	Leu	Gly	
				245				250						255		
aag	atc	atg	ctc	atc	gaa	gcc	ggc	gcc	cga	aga	tgg	cag	ttg	gct	ggc	816
Lys	Ile	Met	Leu	Ile	Glu	Ala	Gly	Ala	Arg	Arg	Trp	Gln	Leu	Ala	Gly	
			260					265					270			
atg	ggg	cct	tat	cgc	agg	cgc	cgt	tgt	cac	ctc	act	gct	cac	ctt	gta	864
Met	Gly	Pro	Tyr	Arg	Arg	Arg	Arg	Cys	His	Leu	Thr	Ala	His	Leu	Val	

275

280

285

.. cac cat ggt tct ggt ctg gtc caa ggc ctt ctg gcg cga ccg 906
 His His Gly Ser Gly Leu Val Gln Gly Leu Leu Ala Arg Pro
 290 295 300

taaagacgcc cccgatggag caa 929

<210> 714

<211> 302

<212> PRT

<213> Corynebacterium glutamicum

<400> 714

Tyr Val Gly Phe Glu Val Leu Leu Val Ala Ser Tyr Val Leu Leu Thr
 1 5 10 15

Leu Gly Ala Ser Pro Ala Arg Val Arg Ser Gly Val Gly Tyr Val Met
 20 25 30

Val Ser Met Ala Ser Ser Met Val Phe Leu Phe Gly Leu Ala Met Val
 35 40 45

Tyr Ala Ser Val Gly Thr Leu Asn Met Ala His Val Gly Leu Arg Met
 50 55 60

Glu Asp Val Pro Ser Gly Thr Arg Ser Ala Ile Phe Ala Val Leu Leu
 65 70 75 80

Val Ala Phe Gly Ile Lys Ala Ala Val Phe Pro Leu Asp Ser Trp Leu
 85 90 95

Pro Asp Ser Tyr Pro Thr Ala Pro Ser Leu Val Thr Ala Val Phe Ala
 100 105 110

Gly Leu Leu Thr Lys Val Gly Val Tyr Ser Ile Ile Arg Ala Arg Ser
 115 120 125

Ile Ile Phe Thr Asp Gly Ser Leu Asp Thr Met Leu Met Trp Val Ala
 130 135 140

Leu Ala Thr Met Leu Ile Gly Ile Leu Gly Ala Met Ala Gln Asn Asp
 145 150 155 160

Ile Lys Arg Leu Leu Ser Phe Thr Leu Val Ser His Ile Gly Tyr Met
 165 170 175

Ile Phe Gly Val Ala Leu Gly Ser Ala Gln Gly Leu Ser Gly Ala Ile
 180 185 190

Phe Tyr Ala Ile His His Ile Leu Val Gln Thr Ser Leu Phe Leu Val
 195 200 205

Val Gly Leu Val Glu Arg Gln Ala Gly Ser Ser Ser Leu Arg Arg Leu
 210 215 220

Gly Ser Leu Ala Tyr Ile Ser Pro Leu Leu Ala Ile Leu Tyr Phe Ile
 225 230 235 240

Pro Ala Ile Asn Leu Gly Gly Ile Pro Pro Phe Ser Gly Phe Leu Gly

145	150	155	160	
atc aaa cgt ttg ttg tca ttt act ctg gtc agc cac atc ggc tac atg Ile Lys Arg Leu Leu Ser Phe Thr Leu Val Ser His Ile Gly Tyr Met	165	170	175	528
atc ttc ggc gta gcc ctt gga tct gca cag ggt ttg tct ggt gcg atc Ile Phe Gly Val Ala Leu Gly Ser Ala Gln Gly Leu Ser Gly Ala Ile	180	185	190	576
ttc tac gca atc cac cac att ctg gtt cag act tcc ctg ttc ctg gtg Phe Tyr Ala Ile His His Ile Leu Val Gln Thr Ser Leu Phe Leu Val	195	200	205	624
gtc ggt ctg gtg gaa cgc caa gcc gga tcc tcc tcg ctg cga cgc ctt Val Gly Leu Val Glu Arg Gln Ala Gly Ser Ser Ser Leu Arg Arg Leu	210	215	220	672
gga tcc ctg gca tat atc tcc cca ctt ctt gcg att ttg tac ttc atc Gly Ser Leu Ala Tyr Ile Ser Pro Leu Leu Ala Ile Leu Tyr Phe Ile	225	230	235	720
ccc gcc atc aac ctg ggt ggt atc cca ccg ttc tcc ggc ttc ctg ggc Pro Ala Ile Asn Leu Gly Gly Ile Pro Pro Phe Ser Gly Phe Leu Gly	245	250	255	768
aag atc atg ctc atc gaa gcc ggc gcc gaa gat ggc agt tgg ctg gca Lys Ile Met Leu Ile Glu Ala Gly Ala Glu Asp Gly Ser Trp Leu Ala	260	265	270	816
tgg gtc ctt atc gca ggc gcc gtt gtc acc tca ctg ctc acc ttg tac Trp Val Leu Ile Ala Gly Ala Val Val Thr Ser Leu Leu Thr Leu Tyr	275	280	285	864
acc atg gtt ctg gtc tgg tcc aag gcc ttc tgg cgc gac cgt aaa gac Thr Met Val Leu Val Trp Ser Lys Ala Phe Trp Arg Asp Arg Lys Asp	290	295	300	912
gcc ccc gat gga gca acc gca ctt gcg cga ccc gca cct ttg gta gat Ala Pro Asp Gly Ala Thr Ala Leu Ala Arg Pro Ala Pro Leu Val Asp	305	310	315	960
gtc caa gac gaa gtc gcc gtt aaa gac cgc aac gat gtc gga cgg atg Val Gln Asp Glu Val Ala Val Lys Asp Arg Asn Asp Val Gly Arg Met	325	330	335	1008
cct tgg ggc atg gtc ttc tcc act gct ctc ctg gtt tca gca tct ctt Pro Trp Gly Met Val Phe Ser Thr Ala Leu Leu Val Ser Ala Ser Leu	340	345	350	1056
gct gta tcc gtg ctc gca gga cca ctg tca tct att act gga cgc gcc Ala Val Ser Val Leu Ala Gly Pro Leu Ser Ser Ile Thr Gly Arg Ala	355	360	365	1104
gcc gaa tcc gca caa gat gtc aac atc tac cgc gcc gca gta ctc ggc Ala Glu Ser Ala Gln Asp Val Asn Ile Tyr Arg Ala Ala Val Leu Gly	370	375	380	1152
ccc aac tac ctc gac cca tca cgc aca ctc gag atg gag cgt tac gac Pro Asn Tyr Leu Asp Pro Ser Arg Thr Leu Glu Met Glu Arg Tyr Asp	385	390	395	1200
			400	

	245		250		255
Lys Ile Met	Leu Ile Glu Ala Gly	Ala Arg Arg Trp Gln	Leu Ala Gly		
	260	265	270		
Met Gly Pro Tyr Arg Arg Arg	Arg Cys His Leu Thr	Ala His Leu Val			
	275	280	285		
His His Gly Ser Gly Leu Val	Gln Gly Leu Leu	Ala Arg Pro			
	290	295	300		

<210> 715

<211> 1280

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1257)

<223> FRXA00910

<400> 715

tac gtt ggt ttc gaa gtg ctg ctg gtg gcg tca tac gtg ctg ctc acc	48
Tyr Val Gly Phe Glu Val Leu Leu Val Ala Ser Tyr Val Leu Leu Thr	
1 5 10 15	
ttg ggt gca tgc ccg gca cgt gta cgt tcc ggc gtg ggt tac gtg atg	96
Leu Gly Ala Ser Pro Ala Arg Val Arg Ser Gly Val Gly Tyr Val Met	
20 25 30	
gtg tcc atg gcg tca tgc atg gtg ttc ctg ttt gga ctc gca atg gtt	144
Val Ser Met Ala Ser Ser Met Val Phe Leu Phe Gly Leu Ala Met Val	
35 40 45	
tac gcc tca gtg ggc acg ttg aac atg gct cac gtt ggc cta cgc atg	192
Tyr Ala Ser Val Gly Thr Leu Asn Met Ala His Val Gly Leu Arg Met	
50 55 60	
gaa gat gtt ccg tct gga act cgc tcc gcg atc ttc gca gtg ttg ctc	240
Glu Asp Val Pro Ser Gly Thr Arg Ser Ala Ile Phe Ala Val Leu Leu	
65 70 75 80	
gtg gca ttc ggt att aaa gct gcc gtg ttc ccc cta gat tcc tgg ctg	288
Val Ala Phe Gly Ile Lys Ala Ala Val Phe Pro Leu Asp Ser Trp Leu	
85 90 95	
ccg gac tcc tac ccc acc gcg cca tgc ctg gtc acc gcg gtg ttc gca	336
Pro Asp Ser Tyr Pro Thr Ala Pro Ser Leu Val Thr Ala Val Phe Ala	
100 105 110	
ggt ctg ttg acc aag gtg ggt gtg tat tcc atc att cga gca cgc tgc	384
Gly Leu Leu Thr Lys Val Gly Val Tyr Ser Ile Ile Arg Ala Arg Ser	
115 120 125	
att att ttc acc gat gga tcc ctt gac acc atg ctg atg tgg gtg gca	432
Ile Ile Phe Thr Asp Gly Ser Leu Asp Thr Met Leu Met Trp Val Ala	
130 135 140	
ctc gcc acc atg ctc att ggt att ttg ggc gcg atg gcg caa aac gat	480
Leu Ala Thr Met Leu Ile Gly Ile Leu Gly Ala Met Ala Gln Asn Asp	

gcc aac cgc gat gac atc aac cac cgc gtc gac acc aac gga acg gag 1248
 Ala Asn Arg Asp Asp Ile Asn His Arg Val Asp Thr Asn Gly Thr Glu
 405 410 415

gac caa cca tgatcagtgg attcaaacga cga 1280
 Asp Gln Pro

<210> 716

<211> 419

<212> PRT

<213> Corynebacterium glutamicum

<400> 716

Tyr Val Gly Phe Glu Val Leu Leu Val Ala Ser Tyr Val Leu Leu Thr
 1 5 10 15

Leu Gly Ala Ser Pro Ala Arg Val Arg Ser Gly Val Gly Tyr Val Met
 20 25 30

Val Ser Met Ala Ser Ser Met Val Phe Leu Phe Gly Leu Ala Met Val
 35 40 45

Tyr Ala Ser Val Gly Thr Leu Asn Met Ala His Val Gly Leu Arg Met
 50 55 60

Glu Asp Val Pro Ser Gly Thr Arg Ser Ala Ile Phe Ala Val Leu Leu
 65 70 75 80

Val Ala Phe Gly Ile Lys Ala Ala Val Phe Pro Leu Asp Ser Trp Leu
 85 90 95

Pro Asp Ser Tyr Pro Thr Ala Pro Ser Leu Val Thr Ala Val Phe Ala
 100 105 110

Gly Leu Leu Thr Lys Val Gly Val Tyr Ser Ile Ile Arg Ala Arg Ser
 115 120 125

Ile Ile Phe Thr Asp Gly Ser Leu Asp Thr Met Leu Met Trp Val Ala
 130 135 140

Leu Ala Thr Met Leu Ile Gly Ile Leu Gly Ala Met Ala Gln Asn Asp
 145 150 155 160

Ile Lys Arg Leu Leu Ser Phe Thr Leu Val Ser His Ile Gly Tyr Met
 165 170 175

Ile Phe Gly Val Ala Leu Gly Ser Ala Gln Gly Leu Ser Gly Ala Ile
 180 185 190

Phe Tyr Ala Ile His His Ile Leu Val Gln Thr Ser Leu Phe Leu Val
 195 200 205

Val Gly Leu Val Glu Arg Gln Ala Gly Ser Ser Ser Leu Arg Arg Leu
 210 215 220

Gly Ser Leu Ala Tyr Ile Ser Pro Leu Leu Ala Ile Leu Tyr Phe Ile
 225 230 235 240

Pro Ala Ile Asn Leu Gly Gly Ile Pro Pro Phe Ser Gly Phe Leu Gly
 245 250 255

Lys Ile Met Leu Ile Glu Ala Gly Ala Glu Asp Gly Ser Trp Leu Ala
 260 265 270

Trp Val Leu Ile Ala Gly Ala Val Val Thr Ser Leu Leu Thr Leu Tyr
 275 280 285

Thr Met Val Leu Val Trp Ser Lys Ala Phe Trp Arg Asp Arg Lys Asp
 290 295 300

Ala Pro Asp Gly Ala Thr Ala Leu Ala Arg Pro Ala Pro Leu Val Asp
 305 310 315 320

Val Gln Asp Glu Val Ala Val Lys Asp Arg Asn Asp Val Gly Arg Met
 325 330 335

Pro Trp Gly Met Val Phe Ser Thr Ala Leu Leu Val Ser Ala Ser Leu
 340 345 350

Ala Val Ser Val Leu Ala Gly Pro Leu Ser Ser Ile Thr Gly Arg Ala
 355 360 365

Ala Glu Ser Ala Gln Asp Val Asn Ile Tyr Arg Ala Ala Val Leu Gly
 370 375 380

Pro Asn Tyr Leu Asp Pro Ser Arg Thr Leu Glu Met Glu Arg Tyr Asp
 385 390 395 400

Ala Asn Arg Asp Asp Ile Asn His Arg Val Asp Thr Asn Gly Thr Glu
 405 410 415

Asp Gln Pro

<210> 717
 <211> 1051
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1051)
 <223> RXN01895

<400> 717
 cgcgtacacg tgctcaacac gacaacgctt aaacggctgc acgcgtaaca cggcagaccg 60

cacaagcttt aagatccacg atcaggagac ttgacaaat atg tca gtt aac cca 115
 Met Ser Val Asn Pro
 1 5

acc cgc ccc gaa ggc ggc cgt cac cac gtc gtc gtc atc ggt tct ggt 163
 Thr Arg Pro Glu Gly Gly Arg His His Val Val Val Ile Gly Ser Gly
 10 15 20

ttt ggt ggc ctt ttt gct gcc aag aac ctg gcc aag gca gac gtc gat 211
 Phe Gly Gly Leu Phe Ala Ala Lys Asn Leu Ala Lys Ala Asp Val Asp
 25 30 35

```

gtc act ctg att gac cgc acc aac cac cac ctc ttc cag cca ctg ctg 259
Val Thr Leu Ile Asp Arg Thr Asn His His Leu Phe Gln Pro Leu Leu
      40                      45                      50

tac caa gtg gca acc ggt atc ctc tcc tcc ggt gaa atc gca cct tcc 307
Tyr Gln Val Ala Thr Gly Ile Leu Ser Ser Gly Glu Ile Ala Pro Ser
      55                      60                      65

act cga cag atc ctg ggc tcc cag gaa aac gtc aac gtc atc aag ggc 355
Thr Arg Gln Ile Leu Gly Ser Gln Glu Asn Val Asn Val Ile Lys Gly
      70                      75                      80                      85

gaa gtc acc gac atc aac gtc gag tcc cag act gtg acc gcc tcc ctg 403
Glu Val Thr Asp Ile Asn Val Glu Ser Gln Thr Val Thr Ala Ser Leu
      90                      95                      100

ggc gag ttc acc cgc gtt ttt gag tac gat tcc ttg gtc gtt ggt gct 451
Gly Glu Phe Thr Arg Val Phe Glu Tyr Asp Ser Leu Val Val Gly Ala
      105                      110                      115

ggc gca ggt cag tcc tac ttc ggc aat gat cac ttc gct gag ttc gca 499
Gly Ala Gly Gln Ser Tyr Phe Gly Asn Asp His Phe Ala Glu Phe Ala
      120                      125                      130

cct ggc atg aag tcc atc gac gat gca ctg gag att cgt gca cgc atc 547
Pro Gly Met Lys Ser Ile Asp Asp Ala Leu Glu Ile Arg Ala Arg Ile
      135                      140                      145

atc ggt gct ttc gag cgc gct gag atc tgc gag gat cca gct gag cgc 595
Ile Gly Ala Phe Glu Arg Ala Glu Ile Cys Glu Asp Pro Ala Glu Arg
      150                      155                      160                      165

gaa cgc ctg ctc acc ttc gtc gtt gtt ggc gct ggc cca acc ggt gtt 643
Glu Arg Leu Leu Thr Phe Val Val Val Gly Ala Gly Pro Thr Gly Val
      170                      175                      180

gag ctt gct ggc cag ttg gct gag atg gct cac cgc acc ctt gct ggt 691
Glu Leu Ala Gly Gln Leu Ala Glu Met Ala His Arg Thr Leu Ala Gly
      185                      190                      195

gag tac aag aac ttc aac acc aac tcc gca aag atc atc ctg ctt gat 739
Glu Tyr Lys Asn Phe Asn Thr Asn Ser Ala Lys Ile Ile Leu Leu Asp
      200                      205                      210

ggt gct cca cag gtt ctt cct cca ttc ggt aag cgc cta ggc cgc aac 787
Gly Ala Pro Gln Val Leu Pro Pro Phe Gly Lys Arg Leu Gly Arg Asn
      215                      220                      225

gca cag cgc acc ctg gaa aag atg ggt gtc aac gtt cgc ctg aac gct 835
Ala Gln Arg Thr Leu Glu Lys Met Gly Val Asn Val Arg Leu Asn Ala
      230                      235                      240                      245

atg gtc acc aac gtt gac gct acc tcg gtc acc tac aag acc aag gac 883
Met Val Thr Asn Val Asp Ala Thr Ser Val Thr Tyr Lys Thr Lys Asp
      250                      255                      260

ggc gaa gag cac acc atc gaa tct ttc tgc aag att tgg tcc gct ggt 931
Gly Glu Glu His Thr Ile Glu Ser Phe Cys Lys Ile Trp Ser Ala Gly
      265                      270                      275

```

```

gtt gcg gca tcc cca ctg ggc aag ctc gtc gca gag cag acc ggt gtt 979
Val Ala Ala Ser Pro Leu Gly Lys Leu Val Ala Glu Gln Thr Gly Val
      280                      285                      290

gag acc gac cgc gca ggc cgc gtc atg gtt aac gat gac ctg tct gtt 1027
Glu Thr Asp Arg Ala Gly Arg Val Met Val Asn Asp Asp Leu Ser Val
      295                      300                      305

ggc gat cag aag aac gtc ttc gtt 1051
Gly Asp Gln Lys Asn Val Phe Val
310                      315

<210> 718
<211> 317
<212> PRT
<213> Corynebacterium glutamicum

<400> 718
Met Ser Val Asn Pro Thr Arg Pro Glu Gly Gly Arg His His Val Val
  1                      5                      10                      15

Val Ile Gly Ser Gly Phe Gly Gly Leu Phe Ala Ala Lys Asn Leu Ala
      20                      25                      30

Lys Ala Asp Val Asp Val Thr Leu Ile Asp Arg Thr Asn His His Leu
      35                      40                      45

Phe Gln Pro Leu Leu Tyr Gln Val Ala Thr Gly Ile Leu Ser Ser Gly
      50                      55                      60

Glu Ile Ala Pro Ser Thr Arg Gln Ile Leu Gly Ser Gln Glu Asn Val
      65                      70                      75                      80

Asn Val Ile Lys Gly Glu Val Thr Asp Ile Asn Val Glu Ser Gln Thr
      85                      90                      95

Val Thr Ala Ser Leu Gly Glu Phe Thr Arg Val Phe Glu Tyr Asp Ser
      100                      105                      110

Leu Val Val Gly Ala Gly Ala Gly Gln Ser Tyr Phe Gly Asn Asp His
      115                      120                      125

Phe Ala Glu Phe Ala Pro Gly Met Lys Ser Ile Asp Asp Ala Leu Glu
      130                      135                      140

Ile Arg Ala Arg Ile Ile Gly Ala Phe Glu Arg Ala Glu Ile Cys Glu
      145                      150                      155                      160

Asp Pro Ala Glu Arg Glu Arg Leu Leu Thr Phe Val Val Val Gly Ala
      165                      170                      175

Gly Pro Thr Gly Val Glu Leu Ala Gly Gln Leu Ala Glu Met Ala His
      180                      185                      190

Arg Thr Leu Ala Gly Glu Tyr Lys Asn Phe Asn Thr Asn Ser Ala Lys
      195                      200                      205

Ile Ile Leu Leu Asp Gly Ala Pro Gln Val Leu Pro Pro Phe Gly Lys
      210                      215                      220

```

Arg Leu Gly Arg Asn Ala Gln Arg Thr Leu Glu Lys Met Gly Val Asn
 225 230 235 240

Val Arg Leu Asn Ala Met Val Thr Asn Val Asp Ala Thr Ser Val Thr
 245 250 255

Tyr Lys Thr Lys Asp Gly Glu Glu His Thr Ile Glu Ser Phe Cys Lys
 260 265 270

Ile Trp Ser Ala Gly Val Ala Ala Ser Pro Leu Gly Lys Leu Val Ala
 275 280 285

Glu Gln Thr Gly Val Glu Thr Asp Arg Ala Gly Arg Val Met Val Asn
 290 295 300

Asp Asp Leu Ser Val Gly Asp Gln Lys Asn Val Phe Val
 305 310 315

<210> 719

<211> 816

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(816)

<223> FRXA01895

<400> 719

cac cac ctc ttc cag cca ctg ctg tac caa gtg gca acc ggt atc ctc 48
 His His Leu Phe Gln Pro Leu Leu Tyr Gln Val Ala Thr Gly Ile Leu
 1 5 10 15

tcc tcc ggt gaa atc gca cct tcc act cga cag atc ctg ggc tcc cag 96
 Ser Ser Gly Glu Ile Ala Pro Ser Thr Arg Gln Ile Leu Gly Ser Gln
 20 25 30

gaa aac gtc aac gtc atc aag ggc gaa gtc acc gac atc aac gtc gag 144
 Glu Asn Val Asn Val Ile Lys Gly Glu Val Thr Asp Ile Asn Val Glu
 35 40 45

tcc cag act gtg acc gcc tcc ctg ggc gag ttc acc cgc gtt ttt gag 192
 Ser Gln Thr Val Thr Ala Ser Leu Gly Glu Phe Thr Arg Val Phe Glu
 50 55 60

tac gat tcc ttg gtc gtt ggt gct ggc gca ggt cag tcc tac ttc ggc 240
 Tyr Asp Ser Leu Val Val Gly Ala Gly Ala Gly Gln Ser Tyr Phe Gly
 65 70 75 80

aat gat cac ttc gct gag ttc gca cct ggc atg aag tcc atc gac gat 288
 Asn Asp His Phe Ala Glu Phe Ala Pro Gly Met Lys Ser Ile Asp Asp
 85 90 95

gca ctg gag att cgt gca cgc atc atc ggt gct ttc gag cgc gct gag 336
 Ala Leu Glu Ile Arg Ala Arg Ile Ile Gly Ala Phe Glu Arg Ala Glu
 100 105 110

atc tgc gag gat cca gct gag cgc gaa cgc ctg ctc acc ttc gtc gtt 384
 Ile Cys Glu Asp Pro Ala Glu Arg Glu Arg Leu Leu Thr Phe Val Val
 115 120 125

```

gtt ggc gct ggc cca acc ggt gtt gag ctt gct ggc cag ttg gct gag 432
Val Gly Ala Gly Pro Thr Gly Val Glu Leu Ala Gly Gln Leu Ala Glu
130 135 140

atg gct cac cgc acc ctt gct ggt gag tac aag aac ttc aac acc aac 480
Met Ala His Arg Thr Leu Ala Gly Glu Tyr Lys Asn Phe Asn Thr Asn
145 150 155 160

tcc gca aag atc atc ctg ctt gat ggt gct cca cag gtt ctt cct cca 528
Ser Ala Lys Ile Ile Leu Leu Asp Gly Ala Pro Gln Val Leu Pro Pro
165 170 175

ttc ggt aag cgc cta ggc cgc aac gca cag cgc acc ctg gaa aag atg 576
Phe Gly Lys Arg Leu Gly Arg Asn Ala Gln Arg Thr Leu Glu Lys Met
180 185 190

ggg gtc aac gtt cgc ctg aac gct atg gtc acc aac gtt gac gct acc 624
Gly Val Asn Val Arg Leu Asn Ala Met Val Thr Asn Val Asp Ala Thr
195 200 205

tcg gtc acc tac aag acc aag gac ggc gaa gag cac acc atc gaa tct 672
Ser Val Thr Tyr Lys Thr Lys Asp Gly Glu Glu His Thr Ile Glu Ser
210 215 220

ttc tgc aag att tgg tcc gct ggt gtt gcg gca tcc cca ctg ggc aag 720
Phe Cys Lys Ile Trp Ser Ala Gly Val Ala Ala Ser Pro Leu Gly Lys
225 230 235 240

ctc gtc gca gag cag acc ggt gtt gag acc gac cgc gca ggc cgc gtc 768
Leu Val Ala Glu Gln Thr Gly Val Glu Thr Asp Arg Ala Gly Arg Val
245 250 255

atg gtt aac gat gac ctg tct gtt ggc gat cag aag aac gtc ttc gtt 816
Met Val Asn Asp Asp Leu Ser Val Gly Asp Gln Lys Asn Val Phe Val
260 265 270

```

<210> 720

<211> 272

<212> PRT

<213> Corynebacterium glutamicum

<400> 720

```

His His Leu Phe Gln Pro Leu Leu Tyr Gln Val Ala Thr Gly Ile Leu
1 5 10 15

Ser Ser Gly Glu Ile Ala Pro Ser Thr Arg Gln Ile Leu Gly Ser Gln
20 25 30

Glu Asn Val Asn Val Ile Lys Gly Glu Val Thr Asp Ile Asn Val Glu
35 40 45

Ser Gln Thr Val Thr Ala Ser Leu Gly Glu Phe Thr Arg Val Phe Glu
50 55 60

Tyr Asp Ser Leu Val Val Gly Ala Gly Ala Gly Gln Ser Tyr Phe Gly
65 70 75 80

Asn Asp His Phe Ala Glu Phe Ala Pro Gly Met Lys Ser Ile Asp Asp
85 90 95

```

Ala Leu Glu Ile Arg Ala Arg Ile Ile Gly Ala Phe Glu Arg Ala Glu
 100 105 110

Ile Cys Glu Asp Pro Ala Glu Arg Glu Arg Leu Leu Thr Phe Val Val
 115 120 125

Val Gly Ala Gly Pro Thr Gly Val Glu Leu Ala Gly Gln Leu Ala Glu
 130 135 140

Met Ala His Arg Thr Leu Ala Gly Glu Tyr Lys Asn Phe Asn Thr Asn
 145 150 155 160

Ser Ala Lys Ile Ile Leu Leu Asp Gly Ala Pro Gln Val Leu Pro Pro
 165 170 175

Phe Gly Lys Arg Leu Gly Arg Asn Ala Gln Arg Thr Leu Glu Lys Met
 180 185 190

Gly Val Asn Val Arg Leu Asn Ala Met Val Thr Asn Val Asp Ala Thr
 195 200 205

Ser Val Thr Tyr Lys Thr Lys Asp Gly Glu Glu His Thr Ile Glu Ser
 210 215 220

Phe Cys Lys Ile Trp Ser Ala Gly Val Ala Ala Ser Pro Leu Gly Lys
 225 230 235 240

Leu Val Ala Glu Gln Thr Gly Val Glu Thr Asp Arg Ala Gly Arg Val
 245 250 255

Met Val Asn Asp Asp Leu Ser Val Gly Asp Gln Lys Asn Val Phe Val
 260 265 270

<210> 721
 <211> 2409
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(2386)
 <223> RXA00703

<400> 721
 ctgggagtc tcttgat ttt aggttttcca cataccccca tatagattga agaattcatt 60

tttcggcatg ggttcaattg ccgggtctag actgtgacct atg aca acc cct cca 115
 Met Thr Thr Pro Pro
 1 5

act gag att tcg aac gtg aat ccc acc gcg aat gaa ttt gat gat ccg 163
 Thr Glu Ile Ser Asn Val Asn Pro Thr Ala Asn Glu Phe Asp Asp Pro
 10 15 20

gat gtg gga cgg cgc att act tct gct gct ggt gtg cca ggc gtt ttg 211
 Asp Val Gly Arg Arg Ile Thr Ser Ala Ala Gly Val Pro Gly Val Leu

	25	30	35	
cat gcg ctc cag cat gct gtt ccg aat cgt gcc ctg ctg ccg ttg ctc				259
His Ala Leu Gln His Ala Val Pro Asn Arg Ala Leu Leu Pro Leu Leu				
	40	45	50	
acc atg aat aaa cca ggc ggc atc gac tgt cct ggt tgt gct tgg cct				307
Thr Met Asn Lys Pro Gly Gly Ile Asp Cys Pro Gly Cys Ala Trp Pro				
	55	60	65	
gag cct tcc act gcc aac ctt ggt gtg gtt gag ttc tgc gag aac ggt				355
Glu Pro Ser Thr Ala Asn Leu Gly Val Val Glu Phe Cys Glu Asn Gly				
	70	75	80	85
gcc aag gcg gtc gcc gag gaa aca aca cct gat cgt gcc ggc aaa gag				403
Ala Lys Ala Val Ala Glu Glu Thr Thr Pro Asp Arg Ala Gly Lys Glu				
	90	95	100	
ttc tgg gca gag cat tct att tat gat ctg ccg gaa aag acc gat cac				451
Phe Trp Ala Glu His Ser Ile Tyr Asp Leu Arg Glu Lys Thr Asp His				
	105	110	115	
tgg ctg gga aag cgt ggc cga atc acc gag ccc atg ttt tat gat cgt				499
Trp Leu Gly Lys Arg Gly Arg Ile Thr Glu Pro Met Phe Tyr Asp Arg				
	120	125	130	
tct tct ggc gat gat cac tac cgc cct att tct tgg gat cgt gca ttt				547
Ser Ser Gly Asp Asp His Tyr Arg Pro Ile Ser Trp Asp Arg Ala Phe				
	135	140	145	
gcg atc att gcg tcg aag ctc cgc gag atc gag cca gat gaa gcg gtg				595
Ala Ile Ile Ala Ser Lys Leu Arg Glu Ile Glu Pro Asp Glu Ala Val				
	150	155	160	165
ttt tac acc tct ggt cga gca ccc aat gag ccg gct tat atg ctg cag				643
Phe Tyr Thr Ser Gly Arg Ala Pro Asn Glu Pro Ala Tyr Met Leu Gln				
	170	175	180	
ctt cta gcc cgc cga ctt ggc aca aat aat ctt cca gac tgt gga aac				691
Leu Leu Ala Arg Arg Leu Gly Thr Asn Asn Leu Pro Asp Cys Gly Asn				
	185	190	195	
atg tgc cac gag tcc acc ggt act gcc ttg ggt gag acc ttg ggt ttg				739
Met Cys His Glu Ser Thr Gly Thr Ala Leu Gly Glu Thr Leu Gly Leu				
	200	205	210	
ggc aag gga tcc gtg gtg atg gag gat ttc tac aac act gat ttg ttg				787
Gly Lys Gly Ser Val Val Met Glu Asp Phe Tyr Asn Thr Asp Leu Leu				
	215	220	225	
att tcc gtg gga caa aac ccg ggc acc aac cac cca cgt gcg ttg acg				835
Ile Ser Val Gly Gln Asn Pro Gly Thr Asn His Pro Arg Ala Leu Thr				
	230	235	240	245
gct ttc aaa gaa ttg aag gaa aac ggt ggc aag att ctg gcg ctg aac				883
Ala Phe Lys Glu Leu Lys Glu Asn Gly Gly Lys Ile Leu Ala Leu Asn				
	250	255	260	
ccc atg cca gag acc ggt ctg atg aaa ttc cgt gag ccc caa tca gtc				931
Pro Met Pro Glu Thr Gly Leu Met Lys Phe Arg Glu Pro Gln Ser Val				
	265	270	275	

aag ggc gcg ttg agc att tca gac aaa ctt gct gat gaa tac ttg cag	979
Lys Gly Ala Leu Ser Ile Ser Asp Lys Leu Ala Asp Glu Tyr Leu Gln	
280 285 290	
atc cgt ctt gat gga gac cgc gca ttc ttc cag gcg ctc aac aag gaa	1027
Ile Arg Leu Asp Gly Asp Arg Ala Phe Phe Gln Ala Leu Asn Lys Glu	
295 300 305	
ctc atc cgt aga gat gcc cta gat cat gca ttc ttg gat aaa ttc tgt	1075
Leu Ile Arg Arg Asp Ala Leu Asp His Ala Phe Leu Asp Lys Phe Cys	
310 315 320 325	
tca ggt gtg gat gaa acc atc gag cac ctc aaa tca ctc gat gat gag	1123
Ser Gly Val Asp Glu Thr Ile Glu His Leu Lys Ser Leu Asp Asp Glu	
330 335 340	
gtt ctg ctc aag gga tgc ggt ctg acg gca gcg gag atc aac aag gcc	1171
Val Leu Leu Lys Gly Cys Gly Leu Thr Ala Ala Glu Ile Asn Lys Ala	
345 350 355	
gct gac atg gtg gaa aag tct gac acc gtg gtg gtg tca tgg act ctc	1219
Ala Asp Met Val Glu Lys Ser Asp Thr Val Val Val Ser Trp Thr Leu	
360 365 370	
ggg gtc acc cag cat aag aac gct gtg tac acc atc cgt gaa atg gtg	1267
Gly Val Thr Gln His Lys Asn Ala Val Tyr Thr Ile Arg Glu Met Val	
375 380 385	
aac ttc ctg ctg ctt act gga aat att ggt aag cct ggc gca ggc act	1315
Asn Phe Leu Leu Leu Thr Gly Asn Ile Gly Lys Pro Gly Ala Gly Thr	
390 395 400 405	
gcc ccg ctt cgt ggg cac tca aac gtc cag ggt gat cga acc atg ggt	1363
Ala Pro Leu Arg Gly His Ser Asn Val Gln Gly Asp Arg Thr Met Gly	
410 415 420	
att tgg gag aaa atg ccg gag gca ttc ctt gct gct ctt gaa aac gag	1411
Ile Trp Glu Lys Met Pro Glu Ala Phe Leu Ala Ala Leu Glu Asn Glu	
425 430 435	
ttt ggt ttc gat gtg ccc cgc aag cac ggc ttc gac acg gta aat tcc	1459
Phe Gly Phe Asp Val Pro Arg Lys His Gly Phe Asp Thr Val Asn Ser	
440 445 450	
ctg cga gcc atg cgc gaa ggc aag acc aag ttc ttt ctc tcc ctc ggt	1507
Leu Arg Ala Met Arg Glu Gly Lys Thr Lys Phe Phe Leu Ser Leu Gly	
455 460 465	
ggc aac ctt gtt cga gtg tcc tca gat acg tct gtt gtc gaa aag ggc	1555
Gly Asn Leu Val Arg Val Ser Ser Asp Thr Ser Val Val Glu Lys Gly	
470 475 480 485	
atg gaa tcc aat gag ctg acg gtg cat ctg tcg acc aag ccc aat ggt	1603
Met Glu Ser Asn Glu Leu Thr Val His Leu Ser Thr Lys Pro Asn Gly	
490 495 500	
tca caa gca tgg cct ggt gag cag tca ctt atc ctt ccg gtg att gct	1651
Ser Gln Ala Trp Pro Gly Glu Gln Ser Leu Ile Leu Pro Val Ile Ala	
505 510 515	

cga aca gat aag gat gtc caa aag tca ggc gtc cag cgt gtg aca gtt	1699
Arg Thr Asp Lys Asp Val Gln Lys Ser Gly Val Gln Arg Val Thr Val	
520 525 530	
gag gat tct gcc ggc gct gtt cac gca tcc act ggt aaa cga acc gcc	1747
Glu Asp Ser Ala Gly Ala Val His Ala Ser Thr Gly Lys Arg Thr Ala	
535 540 545	
aac aag gat ctg aat ttg aag tcc gaa tgc gac atc att gga acc atc	1795
Asn Lys Asp Leu Asn Leu Lys Ser Glu Cys Asp Ile Ile Gly Thr Ile	
550 555 560 565	
ggt aag cag acc ttc ggt gat gcc ttc tgg cag ccg atg att gat aac	1843
Gly Lys Gln Thr Phe Gly Asp Ala Phe Trp Gln Pro Met Ile Asp Asn	
570 575 580	
tac gat gtg gtc cgc gat cac atc gag gcc acc att cct ggg ttc cac	1891
Tyr Asp Val Val Arg Asp His Ile Glu Ala Thr Ile Pro Gly Phe His	
585 590 595	
gat ttc aac cgt cgc atc gac aac ccc ggt gga ttc ctc ctc ccc aac	1939
Asp Phe Asn Arg Arg Ile Asp Asn Pro Gly Gly Phe Leu Leu Pro Asn	
600 605 610	
gga cct cgt gag cgc atc ttc aac aca tcc aat ggc aag gcc caa ttg	1987
Gly Pro Arg Glu Arg Ile Phe Asn Thr Ser Asn Gly Lys Ala Gln Leu	
615 620 625	
acg gtt aat gaa acc aat gtg att gag cta ccc aag gac tat ttg ctt	2035
Thr Val Asn Glu Thr Asn Val Ile Glu Leu Pro Lys Asp Tyr Leu Leu	
630 635 640 645	
atg aac acg gta cgt tca cat gat caa tac aac tcc acg att tac ggt	2083
Met Asn Thr Val Arg Ser His Asp Gln Tyr Asn Ser Thr Ile Tyr Gly	
650 655 660	
ctg gat gac cgc tac cgc ggt gtt cgc aat ggt cgc cgc gta gtg ttc	2131
Leu Asp Asp Arg Tyr Arg Gly Val Arg Asn Gly Arg Arg Val Val Phe	
665 670 675	
gtc aat cct caa gat tgt aag caa cgt ggt ctc aag gat gga gac atc	2179
Val Asn Pro Gln Asp Cys Lys Gln Arg Gly Leu Lys Asp Gly Asp Ile	
680 685 690	
gtc gat atc gtc tct gtc ttt gat gat ggc gaa cgc cga gca ccg aat	2227
Val Asp Ile Val Ser Val Phe Asp Asp Gly Glu Arg Arg Ala Pro Asn	
695 700 705	
ttc cga gtg gtg gaa tat gac acc gcg agg gac tgc gtc acc acg tat	2275
Phe Arg Val Val Glu Tyr Asp Thr Ala Arg Asp Cys Val Thr Thr Tyr	
710 715 720 725	
ttc cct gag gcc aac gta ttg gtt cca ttg gat tca gta gct gaa aaa	2323
Phe Pro Glu Ala Asn Val Leu Val Pro Leu Asp Ser Val Ala Glu Lys	
730 735 740	
tcc aac act cca gtg tcc aag tca gtt gtg gtt cgc ctt gaa gca aca	2371
Ser Asn Thr Pro Val Ser Lys Ser Val Val Val Arg Leu Glu Ala Thr	
745 750 755	
gga cgt act gct tct tagaaaaaca ccagggaatt ttc	2409

Gly Arg Thr Ala Ser
760

<210> 722

<211> 762

<212> PRT

<213> Corynebacterium glutamicum

<400> 722

Met Thr Thr Pro Pro Thr Glu Ile Ser Asn Val Asn Pro Thr Ala Asn
1 5 10 15

Glu Phe Asp Asp Pro Asp Val Gly Arg Arg Ile Thr Ser Ala Ala Gly
20 25 30

Val Pro Gly Val Leu His Ala Leu Gln His Ala Val Pro Asn Arg Ala
35 40 45

Leu Leu Pro Leu Leu Thr Met Asn Lys Pro Gly Gly Ile Asp Cys Pro
50 55 60

Gly Cys Ala Trp Pro Glu Pro Ser Thr Ala Asn Leu Gly Val Val Glu
65 70 75 80

Phe Cys Glu Asn Gly Ala Lys Ala Val Ala Glu Glu Thr Thr Pro Asp
85 90 95

Arg Ala Gly Lys Glu Phe Trp Ala Glu His Ser Ile Tyr Asp Leu Arg
100 105 110

Glu Lys Thr Asp His Trp Leu Gly Lys Arg Gly Arg Ile Thr Glu Pro
115 120 125

Met Phe Tyr Asp Arg Ser Ser Gly Asp Asp His Tyr Arg Pro Ile Ser
130 135 140

Trp Asp Arg Ala Phe Ala Ile Ile Ala Ser Lys Leu Arg Glu Ile Glu
145 150 155 160

Pro Asp Glu Ala Val Phe Tyr Thr Ser Gly Arg Ala Pro Asn Glu Pro
165 170 175

Ala Tyr Met Leu Gln Leu Leu Ala Arg Arg Leu Gly Thr Asn Asn Leu
180 185 190

Pro Asp Cys Gly Asn Met Cys His Glu Ser Thr Gly Thr Ala Leu Gly
195 200 205

Glu Thr Leu Gly Leu Gly Lys Gly Ser Val Val Met Glu Asp Phe Tyr
210 215 220

Asn Thr Asp Leu Leu Ile Ser Val Gly Gln Asn Pro Gly Thr Asn His
225 230 235 240

Pro Arg Ala Leu Thr Ala Phe Lys Glu Leu Lys Glu Asn Gly Gly Lys
245 250 255

Ile Leu Ala Leu Asn Pro Met Pro Glu Thr Gly Leu Met Lys Phe Arg
260 265 270

Glu Pro Gln Ser Val Lys Gly Ala Leu Ser Ile Ser Asp Lys Leu Ala
 275 280 285
 Asp Glu Tyr Leu Gln Ile Arg Leu Asp Gly Asp Arg Ala Phe Phe Gln
 290 295 300
 Ala Leu Asn Lys Glu Leu Ile Arg Arg Asp Ala Leu Asp His Ala Phe
 305 310 315 320
 Leu Asp Lys Phe Cys Ser Gly Val Asp Glu Thr Ile Glu His Leu Lys
 325 330 335
 Ser Leu Asp Asp Glu Val Leu Leu Lys Gly Cys Gly Leu Thr Ala Ala
 340 345 350
 Glu Ile Asn Lys Ala Ala Asp Met Val Glu Lys Ser Asp Thr Val Val
 355 360 365
 Val Ser Trp Thr Leu Gly Val Thr Gln His Lys Asn Ala Val Tyr Thr
 370 375 380
 Ile Arg Glu Met Val Asn Phe Leu Leu Leu Thr Gly Asn Ile Gly Lys
 385 390 395 400
 Pro Gly Ala Gly Thr Ala Pro Leu Arg Gly His Ser Asn Val Gln Gly
 405 410 415
 Asp Arg Thr Met Gly Ile Trp Glu Lys Met Pro Glu Ala Phe Leu Ala
 420 425 430
 Ala Leu Glu Asn Glu Phe Gly Phe Asp Val Pro Arg Lys His Gly Phe
 435 440 445
 Asp Thr Val Asn Ser Leu Arg Ala Met Arg Glu Gly Lys Thr Lys Phe
 450 455 460
 Phe Leu Ser Leu Gly Gly Asn Leu Val Arg Val Ser Ser Asp Thr Ser
 465 470 475 480
 Val Val Glu Lys Gly Met Glu Ser Asn Glu Leu Thr Val His Leu Ser
 485 490 495
 Thr Lys Pro Asn Gly Ser Gln Ala Trp Pro Gly Glu Gln Ser Leu Ile
 500 505 510
 Leu Pro Val Ile Ala Arg Thr Asp Lys Asp Val Gln Lys Ser Gly Val
 515 520 525
 Gln Arg Val Thr Val Glu Asp Ser Ala Gly Ala Val His Ala Ser Thr
 530 535 540
 Gly Lys Arg Thr Ala Asn Lys Asp Leu Asn Leu Lys Ser Glu Cys Asp
 545 550 555 560
 Ile Ile Gly Thr Ile Gly Lys Gln Thr Phe Gly Asp Ala Phe Trp Gln
 565 570 575
 Pro Met Ile Asp Asn Tyr Asp Val Val Arg Asp His Ile Glu Ala Thr
 580 585 590
 Ile Pro Gly Phe His Asp Phe Asn Arg Arg Ile Asp Asn Pro Gly Gly

595					600					605						
Phe	Leu	Leu	Pro	Asn	Gly	Pro	Arg	Glu	Arg	Ile	Phe	Asn	Thr	Ser	Asn	
610					615					620						
Gly	Lys	Ala	Gln	Leu	Thr	Val	Asn	Glu	Thr	Asn	Val	Ile	Glu	Leu	Pro	
625					630					635					640	
Lys	Asp	Tyr	Leu	Leu	Met	Asn	Thr	Val	Arg	Ser	His	Asp	Gln	Tyr	Asn	
645					650					655						
Ser	Thr	Ile	Tyr	Gly	Leu	Asp	Asp	Arg	Tyr	Arg	Gly	Val	Arg	Asn	Gly	
660					665					670						
Arg	Arg	Val	Val	Phe	Val	Asn	Pro	Gln	Asp	Cys	Lys	Gln	Arg	Gly	Leu	
675					680					685						
Lys	Asp	Gly	Asp	Ile	Val	Asp	Ile	Val	Ser	Val	Phe	Asp	Asp	Gly	Glu	
690					695					700						
Arg	Arg	Ala	Pro	Asn	Phe	Arg	Val	Val	Glu	Tyr	Asp	Thr	Ala	Arg	Asp	
705					710					715					720	
Cys	Val	Thr	Thr	Tyr	Phe	Pro	Glu	Ala	Asn	Val	Leu	Val	Pro	Leu	Asp	
725					730					735						
Ser	Val	Ala	Glu	Lys	Ser	Asn	Thr	Pro	Val	Ser	Lys	Ser	Val	Val	Val	
740					745					750						
Arg	Leu	Glu	Ala	Thr	Gly	Arg	Thr	Ala	Ser							
755					760											

<210> 723

<211> 1038

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1015)

<223> RXN00705

<400> 723

gttctggaac aagcactgat gattgggccg agtccacggtt gggttaatgct ctgcatcttc 60

aagaaatcat	cgctaaaaat	taccgggagg	ctaaataaaa	atg	ggt	cgg	att	acc	115
				Met	Gly	Arg	Ile	Thr	
				1				5	

caa	aac	ttg	cag	gtc	cca	cgc	ggt	gtg	tcc	act	gac	gag	caa	gtt	ttt	163
Gln	Asn	Leu	Gln	Val	Pro	Arg	Val	Val	Ser	Thr	Asp	Glu	Gln	Val	Phe	
			10					15						20		

gtt	aac	act	cgt	ccg	gat	act	gtt	gcg	gtg	gag	gag	cct	cta	gaa	att	211
Val	Asn	Thr	Arg	Pro	Asp	Thr	Val	Ala	Val	Glu	Glu	Pro	Leu	Glu	Ile	
			25					30					35			

cgg	gtt	aat	ggc	act	gcg	ctt	acc	acc	act	atg	cgc	acg	ccc	ggc	cat	259
Arg	Val	Asn	Gly	Thr	Ala	Leu	Thr	Thr	Thr	Met	Arg	Thr	Pro	Gly	His	
			40				45					50				

gat att gag ttg gtg cat ggc ctc ctc ttg tca gaa ggt ctg atc acg	307
Asp Ile Glu Leu Val His Gly Leu Leu Leu Ser Glu Gly Leu Ile Thr	
55 60 65	
gat gct tct gag gtt ttt acc gcc cgc tat tgt gca gga gct gtt ggc	355
Asp Ala Ser Glu Val Phe Thr Ala Arg Tyr Cys Ala Gly Ala Val Gly	
70 75 80 85	
cca gat aat caa aat acg tac aac gtc tta gaa ctt gat gtc atc ccc	403
Pro Asp Asn Gln Asn Thr Tyr Asn Val Leu Glu Leu Asp Val Ile Pro	
90 95 100	
aaa gac aat ccg gcc cgg gat ccc gtc cag aat ccc tcc cat aat ccc	451
Lys Asp Asn Pro Ala Arg Asp Pro Val Gln Asn Pro Ser His Asn Pro	
105 110 115	
gaa ggc agc caa cac gaa gca ctc cac atc cca act ttc caa ccg gta	499
Glu Gly Ser Gln His Glu Ala Leu His Ile Pro Thr Phe Gln Pro Val	
120 125 130	
cgc gaa cta aac ctc gtg gca gcc caa cgc aat gtg ctg act acg tct	547
Arg Glu Leu Asn Leu Val Ala Ala Gln Arg Asn Val Leu Thr Thr Ser	
135 140 145	
gct tgt ggt gtt tgt ggc acg acg tct att gag cag ttg atg aac aag	595
Ala Cys Gly Val Cys Gly Thr Thr Ser Ile Glu Gln Leu Met Asn Lys	
150 155 160 165	
aag ggc tgg ccc att acg ccg att aca ccg gat cct cgg atg att gtg	643
Lys Gly Trp Pro Ile Thr Pro Ile Thr Pro Asp Pro Arg Met Ile Val	
170 175 180	
tcg ttg cca gat aag ttg aag tcg aag cag aag att ttc gac aaa act	691
Ser Leu Pro Asp Lys Leu Lys Ser Lys Gln Lys Ile Phe Asp Lys Thr	
185 190 195	
ggt ggg gtt cat gct gct ggt ttg gcc acg ctt gat ggt gag atg ttg	739
Gly Gly Val His Ala Ala Gly Leu Ala Thr Leu Asp Gly Glu Met Leu	
200 205 210	
att att cga gag gat gtc ggt cgg cat aac gca gct gac aaa gtt ata	787
Ile Ile Arg Glu Asp Val Gly Arg His Asn Ala Ala Asp Lys Val Ile	
215 220 225	
gga aac atg ctg atg gcg gga aag ctc ccc ttg gaa aac act att ttg	835
Gly Asn Met Leu Met Ala Gly Lys Leu Pro Leu Glu Asn Thr Ile Leu	
230 235 240 245	
gtg atg agt tct agg gcg tct ttt gag ctt gtc caa aag gct gcc atg	883
Val Met Ser Ser Arg Ala Ser Phe Glu Leu Val Gln Lys Ala Ala Met	
250 255 260	
gct gga att tcg ggt gta atc gct gtt ggt gct gca aca tcg ctg gca	931
Ala Gly Ile Ser Gly Val Ile Ala Val Gly Ala Ala Thr Ser Leu Ala	
265 270 275	
atc gag gcg gcg cag gat tca ggt att ttc ctt gct ggt ttt gtt cgg	979
Ile Glu Ala Ala Gln Asp Ser Gly Ile Phe Leu Ala Gly Phe Val Arg	
280 285 290	

ggc aac aag ttt aac cac tat gcg ggc gag ctc gga taatgccaga 1025
 Gly Asn Lys Phe Asn His Tyr Ala Gly Glu Leu Gly
 295 300 305

acaggtagaa cag 1038

<210> 724

<211> 305

<212> PRT

<213> Corynebacterium glutamicum

<400> 724

Met Gly Arg Ile Thr Gln Asn Leu Gln Val Pro Arg Val Val Ser Thr
 1 5 10 15

Asp Glu Gln Val Phe Val Asn Thr Arg Pro Asp Thr Val Ala Val Glu
 20 25 30

Glu Pro Leu Glu Ile Arg Val Asn Gly Thr Ala Leu Thr Thr Thr Met
 35 40 45

Arg Thr Pro Gly His Asp Ile Glu Leu Val His Gly Leu Leu Leu Ser
 50 55 60

Glu Gly Leu Ile Thr Asp Ala Ser Glu Val Phe Thr Ala Arg Tyr Cys
 65 70 75 80

Ala Gly Ala Val Gly Pro Asp Asn Gln Asn Thr Tyr Asn Val Leu Glu
 85 90 95

Leu Asp Val Ile Pro Lys Asp Asn Pro Ala Arg Asp Pro Val Gln Asn
 100 105 110

Pro Ser His Asn Pro Glu Gly Ser Gln His Glu Ala Leu His Ile Pro
 115 120 125

Thr Phe Gln Pro Val Arg Glu Leu Asn Leu Val Ala Ala Gln Arg Asn
 130 135 140

Val Leu Thr Thr Ser Ala Cys Gly Val Cys Gly Thr Thr Ser Ile Glu
 145 150 155 160

Gln Leu Met Asn Lys Lys Gly Trp Pro Ile Thr Pro Ile Thr Pro Asp
 165 170 175

Pro Arg Met Ile Val Ser Leu Pro Asp Lys Leu Lys Ser Lys Gln Lys
 180 185 190

Ile Phe Asp Lys Thr Gly Gly Val His Ala Ala Gly Leu Ala Thr Leu
 195 200 205

Asp Gly Glu Met Leu Ile Ile Arg Glu Asp Val Gly Arg His Asn Ala
 210 215 220

Ala Asp Lys Val Ile Gly Asn Met Leu Met Ala Gly Lys Leu Pro Leu
 225 230 235 240

Glu Asn Thr Ile Leu Val Met Ser Ser Arg Ala Ser Phe Glu Leu Val
 245 250 255

Gln Lys Ala Ala Met Ala Gly Ile Ser Gly Val Ile Ala Val Gly Ala
 260 265 270

Ala Thr Ser Leu Ala Ile Glu Ala Ala Gln Asp Ser Gly Ile Phe Leu
 275 280 285

Ala Gly Phe Val Arg Gly Asn Lys Phe Asn His Tyr Ala Gly Glu Leu
 290 295 300

Gly
 305

<210> 725
 <211> 908
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (1)..(885)
 <223> FRXA00705

<400> 725
 cca cgc gtt gtg tcc act gac gag caa gtt ttt gtt aac act cgt ccg 48
 Pro Arg Val Val Ser Thr Asp Glu Gln Val Phe Val Asn Thr Arg Pro
 1 5 10 15

gat act gtt gcg gtg gag gag cct cta gaa att cgg gtt aat ggc act 96
 Asp Thr Val Ala Val Glu Glu Pro Leu Glu Ile Arg Val Asn Gly Thr
 20 25 30

gcg ctt acc acc act atg cgc acg ccc ggc cat gat att gag ttg gtg 144
 Ala Leu Thr Thr Thr Met Arg Thr Pro Gly His Asp Ile Glu Leu Val
 35 40 45

cat ggc ctc ctc ttg tca gaa ggt ctg atc acg gat gct tct gag gtt 192
 His Gly Leu Leu Leu Ser Glu Gly Leu Ile Thr Asp Ala Ser Glu Val
 50 55 60

ttt acc gcc cgc tat tgt gca gga gct gtt ggc cca gat aat caa aat 240
 Phe Thr Ala Arg Tyr Cys Ala Gly Ala Val Gly Pro Asp Asn Gln Asn
 65 70 75 80

acg tac aac gtc tta gaa ctt gat gtc atc ccc aaa gac aat ccg gcc 288
 Thr Tyr Asn Val Leu Glu Leu Asp Val Ile Pro Lys Asp Asn Pro Ala
 85 90 95

cgg gat ccc gtc cag aat ccc tcc cat aat ccc gaa ggc agc caa cac 336
 Arg Asp Pro Val Gln Asn Pro Ser His Asn Pro Glu Gly Ser Gln His
 100 105 110

gaa gca ctc cac atc cca act ttc caa ccg gta cgc gaa cta aac ctc 384
 Glu Ala Leu His Ile Pro Thr Phe Gln Pro Val Arg Glu Leu Asn Leu
 115 120 125

gtg gca gcc caa cgc aat gtg ctg act acg tct gct tgt ggt gtt tgt 432
 Val Ala Ala Gln Arg Asn Val Leu Thr Thr Ser Ala Cys Gly Val Cys
 130 135 140

ggc acg acg tct att gag cag ttg atg aac aag aag ggc tgg ccc att 480

Gly Thr Thr Ser Ile Glu Gln Leu Met Asn Lys Lys Gly Trp Pro Ile
 145 150 155 160
 acg ccg att aca ccg gat cct cgg atg att gtg tcg ttg cca gat aag 528
 Thr Pro Ile Thr Pro Asp Pro Arg Met Ile Val Ser Leu Pro Asp Lys
 165 170 175
 ttg aag tcg aag cag aag att ttc gac aaa act ggt ggg gtt cat gct 576
 Leu Lys Ser Lys Gln Lys Ile Phe Asp Lys Thr Gly Gly Val His Ala
 180 185 190
 gct ggt ttg gcc acg ctt gat ggt gag atg ttg att att cga gag gat 624
 Ala Gly Leu Ala Thr Leu Asp Gly Glu Met Leu Ile Ile Arg Glu Asp
 195 200 205
 gtc ggt cgg cat aac gca gct gac aaa gtt ata gga aac atg ctg atg 672
 Val Gly Arg His Asn Ala Ala Asp Lys Val Ile Gly Asn Met Leu Met
 210 215 220
 gcg gga aag ctc ccc ttg gaa aac act att ttg gtg atg agt tct agg 720
 Ala Gly Lys Leu Pro Leu Glu Asn Thr Ile Leu Val Met Ser Ser Arg
 225 230 235 240
 gcg tct ttt gag ctt gtc caa aag gct gcc atg gct gga att tcg ggt 768
 Ala Ser Phe Glu Leu Val Gln Lys Ala Ala Met Ala Gly Ile Ser Gly
 245 250 255
 gta atc gct gtt ggt gct gca aca tcg ctg gca atc gag gcg gcg cag 816
 Val Ile Ala Val Gly Ala Ala Thr Ser Leu Ala Ile Glu Ala Ala Gln
 260 265 270
 gat tca ggt att ttc ctt gct ggt ttt gtt cgg ggc aac aag ttt aac 864
 Asp Ser Gly Ile Phe Leu Ala Gly Phe Val Arg Gly Asn Lys Phe Asn
 275 280 285
 cac tat gcg ggc gag ctc gga taatgccaga acaggtagaa cag 908
 His Tyr Ala Gly Glu Leu Gly
 290 295

<210> 726

<211> 295

<212> PRT

<213> Corynebacterium glutamicum

<400> 726

Pro Arg Val Val Ser Thr Asp Glu Gln Val Phe Val Asn Thr Arg Pro
 1 5 10 15
 Asp Thr Val Ala Val Glu Glu Pro Leu Glu Ile Arg Val Asn Gly Thr
 20 25 30
 Ala Leu Thr Thr Thr Met Arg Thr Pro Gly His Asp Ile Glu Leu Val
 35 40 45
 His Gly Leu Leu Leu Ser Glu Gly Leu Ile Thr Asp Ala Ser Glu Val
 50 55 60
 Phe Thr Ala Arg Tyr Cys Ala Gly Ala Val Gly Pro Asp Asn Gln Asn
 65 70 75 80

Thr	Tyr	Asn	Val	Leu	Glu	Leu	Asp	Val	Ile	Pro	Lys	Asp	Asn	Pro	Ala
				85					90						95
Arg	Asp	Pro	Val	Gln	Asn	Pro	Ser	His	Asn	Pro	Glu	Gly	Ser	Gln	His
			100					105					110		
Glu	Ala	Leu	His	Ile	Pro	Thr	Phe	Gln	Pro	Val	Arg	Glu	Leu	Asn	Leu
		115					120					125			
Val	Ala	Ala	Gln	Arg	Asn	Val	Leu	Thr	Thr	Ser	Ala	Cys	Gly	Val	Cys
	130					135					140				
Gly	Thr	Thr	Ser	Ile	Glu	Gln	Leu	Met	Asn	Lys	Lys	Gly	Trp	Pro	Ile
145				150						155					160
Thr	Pro	Ile	Thr	Pro	Asp	Pro	Arg	Met	Ile	Val	Ser	Leu	Pro	Asp	Lys
				165					170					175	
Leu	Lys	Ser	Lys	Gln	Lys	Ile	Phe	Asp	Lys	Thr	Gly	Gly	Val	His	Ala
			180					185					190		
Ala	Gly	Leu	Ala	Thr	Leu	Asp	Gly	Glu	Met	Leu	Ile	Ile	Arg	Glu	Asp
		195					200					205			
Val	Gly	Arg	His	Asn	Ala	Ala	Asp	Lys	Val	Ile	Gly	Asn	Met	Leu	Met
	210				215						220				
Ala	Gly	Lys	Leu	Pro	Leu	Glu	Asn	Thr	Ile	Leu	Val	Met	Ser	Ser	Arg
225					230					235					240
Ala	Ser	Phe	Glu	Leu	Val	Gln	Lys	Ala	Ala	Met	Ala	Gly	Ile	Ser	Gly
				245					250					255	
Val	Ile	Ala	Val	Gly	Ala	Ala	Thr	Ser	Leu	Ala	Ile	Glu	Ala	Ala	Gln
			260					265					270		
Asp	Ser	Gly	Ile	Phe	Leu	Ala	Gly	Phe	Val	Arg	Gly	Asn	Lys	Phe	Asn
		275					280					285			
His	Tyr	Ala	Gly	Glu	Leu	Gly									
	290					295									

```
<210> 727
<211> 1134
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(1111)  
<223> RXN00388
```

```

<400> 727
gaagagtact tcgaccacga cgactaacac cgcaatttaa aggcttttca agcctgcccc 60

acatcgaagc agttttcaca aagaataagg ttggaaaatt atg ttg ccc gtc aac    115
                                         Met Leu Pro Val Asn
                                         1             5

caa acg tat gcg cag ttc tca gac act gcc ttc gta tcg gca tac atc    163

```

Gln	Thr	Tyr	Ala	Gln	Phe	Ser	Asp	Thr	Ala	Phe	Val	Ser	Ala	Tyr	Ile	
				10					15					20		
atc	tac	gtt	ctg	gca	ctc	atc	ctc	tcc	ctc	gtc	tac	tac	gta	aaa	caa	211
Ile	Tyr	Val	Leu	Ala	Leu	Ile	Leu	Ser	Leu	Val	Tyr	Tyr	Val	Lys	Gln	
			25					30					35			
caa	ggc	att	atc	gac	gcc	cgc	cgc	gag	caa	acc	cgc	gtc	agc	gaa	ctc	259
Gln	Gly	Ile	Ile	Asp	Ala	Arg	Arg	Glu	Gln	Thr	Arg	Val	Ser	Glu	Leu	
		40					45					50				
gtt	ggt	gca	ggc	ggc	agc	gct	gat	gtt	gat	act	gac	ctg	cct	gat	gac	307
Val	Gly	Ala	Gly	Gly	Ser	Ala	Asp	Val	Asp	Thr	Asp	Leu	Pro	Asp	Asp	
	55					60					65					
atc	gcc	gac	ggt	gtc	ctc	gcc	gac	gaa	gac	ctt	gca	aaa	cgc	gaa	gaa	355
Ile	Ala	Asp	Gly	Val	Leu	Ala	Asp	Glu	Asp	Leu	Ala	Lys	Arg	Glu	Glu	
70					75				80					85		
acc	gca	cgc	aaa	cta	gcc	aac	atg	acc	caa	tct	ctc	atg	tgg	ctc	ggc	403
Thr	Ala	Arg	Lys	Leu	Ala	Asn	Met	Thr	Gln	Ser	Leu	Met	Trp	Leu	Gly	
				90					95					100		
gtc	atg	gtg	cac	ctc	gta	tcc	gtc	gtg	atg	cgc	gcg	ctg	tct	gcc	agc	451
Val	Met	Val	His	Leu	Val	Ser	Val	Val	Met	Arg	Ala	Leu	Ser	Ala	Ser	
			105					110					115			
cga	ttc	ccc	ttc	ggc	aac	ctg	tat	gaa	tac	atc	ctc	atg	gtc	acc	ctc	499
Arg	Phe	Pro	Phe	Gly	Asn	Leu	Tyr	Glu	Tyr	Ile	Leu	Met	Val	Thr	Leu	
		120					125					130				
ttc	gcc	atg	atc	gga	gcc	gta	ctc	atc	ctg	cag	cgc	cca	caa	ttc	cgc	547
Phe	Ala	Met	Ile	Gly	Ala	Val	Leu	Ile	Leu	Gln	Arg	Pro	Gln	Phe	Arg	
	135					140					145					
gtg	gta	tgg	cca	tgg	atc	ctc	acc	cca	atg	ctg	gca	ctg	ctc	ttc	tac	595
Val	Val	Trp	Pro	Trp	Ile	Leu	Thr	Pro	Met	Leu	Ala	Leu	Leu	Phe	Tyr	
150					155				160					165		
ggt	ggc	acc	cag	ctg	tac	tcc	gac	gca	gca	cca	gtc	gtt	cca	gca	ctg	643
Gly	Gly	Thr	Gln	Leu	Tyr	Ser	Asp	Ala	Ala	Pro	Val	Val	Pro	Ala	Leu	
			170						175					180		
cag	tcc	ttc	tgg	ttc	ccg	atc	cac	gtt	tcc	tcc	gtc	tcc	atc	ggc	gca	691
Gln	Ser	Phe	Trp	Phe	Pro	Ile	His	Val	Ser	Ser	Val	Ser	Ile	Gly	Ala	
			185					190					195			
tcc	atc	ggt	atc	gtc	tcc	ggt	att	gca	tcc	ctg	ctg	tac	ata	ctg	cgc	739
Ser	Ile	Gly	Ile	Val	Ser	Gly	Ile	Ala	Ser	Leu	Leu	Tyr	Ile	Leu	Arg	
		200					205					210				
atg	tgg	caa	cca	aag	ggt	aaa	gaa	aag	ggc	ttc	ttc	ggc	gca	gta	gca	787
Met	Trp	Gln	Pro	Lys	Gly	Lys	Glu	Lys	Gly	Phe	Phe	Gly	Ala	Val	Ala	
	215					220					225					
aaa	cca	ctc	cca	tcc	gga	aaa	acc	ctg	gat	aac	ctg	gca	tac	aag	acc	835
Lys	Pro	Leu	Pro	Ser	Gly	Lys	Thr	Leu	Asp	Asn	Leu	Ala	Tyr	Lys	Thr	
230					235					240				245		
gcg	atc	tgg	act	gtc	cca	atc	ttc	ggc	ctg	ggc	atc	atc	ttg	ggt	gcc	883
Ala	Ile	Trp	Thr	Val	Pro	Ile	Phe	Gly	Leu	Gly	Ile	Ile	Leu	Gly	Ala	

	250	255	260	
atc tgg gca gaa gca gcc tgg ggt cgt ttc tgg gga tgg gat cct aag				931
Ile Trp Ala Glu Ala Ala Trp Gly Arg Phe Trp Gly Trp Asp Pro Lys				
	265	270	275	
gaa aca gtc tcc ttc atc acc tgg gtt ctc tac gct ggt tac ctc cac				979
Glu Thr Val Ser Phe Ile Thr Trp Val Leu Tyr Ala Gly Tyr Leu His				
	280	285	290	
gca cgt gca act gct ggt tgg cgc aac acc aac gct gca tgg atc aac				1027
Ala Arg Ala Thr Ala Gly Trp Arg Asn Thr Asn Ala Ala Trp Ile Asn				
	295	300	305	
atc ctg gcg ctg gtc acg atg att ttt aat ctg ttc ttc atc aac atg				1075
Ile Leu Ala Leu Val Thr Met Ile Phe Asn Leu Phe Phe Ile Asn Met				
	310	315	320	325
gtc gta tct ggt ctg cac tct tac gcc gga ctg aac taagcacttt				1121
Val Val Ser Gly Leu His Ser Tyr Ala Gly Leu Asn				
	330	335		
tggttggcgg ggt				1134
<210> 728				
<211> 337				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 728				
Met Leu Pro Val Asn Gln Thr Tyr Ala Gln Phe Ser Asp Thr Ala Phe				
1 5 10 15				
Val Ser Ala Tyr Ile Ile Tyr Val Leu Ala Leu Ile Leu Ser Leu Val				
20 25 30				
Tyr Tyr Val Lys Gln Gln Gly Ile Ile Asp Ala Arg Arg Glu Gln Thr				
35 40 45				
Arg Val Ser Glu Leu Val Gly Ala Gly Gly Ser Ala Asp Val Asp Thr				
50 55 60				
Asp Leu Pro Asp Asp Ile Ala Asp Gly Val Leu Ala Asp Glu Asp Leu				
65 70 75 80				
Ala Lys Arg Glu Glu Thr Ala Arg Lys Leu Ala Asn Met Thr Gln Ser				
85 90 95				
Leu Met Trp Leu Gly Val Met Val His Leu Val Ser Val Val Met Arg				
100 105 110				
Ala Leu Ser Ala Ser Arg Phe Pro Phe Gly Asn Leu Tyr Glu Tyr Ile				
115 120 125				
Leu Met Val Thr Leu Phe Ala Met Ile Gly Ala Val Leu Ile Leu Gln				
130 135 140				
Arg Pro Gln Phe Arg Val Val Trp Pro Trp Ile Leu Thr Pro Met Leu				
145 150 155 160				

Ala Leu Leu Phe Tyr Gly Gly Thr Gln Leu Tyr Ser Asp Ala Ala Pro
 165 170 175

Val Val Pro Ala Leu Gln Ser Phe Trp Phe Pro Ile His Val Ser Ser
 180 185 190

Val Ser Ile Gly Ala Ser Ile Gly Ile Val Ser Gly Ile Ala Ser Leu
 195 200 205

Leu Tyr Ile Leu Arg Met Trp Gln Pro Lys Gly Lys Glu Lys Gly Phe
 210 215 220

Phe Gly Ala Val Ala Lys Pro Leu Pro Ser Gly Lys Thr Leu Asp Asn
 225 230 235 240

Leu Ala Tyr Lys Thr Ala Ile Trp Thr Val Pro Ile Phe Gly Leu Gly
 245 250 255

Ile Ile Leu Gly Ala Ile Trp Ala Glu Ala Ala Trp Gly Arg Phe Trp
 260 265 270

Gly Trp Asp Pro Lys Glu Thr Val Ser Phe Ile Thr Trp Val Leu Tyr
 275 280 285

Ala Gly Tyr Leu His Ala Arg Ala Thr Ala Gly Trp Arg Asn Thr Asn
 290 295 300

Ala Ala Trp Ile Asn Ile Leu Ala Leu Val Thr Met Ile Phe Asn Leu
 305 310 315 320

Phe Phe Ile Asn Met Val Val Ser Gly Leu His Ser Tyr Ala Gly Leu
 325 330 335

Asn

<210> 729
 <211> 326
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(303)
 <223> FRXA00388

<400> 729

acc	ctg	gat	aac	ctg	gca	tac	aag	acc	gcg	atc	tgg	act	gtc	cca	atc	48
Thr	Leu	Asp	Asn	Leu	Ala	Tyr	Lys	Thr	Ala	Ile	Trp	Thr	Val	Pro	Ile	
1				5					10					15		

ttc	ggc	ctg	ggc	atc	atc	ttg	ggt	gcc	atc	tgg	gca	gaa	gca	gcc	tgg	96
Phe	Gly	Leu	Gly	Ile	Ile	Leu	Gly	Ala	Ile	Trp	Ala	Glu	Ala	Ala	Trp	
			20					25					30			

ggt	cgt	ttc	tgg	gga	tgg	gat	cct	aag	gaa	aca	gtc	tcc	ttc	atc	acc	144
Gly	Arg	Phe	Trp	Gly	Trp	Asp	Pro	Lys	Glu	Thr	Val	Ser	Phe	Ile	Thr	
		35					40					45				

tgg	ggt	ctc	tac	gct	ggt	tac	ctc	cac	gca	cgt	gca	act	gct	ggt	tgg	192
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Trp Val Leu Tyr Ala Gly Tyr Leu His Ala Arg Ala Thr Ala Gly Trp
 50 55 60

cgc aac acc aac gct gca tgg atc aac atc ctg gcg ctg gtc acg atg 240
 Arg Asn Thr Asn Ala Ala Trp Ile Asn Ile Leu Ala Leu Val Thr Met
 65 70 75 80

att ttt aat ctg ttc ttc atc aac atg gtc gta tct ggt ctg cac tct 288
 Ile Phe Asn Leu Phe Phe Ile Asn Met Val Val Ser Gly Leu His Ser
 85 90 95

tac gcc gga ctg aac taagcacttt tgggtggcgg ggt 326
 Tyr Ala Gly Leu Asn
 100

<210> 730
 <211> 101
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 730
 Thr Leu Asp Asn Leu Ala Tyr Lys Thr Ala Ile Trp Thr Val Pro Ile
 1 5 10 15

Phe Gly Leu Gly Ile Ile Leu Gly Ala Ile Trp Ala Glu Ala Ala Trp
 20 25 30

Gly Arg Phe Trp Gly Trp Asp Pro Lys Glu Thr Val Ser Phe Ile Thr
 35 40 45

Trp Val Leu Tyr Ala Gly Tyr Leu His Ala Arg Ala Thr Ala Gly Trp
 50 55 60

Arg Asn Thr Asn Ala Ala Trp Ile Asn Ile Leu Ala Leu Val Thr Met
 65 70 75 80

Ile Phe Asn Leu Phe Phe Ile Asn Met Val Val Ser Gly Leu His Ser
 85 90 95

Tyr Ala Gly Leu Asn
 100

<210> 731
 <211> 610
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(610)
 <223> FRXA00386

<400> 731
 gaagagtact tcgaccacga cgactaacac cgcaatttaa aggcttttca agcctgcccc 60

acatcgaagc agttttcaca aagaataagg ttggaaaatt atg ttg ccc gtc aac 115
 Met Leu Pro Val Asn
 1 5

caa acg tat gcg cag ttc tca gac act gcc ttc gta tcg gca tac atc 163
 Gln Thr Tyr Ala Gln Phe Ser Asp Thr Ala Phe Val Ser Ala Tyr Ile
 10 15 20

atc tac gtt ctg gca ctc atc ctc tcc ctc gtc tac tac gta aaa caa 211
 Ile Tyr Val Leu Ala Leu Ile Leu Ser Leu Val Tyr Tyr Val Lys Gln
 25 30 35

caa ggc att atc gac gcc cgc cgc gag caa acc cgc gtc agc gaa ctc 259
 Gln Gly Ile Ile Asp Ala Arg Arg Glu Gln Thr Arg Val Ser Glu Leu
 40 45 50

gtt ggt gca ggc ggc agc gct gat gtt gat act gac ctg cct gat gac 307
 Val Gly Ala Gly Gly Ser Ala Asp Val Asp Thr Asp Leu Pro Asp Asp
 55 60 65

atc gcc gac ggt gtc ctc gcc gac gaa gac ctt gca aaa cgc gaa gaa 355
 Ile Ala Asp Gly Val Leu Ala Asp Glu Asp Leu Ala Lys Arg Glu Glu
 70 75 80 85

acc gca cgc aaa cta gcc aac atg acc caa tct ctc atg tgg ctc ggc 403
 Thr Ala Arg Lys Leu Ala Asn Met Thr Gln Ser Leu Met Trp Leu Gly
 90 95 100

gtc atg gtg cac ctc gta tcc gtc gtg atg cgc gcg ctg tct gcc agc 451
 Val Met Val His Leu Val Ser Val Val Met Arg Ala Leu Ser Ala Ser
 105 110 115

cga ttc ccc ttc ggc aac ctg tat gaa tac atc ctc atg gtc acc ctc 499
 Arg Phe Pro Phe Gly Asn Leu Tyr Glu Tyr Ile Leu Met Val Thr Leu
 120 125 130

ttc gcc atg atc gga gcc gta ctc atc ctg cag cgc cca caa ttc cgc 547
 Phe Ala Met Ile Gly Ala Val Leu Ile Leu Gln Arg Pro Gln Phe Arg
 135 140 145

gtg gta tgg cca tgg atc ctc acc cca atg gct ggc act tgg ttt tct 595
 Val Val Trp Pro Trp Ile Leu Thr Pro Met Ala Gly Thr Trp Phe Ser
 150 155 160 165

acg gtg gca ccc agc 610
 Thr Val Ala Pro Ser
 170

<210> 732

<211> 170

<212> PRT

<213> Corynebacterium glutamicum

<400> 732

Met Leu Pro Val Asn Gln Thr Tyr Ala Gln Phe Ser Asp Thr Ala Phe
 1 5 10 15

Val Ser Ala Tyr Ile Ile Tyr Val Leu Ala Leu Ile Leu Ser Leu Val
 20 25 30

Tyr Tyr Val Lys Gln Gln Gly Ile Ile Asp Ala Arg Arg Glu Gln Thr
 35 40 45

Arg Val Ser Glu Leu Val Gly Ala Gly Gly Ser Ala Asp Val Asp Thr

50	55	60
Asp Leu Pro Asp Asp Ile Ala Asp Gly Val Leu Ala Asp Glu Asp Leu		
65	70	75
Ala Lys Arg Glu Glu Thr Ala Arg Lys Leu Ala Asn Met Thr Gln Ser		
	85	90
Leu Met Trp Leu Gly Val Met Val His Leu Val Ser Val Val Met Arg		
	100	105
Ala Leu Ser Ala Ser Arg Phe Pro Phe Gly Asn Leu Tyr Glu Tyr Ile		
	115	120
Leu Met Val Thr Leu Phe Ala Met Ile Gly Ala Val Leu Ile Leu Gln		
	130	135
Arg Pro Gln Phe Arg Val Val Trp Pro Trp Ile Leu Thr Pro Met Ala		
145	150	155
Gly Thr Trp Phe Ser Thr Val Ala Pro Ser		
	165	170

<210> 733

<211> 1095

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1072)

<223> RXA00945

<400> 733

tcacagtacc acccacaagc cacaaggagg gtatggaggt. gggcgtctaa agccaaattt 60

ttcccgtgtg	ttgaggcgat	tgacccgtac	actaatgtgc	atg ctt gaa cgc ctc	115
				Met Leu Glu Arg Leu	
				1	5

aaa cgc cta gat ccg ctc att gtc ctc att gtg ctg gct gtc att gtg	163
Lys Arg Leu Asp Pro Leu Ile Val Leu Ile Val Leu Ala Val Ile Val	
	10
	15
	20

gcg atc atc att cca gtt cgc ggg gtt gct gcg gat tgg ttt gat gtc	211
Ala Ile Ile Ile Pro Val Arg Gly Val Ala Ala Asp Trp Phe Asp Val	
	25
	30
	35

gcc gtc aag att gcc att gcg ctg ctg ttt ttt ctt tat ggt gcc cgc	259
Ala Val Lys Ile Ala Ile Ala Leu Leu Phe Phe Leu Tyr Gly Ala Arg	
	40
	45
	50

cta tcc acc caa gag gcg ctg aat ggt ctg aag cac tgg agg ctt cac	307
Leu Ser Thr Gln Glu Ala Leu Asn Gly Leu Lys His Trp Arg Leu His	
	55
	60
	65

ctg act att ttg gcg atc act ttc gga ata ttc cca ctt atc ggc att	355
Leu Thr Ile Leu Ala Ile Thr Phe Gly Ile Phe Pro Leu Ile Gly Ile	
	70
	75
	80
	85

ggg ctc gag ccg atg act gca ttt gtg tcg gaa gat att tat cgg gga	403
Gly Leu Glu Pro Met Thr Ala Phe Val Ser Glu Asp Ile Tyr Arg Gly	
90 95 100	
att ttg ttc ctc acg ctc gtt ccg tcc acc gtg cag tca tcg gtg gcg	451
Ile Leu Phe Leu Thr Leu Val Pro Ser Thr Val Gln Ser Ser Val Ala	
105 110 115	
ttt acc tcg atc gct aaa ggc aac gta gct ggt gcg att gtg tcg gca	499
Phe Thr Ser Ile Ala Lys Gly Asn Val Ala Gly Ala Ile Val Ser Ala	
120 125 130	
tcg ctc tcc aac ctt gcg ggt gtt ttc ctc act ccg ctg ctg gtc atg	547
Ser Leu Ser Asn Leu Ala Gly Val Phe Leu Thr Pro Leu Leu Val Met	
135 140 145	
ctc atc atg tct gcg ggc ggg gga gtt cac gtg gat tcc cag gtc ttc	595
Leu Ile Met Ser Ala Gly Gly Gly Val His Val Asp Ser Gln Val Phe	
150 155 160 165	
ctc gac att gcg att cag ctt ctg ctg ccg ttc atc ctc ggc cag gta	643
Leu Asp Ile Ala Ile Gln Leu Leu Leu Pro Phe Ile Leu Gly Gln Val	
170 175 180	
tgt agg cgt tgg gtg aag aat ttt gcg gcc aac aaa gca aca aaa atc	691
Cys Arg Arg Trp Val Lys Asn Phe Ala Ala Asn Lys Ala Thr Lys Ile	
185 190 195	
gtg gac cgc ggc tcg atc gcg atg gtc gtg tac tcc gcg ttt tct gcc	739
Val Asp Arg Gly Ser Ile Ala Met Val Val Tyr Ser Ala Phe Ser Ala	
200 205 210	
ggc atg gtg gct ggc att tgg tcc act gtg agc gtt cta gag att atc	787
Gly Met Val Ala Gly Ile Trp Ser Thr Val Ser Val Leu Glu Ile Ile	
215 220 225	
tac ctc att gtt ttc gct att ctg ctg gtg atg gcc atg ctg tgg ttc	835
Tyr Leu Ile Val Phe Ala Ile Leu Leu Val Met Ala Met Leu Trp Phe	
230 235 240 245	
acg ctg ttc atg gct aca cgc ctt gga ttt aac cgg gca gat tcc atc	883
Thr Leu Phe Met Ala Thr Arg Leu Gly Phe Asn Arg Ala Asp Ser Ile	
250 255 260	
gct att cag ttc tgc gga acc aag aaa tcc ctg gcc aca ggc ctc cca	931
Ala Ile Gln Phe Cys Gly Thr Lys Lys Ser Leu Ala Thr Gly Leu Pro	
265 270 275	
atg gcg gca gtc atc ttc ggt ggc gcc aat atc ggc ctg ctc atc ttg	979
Met Ala Ala Val Ile Phe Gly Gly Ala Asn Ile Gly Leu Leu Ile Leu	
280 285 290	
ccg ttg atg atc ttc cac caa gtc cag ctg atg att tgt gca tgg ctt	1027
Pro Leu Met Ile Phe His Gln Val Gln Leu Met Ile Cys Ala Trp Leu	
295 300 305	
gca gct cgt tat ggt cgt gat gcg cag gaa cag aaa gcc aac gcc	1072
Ala Ala Arg Tyr Gly Arg Asp Ala Gln Glu Gln Lys Ala Asn Ala	
310 315 320	
taaaagtcct cagtagctag cca	1095

<210> 734

<211> 324

<212> PRT

<213> Corynebacterium glutamicum

<400> 734

Met Leu Glu Arg Leu Lys Arg Leu Asp Pro Leu Ile Val Leu Ile Val
 1 5 10 15

Leu Ala Val Ile Val Ala Ile Ile Ile Pro Val Arg Gly Val Ala Ala
 20 25 30

Asp Trp Phe Asp Val Ala Val Lys Ile Ala Ile Ala Leu Leu Phe Phe
 35 40 45

Leu Tyr Gly Ala Arg Leu Ser Thr Gln Glu Ala Leu Asn Gly Leu Lys
 50 55 60

His Trp Arg Leu His Leu Thr Ile Leu Ala Ile Thr Phe Gly Ile Phe
 65 70 75 80

Pro Leu Ile Gly Ile Gly Leu Glu Pro Met Thr Ala Phe Val Ser Glu
 85 90 95

Asp Ile Tyr Arg Gly Ile Leu Phe Leu Thr Leu Val Pro Ser Thr Val
 100 105 110

Gln Ser Ser Val Ala Phe Thr Ser Ile Ala Lys Gly Asn Val Ala Gly
 115 120 125

Ala Ile Val Ser Ala Ser Leu Ser Asn Leu Ala Gly Val Phe Leu Thr
 130 135 140

Pro Leu Leu Val Met Leu Ile Met Ser Ala Gly Gly Gly Val His Val
 145 150 155 160

Asp Ser Gln Val Phe Leu Asp Ile Ala Ile Gln Leu Leu Leu Pro Phe
 165 170 175

Ile Leu Gly Gln Val Cys Arg Arg Trp Val Lys Asn Phe Ala Ala Asn
 180 185 190

Lys Ala Thr Lys Ile Val Asp Arg Gly Ser Ile Ala Met Val Val Tyr
 195 200 205

Ser Ala Phe Ser Ala Gly Met Val Ala Gly Ile Trp Ser Thr Val Ser
 210 215 220

Val Leu Glu Ile Ile Tyr Leu Ile Val Phe Ala Ile Leu Leu Val Met
 225 230 235 240

Ala Met Leu Trp Phe Thr Leu Phe Met Ala Thr Arg Leu Gly Phe Asn
 245 250 255

Arg Ala Asp Ser Ile Ala Ile Gln Phe Cys Gly Thr Lys Lys Ser Leu
 260 265 270

Ala Thr Gly Leu Pro Met Ala Ala Val Ile Phe Gly Gly Ala Asn Ile
 275 280 285

Gly Leu Leu Ile Leu Pro Leu Met Ile Phe His Gln Val Gln Leu Met
 290 295 300

Ile Cys Ala Trp Leu Ala Ala Arg Tyr Gly Arg Asp Ala Gln Glu Gln
 305 310 315 320

Lys Ala Asn Ala

<210> 735

<211> 1281

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1258)

<223> RXN02556

<400> 735

tgccatcata ttaaggccaa attgcttgga tcctgggatt tatttaatta gattaaatcc 60
 gtagaaatta gcccatgaag catggaaagg cgaaaacccc ttg atc gtt tcc acc 115
 Leu Ile Val Ser Thr
 1 5
 cag ccc att act gat cgc agc gca ctc tcg gca gaa cac gca gag gtg 163
 Gln Pro Ile Thr Asp Arg Ser Ala Leu Ser Ala Glu His Ala Glu Val
 10 15 20
 atc aaa gca acg ctt cct ctc gtg ggc ggc aag att aat gag atc acg 211
 Ile Lys Ala Thr Leu Pro Leu Val Gly Gly Lys Ile Asn Glu Ile Thr
 25 30 35
 ccg gtt ttc tac aac aag atg ttt gcg gct cac cca gaa ttg atc gct 259
 Pro Val Phe Tyr Asn Lys Met Phe Ala Ala His Pro Glu Leu Ile Ala
 40 45 50
 aac acc ttc aac cgt ggc aat cag aag caa ggc gat cag cag aag gcg 307
 Asn Thr Phe Asn Arg Gly Asn Gln Lys Gln Gly Asp Gln Gln Lys Ala
 55 60 65
 ctg gcg gct tcg att gca acg ttt gcc acc atg ctc gtt act cct gat 355
 Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met Leu Val Thr Pro Asp
 70 75 80 85
 gct cct gac cca gtt cag ctg ctg tcc cgc att ggc cac aag cac gtg 403
 Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile Gly His Lys His Val
 90 95 100
 tcc ctc ggc att act gct gat cag tac gac att gtt cac gag cac ctg 451
 Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile Val His Glu His Leu
 105 110 115
 ttc gcc gca atc gtt gag gtt ttg gga gcg gaa act gtc acc gca cct 499
 Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu Thr Val Thr Ala Pro
 120 125 130
 gtc gct gaa gcc tgg gat gct gtc tac tgg atc atg gca aat gtg ctg 547

Val	Ala	Glu	Ala	Trp	Asp	Ala	Val	Tyr	Trp	Ile	Met	Ala	Asn	Val	Leu		
135						140					145						
atc	ggt	ttt	gag	aac	aac	ctt	tat	gct	tcc	aac	gat	ctg	gag	cct	ggc	595	
Ile	Gly	Phe	Glu	Asn	Asn	Leu	Tyr	Ala	Ser	Asn	Asp	Leu	Glu	Pro	Gly		
150					155					160				165			
gac	gtc	ttc	cgc	gaa	gtc	acc	gtg	acc	gcg	aag	aag	cag	ctc	agc	gca	643	
Asp	Val	Phe	Arg	Glu	Val	Thr	Val	Thr	Ala	Lys	Lys	Gln	Leu	Ser	Ala		
				170					175					180			
acc	gtc	tgg	gaa	tac	acc	ctg	gca	ggt	gag	ctg	gtt	gcc	cca	gag	cca	691	
Thr	Val	Trp	Glu	Tyr	Thr	Leu	Ala	Gly	Glu	Leu	Val	Ala	Pro	Glu	Pro		
			185					190					195				
ggt	cag	tac	acc	tcc	atc	gga	gta	gtg	ctt	gac	gac	ggc	gcc	cgc	cag	739	
Gly	Gln	Tyr	Thr	Ser	Ile	Gly	Val	Val	Leu	Asp	Asp	Gly	Ala	Arg	Gln		
		200					205					210					
ctg	cgc	cag	tac	agc	ttg	ctc	ggc	ggc	tcc	gac	acc	gag	tac	cgc	att	787	
Leu	Arg	Gln	Tyr	Ser	Leu	Leu	Gly	Gly	Ser	Asp	Thr	Glu	Tyr	Arg	Ile		
		215				220					225						
gcg	gtt	gag	gat	aac	ggc	gag	gtt	tct	gga	ttc	ctg	cgt	gat	cgc	gta	835	
Ala	Val	Glu	Asp	Asn	Gly	Glu	Val	Ser	Gly	Phe	Leu	Arg	Asp	Arg	Val		
230					235					240					245		
tcc	gtt	ggt	gac	aag	att	gaa	gcc	acc	atc	gcg	gcc	ggc	gac	ctg	gtt	883	
Ser	Val	Gly	Asp	Lys	Ile	Glu	Ala	Thr	Ile	Ala	Ala	Gly	Asp	Leu	Val		
				250					255					260			
ctt	aac	aag	gac	acc	aat	cca	gtt	gtg	ctg	att	tcc	cag	ggc	atc	ggc	931	
Leu	Asn	Lys	Asp	Thr	Asn	Pro	Val	Val	Leu	Ile	Ser	Gln	Gly	Ile	Gly		
			265					270					275				
tcc	acc	cca	atg	gtg	ggc	atg	ctc	gca	ggt	atg	aac	cct	gaa	cgt	gac	979	
Ser	Thr	Pro	Met	Val	Gly	Met	Leu	Ala	Gly	Met	Asn	Pro	Glu	Arg	Asp		
		280					285					290					
gtt	gtg	gtt	ttg	cat	gct	gac	cag	gcc	gag	tcc	acc	tac	gcg	cag	gtg	1027	
Val	Val	Val	Leu	His	Ala	Asp	Gln	Ala	Glu	Ser	Thr	Tyr	Ala	Gln	Val		
		295				300					305						
gag	gaa	gtg	cag	ggg	ctc	gtc	gaa	aag	ctc	cct	aag	gct	gcg	ttt	gaa	1075	
Glu	Glu	Val	Gln	Gly	Leu	Val	Glu	Lys	Leu	Pro	Lys	Ala	Ala	Phe	Glu		
310					315					320					325		
atc	ttc	tac	cgc	gac	aac	gac	cag	tgg	ctc	gag	gtc	gct	ggc	cgc	att	1123	
Ile	Phe	Tyr	Arg	Asp	Asn	Asp	Gln	Trp	Leu	Glu	Val	Ala	Gly	Arg	Ile		
				330					335					340			
cca	tca	ggt	gcg	tcc	gtg	tac	ctg	tgc	ggt	ggc	gtg	gaa	ttc	ttg	aag	1171	
Pro	Ser	Gly	Ala	Ser	Val	Tyr	Leu	Cys	Gly	Gly	Val	Glu	Phe	Leu	Lys		
			345					350					355				
aac	gtg	cgt	gag	cag	atc	gag	gcg	ctc	gat	gag	cag	cct	cgc	gac	gta	1219	
Asn	Val	Arg	Glu	Gln	Ile	Glu	Ala	Leu	Asp	Glu	Gln	Pro	Arg	Asp	Val		
		360				365						370					
aac	ttc	gag	ctc	ttc	gca	cca	aac	gac	tgg	ctg	att	tcc	taagcccaca			1268	
Asn	Phe	Glu	Leu	Phe	Ala	Pro	Asn	Asp	Trp	Leu	Ile	Ser					

375 380 385 1281
 cccagaact tcc

<210> 736
 <211> 386
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 736
 Leu Ile Val Ser Thr Gln Pro Ile Thr Asp Arg Ser Ala Leu Ser Ala
 1 5 10 15
 Glu His Ala Glu Val Ile Lys Ala Thr Leu Pro Leu Val Gly Gly Lys
 20 25 30
 Ile Asn Glu Ile Thr Pro Val Phe Tyr Asn Lys Met Phe Ala Ala His
 35 40 45
 Pro Glu Leu Ile Ala Asn Thr Phe Asn Arg Gly Asn Gln Lys Gln Gly
 50 55 60
 Asp Gln Gln Lys Ala Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met
 65 70 75 80
 Leu Val Thr Pro Asp Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile
 85 90 95
 Gly His Lys His Val Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile
 100 105 110
 Val His Glu His Leu Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu
 115 120 125
 Thr Val Thr Ala Pro Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile
 130 135 140
 Met Ala Asn Val Leu Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn
 145 150 155 160
 Asp Leu Glu Pro Gly Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys
 165 170 175
 Lys Gln Leu Ser Ala Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu
 180 185 190
 Val Ala Pro Glu Pro Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp
 195 200 205
 Asp Gly Ala Arg Gln Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp
 210 215 220
 Thr Glu Tyr Arg Ile Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe
 225 230 235 240
 Leu Arg Asp Arg Val Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala
 245 250 255
 Ala Gly Asp Leu Val Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile
 260 265 270

Ser Gln Gly Ile Gly Ser Thr Pro Met Val Gly Met Leu Ala Gly Met
 275 280 285

Asn Pro Glu Arg Asp Val Val Val Leu His Ala Asp Gln Ala Glu Ser
 290 295 300

Thr Tyr Ala Gln Val Glu Glu Val Gln Gly Leu Val Glu Lys Leu Pro
 305 310 315 320

Lys Ala Ala Phe Glu Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu
 325 330 335

Val Ala Gly Arg Ile Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly
 340 345 350

Val Glu Phe Leu Lys Asn Val Arg Glu Gln Ile Glu Ala Leu Asp Glu
 355 360 365

Gln Pro Arg Asp Val Asn Phe Glu Leu Phe Ala Pro Asn Asp Trp Leu
 370 375 380

Ile Ser
 385

<210> 737
 <211> 1281
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1258)
 <223> FRXA02556

<400> 737
 tgccatcata ttaaggccaa attgcttgga tcctgggatt tatttaatta gattaaatcc 60

gtagaaatta gcccatgaag catggaaagg cgaaaacccc ttg atc gtt tcc acc 115
 Leu Ile Val Ser Thr
 1 5

cag ccc att act gat cgc agc gca ctc tcg gca gaa cac gca gag gtg 163
 Gln Pro Ile Thr Asp Arg Ser Ala Leu Ser Ala Glu His Ala Glu Val
 10 15 20

atc aaa gca acg ctt cct ctc gtg ggc ggc aag att aat gag atc acg 211
 Ile Lys Ala Thr Leu Pro Leu Val Gly Gly Lys Ile Asn Glu Ile Thr
 25 30 35

ccg gtt ttc tac aac aag atg ttt gcg gct cac cca gaa ttg atc gct 259
 Pro Val Phe Tyr Asn Lys Met Phe Ala Ala His Pro Glu Leu Ile Ala
 40 45 50

aac acc ttc aac ggt ggc aat cag aag caa ggc gat cag cag aag gcg 307
 Asn Thr Phe Asn Gly Gly Asn Gln Lys Gln Gly Asp Gln Gln Lys Ala
 55 60 65

ctg gcg gct tcg att gca acg ttt gcc acc atg ctc gtt act cct gat 355
 Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met Leu Val Thr Pro Asp

70	75	80	85
gct cct gac cca gtt cag ctg ctg tcc cgc att ggc cac aag cac gtg Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile Gly His Lys His Val 90 95 100	403		
tcc ctg ggc att act gct gat cag tac gac att gtt cac gag cac ctg Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile Val His Glu His Leu 105 110 115	451		
ttc gcc gca atc gtt gag gtt ttg gga gcg gaa act gtc acc gca cct Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu Thr Val Thr Ala Pro 120 125 130	499		
gtc gct gaa gcc tgg gat gct gtc tac tgg atc atg gca aat gtg ctg Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile Met Ala Asn Val Leu 135 140 145	547		
atc ggt ttt gag aac aac ctt tat gct tcc aac gat ctg gag cct ggc Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn Asp Leu Glu Pro Gly 150 155 160 165	595		
gac gtc ttc cgc gaa gtc acc gtg acc gcg aag aag cag ctg agc gca Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys Lys Gln Leu Ser Ala 170 175 180	643		
acc gtc tgg gaa tac acc ctg gca ggt gag ctg gtt gcc cca gag cca Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu Val Ala Pro Glu Pro 185 190 195	691		
ggt cag tac acc tcc atc gga gta gtg ctt gac gac ggc gcc cgc cag Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp Asp Gly Ala Arg Gln 200 205 210	739		
ctg cgc cag tac agc ttg ctg ggc ggc tcc gac acc gag tac cgc att Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp Thr Glu Tyr Arg Ile 215 220 225	787		
gcg gtt gag gat aac ggc gag gtt tct gga ttc ctg cgt gat cgc gta Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe Leu Arg Asp Arg Val 230 235 240 245	835		
tcc gtt ggt gac aag att gaa gcc acc atc gcg gcc ggc gac ctg gtt Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala Ala Gly Asp Leu Val 250 255 260	883		
ctt aac aag gac acc aat cca gtt gtg ctg att tcc cag ggc atc ggc Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile Ser Gln Gly Ile Gly 265 270 275	931		
tcc acc cca atg gtg ggc atg ctg gca ggt atg aac cct gaa cgt gac Ser Thr Pro Met Val Gly Met Leu Ala Gly Met Asn Pro Glu Arg Asp 280 285 290	979		
gtt gtg gtt ttg cat gct gac cag gcc gag tcc acc tac gcg cag gtg Val Val Val Leu His Ala Asp Gln Ala Glu Ser Thr Tyr Ala Gln Val 295 300 305	1027		
gag gaa gtg cag ggg ctg gtc gaa aag ctg cct aag gct gcg ttt gaa Glu Glu Val Gln Gly Leu Val Glu Lys Leu Pro Lys Ala Ala Phe Glu 310 315 320 325	1075		

atc ttc tac cgc gac aac gac cag tgg ctc gag gtc gct ggc cgc att 1123
 Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu Val Ala Gly Arg Ile
 330 335 340

cca tca ggt gcg tcc gtg tac ctg tgc ggt ggc gtg gaa ttc ttg aag 1171
 Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly Val Glu Phe Leu Lys
 345 350 355

aac gtg cgt gag cag atc gag gcg ctc gat gag cag cct cgc gac gta 1219
 Asn Val Arg Glu Gln Ile Glu Ala Leu Asp Glu Gln Pro Arg Asp Val
 360 365 370

aac ttc gag ctc ttc gca cca aac gac tgg ctg att tcc taagcccaca 1268
 Asn Phe Glu Leu Phe Ala Pro Asn Asp Trp Leu Ile Ser
 375 380 385

ccccagaact tcc 1281

<210> 738

<211> 386

<212> PRT

<213> Corynebacterium glutamicum

<400> 738

Leu Ile Val Ser Thr Gln Pro Ile Thr Asp Arg Ser Ala Leu Ser Ala
 1 5 10 15

Glu His Ala Glu Val Ile Lys Ala Thr Leu Pro Leu Val Gly Gly Lys
 20 25 30

Ile Asn Glu Ile Thr Pro Val Phe Tyr Asn Lys Met Phe Ala Ala His
 35 40 45

Pro Glu Leu Ile Ala Asn Thr Phe Asn Gly Gly Asn Gln Lys Gln Gly
 50 55 60

Asp Gln Gln Lys Ala Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met
 65 70 75 80

Leu Val Thr Pro Asp Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile
 85 90 95

Gly His Lys His Val Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile
 100 105 110

Val His Glu His Leu Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu
 115 120 125

Thr Val Thr Ala Pro Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile
 130 135 140

Met Ala Asn Val Leu Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn
 145 150 155 160

Asp Leu Glu Pro Gly Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys
 165 170 175

Lys Gln Leu Ser Ala Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu
 180 185 190

Val Ala Pro Glu Pro Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp
 195 200 205

Asp Gly Ala Arg Gln Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp
 210 215 220

Thr Glu Tyr Arg Ile Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe
 225 230 235 240

Leu Arg Asp Arg Val Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala
 245 250 255

Ala Gly Asp Leu Val Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile
 260 265 270

Ser Gln Gly Ile Gly Ser Thr Pro Met Val Gly Met Leu Ala Gly Met
 275 280 285

Asn Pro Glu Arg Asp Val Val Val Leu His Ala Asp Gln Ala Glu Ser
 290 295 300

Thr Tyr Ala Gln Val Glu Glu Val Gln Gly Leu Val Glu Lys Leu Pro
 305 310 315 320

Lys Ala Ala Phe Glu Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu
 325 330 335

Val Ala Gly Arg Ile Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly
 340 345 350

Val Glu Phe Leu Lys Asn Val Arg Glu Gln Ile Glu Ala Leu Asp Glu
 355 360 365

Gln Pro Arg Asp Val Asn Phe Glu Leu Phe Ala Pro Asn Asp Trp Leu
 370 375 380

Ile Ser
 385

<210> 739
 <211> 1200
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1177)
 <223> RXA01392

<400> 739
 gtctgcaatc accccgaaca tttgttcaat cggttgatttt cattccactt cgtaatatg 60

ttgacatatc atctaaattt ccaagagagg acaccacaca gtg gct aac acg tca 115
 Val Ala Asn Thr Ser
 1 5

tcc gat tgg gca ggc gcc cca caa aat gca tca gca gac ggc gag ttc 163
 Ser Asp Trp Ala Gly Ala Pro Gln Asn Ala Ser Ala Asp Gly Glu Phe
 10 15 20

gtt cgc gat acc aac tac atc gat gac cgc atc gtc gca gac gtt cca	211
Val Arg Asp Thr Asn Tyr Ile Asp Asp Arg Ile Val Ala Asp Val Pro	
25 30 35	
gcg gga tcc gaa cca att gct cag gaa gat ggc act ttc cat tgg cct	259
Ala Gly Ser Glu Pro Ile Ala Gln Glu Asp Gly Thr Phe His Trp Pro	
40 45 50	
gtc gag gct ggt cgc tac cgt tta gtc gct gcc cgc gca tgt cca tgg	307
Val Glu Ala Gly Arg Tyr Arg Leu Val Ala Ala Arg Ala Cys Pro Trp	
55 60 65	
gca cac cgc act gtt atc acc cgt cgt ctt ctc ggc ctg gag aac gtg	355
Ala His Arg Thr Val Ile Thr Arg Arg Leu Leu Gly Leu Glu Asn Val	
70 75 80 85	
atc tcg ctt ggt ctg acc ggc ccg act cac gac gtt cgt tcc tgg act	403
Ile Ser Leu Gly Leu Thr Gly Pro Thr His Asp Val Arg Ser Trp Thr	
90 95 100	
ttc gat tta gat cca aac cat ctt gat ccc gtg ctg cag att cct cgt	451
Phe Asp Leu Asp Pro Asn His Leu Asp Pro Val Leu Gln Ile Pro Arg	
105 110 115	
cta cag gac gcg tat ttc aac cgc ttc ccc gat tac ccg cgc ggc att	499
Leu Gln Asp Ala Tyr Phe Asn Arg Phe Pro Asp Tyr Pro Arg Gly Ile	
120 125 130	
act gtc cca gcg ctc gtg gag gaa tcg tct aag aag gtc gtc acc aac	547
Thr Val Pro Ala Leu Val Glu Glu Ser Ser Lys Lys Val Val Thr Asn	
135 140 145	
gat tac cct tcc atc acc atc gat ttc aat ctt gag tgg aag cag ttc	595
Asp Tyr Pro Ser Ile Thr Ile Asp Phe Asn Leu Glu Trp Lys Gln Phe	
150 155 160 165	
cac cgt gag ggt gcg cct aac ctc tac ccc gcg gag ctg cgc gag gag	643
His Arg Glu Gly Ala Pro Asn Leu Tyr Pro Ala Glu Leu Arg Glu Glu	
170 175 180	
atg gcg ccg gtg atg aag cgc atc ttc act gag gtc aac aac ggc gta	691
Met Ala Pro Val Met Lys Arg Ile Phe Thr Glu Val Asn Asn Gly Val	
185 190 195	
tac agg acc ggc ttt gcc ggt agc cag gaa gcg cac aac gag gcg tac	739
Tyr Arg Thr Gly Phe Ala Gly Ser Gln Glu Ala His Asn Glu Ala Tyr	
200 205 210	
aag cgg ctt tgg gtt gcg ttg gac tgg cta gaa gat cgc tta tcg acg	787
Lys Arg Leu Trp Val Ala Leu Asp Trp Leu Glu Asp Arg Leu Ser Thr	
215 220 225	
cga cgt tac ctc atg ggg gat cac atc acc gag gcg gat atc cgc ctc	835
Arg Arg Tyr Leu Met Gly Asp His Ile Thr Glu Ala Asp Ile Arg Leu	
230 235 240 245	
tac cca acc ctc gtg cgt ttc gat gcc gtc tac cac gga cac ttc aag	883
Tyr Pro Thr Leu Val Arg Phe Asp Ala Val Tyr His Gly His Phe Lys	
250 255 260	

tgt ggc cgc aac aag atc acc gaa atg ccg aat cta tgg ggc tac ctg 931
 Cys Gly Arg Asn Lys Ile Thr Glu Met Pro Asn Leu Trp Gly Tyr Leu
 265 270 275

 cgg gat ctt ttc cag acc cca ggc ttt ggc gac acc acc gat ttc acc 979
 Arg Asp Leu Phe Gln Thr Pro Gly Phe Gly Asp Thr Thr Asp Phe Thr
 280 285 290

 gaa atc aag cag cac tac tac atc acc cac gcg gag att aac ccc acc 1027
 Glu Ile Lys Gln His Tyr Tyr Ile Thr His Ala Glu Ile Asn Pro Thr
 295 300 305

 cgg atc gtt cca gtc gga cca gat ctg tct ggt ttc gcg aca cca cac 1075
 Arg Ile Val Pro Val Gly Pro Asp Leu Ser Gly Phe Ala Thr Pro His
 310 315 320 325

 ggc cgt gaa aag ctc ggc gga tcc cca ttt gct gaa ggt gtt act ctg 1123
 Gly Arg Glu Lys Leu Gly Gly Ser Pro Phe Ala Glu Gly Val Thr Leu
 330 335 340

 cct ggc cca att cct gcg ggc gaa gaa gtg aaa aac cct gaa cct ttt 1171
 Pro Gly Pro Ile Pro Ala Gly Glu Glu Val Lys Asn Pro Glu Pro Phe
 345 350 355

 cag aag taactaaggc cgcaatccct cga 1200
 Gln Lys

<210> 740

<211> 359

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 740

Val Ala Asn Thr Ser Ser Asp Trp Ala Gly Ala Pro Gln Asn Ala Ser
 1 5 10 15

 Ala Asp Gly Glu Phe Val Arg Asp Thr Asn Tyr Ile Asp Asp Arg Ile
 20 25 30

 Val Ala Asp Val Pro Ala Gly Ser Glu Pro Ile Ala Gln Glu Asp Gly
 35 40 45

 Thr Phe His Trp Pro Val Glu Ala Gly Arg Tyr Arg Leu Val Ala Ala
 50 55 60

 Arg Ala Cys Pro Trp Ala His Arg Thr Val Ile Thr Arg Arg Leu Leu
 65 70 75 80

 Gly Leu Glu Asn Val Ile Ser Leu Gly Leu Thr Gly Pro Thr His Asp
 85 90 95

 Val Arg Ser Trp Thr Phe Asp Leu Asp Pro Asn His Leu Asp Pro Val
 100 105 110

 Leu Gln Ile Pro Arg Leu Gln Asp Ala Tyr Phe Asn Arg Phe Pro Asp
 115 120 125

 Tyr Pro Arg Gly Ile Thr Val Pro Ala Leu Val Glu Glu Ser Ser Lys
 130 135 140

Lys Val Val Thr Asn Asp Tyr Pro Ser Ile Thr Ile Asp Phe Asn Leu
 145 150 155 160
 Glu Trp Lys Gln Phe His Arg Glu Gly Ala Pro Asn Leu Tyr Pro Ala
 165 170 175
 Glu Leu Arg Glu Glu Met Ala Pro Val Met Lys Arg Ile Phe Thr Glu
 180 185 190
 Val Asn Asn Gly Val Tyr Arg Thr Gly Phe Ala Gly Ser Gln Glu Ala
 195 200 205
 His Asn Glu Ala Tyr Lys Arg Leu Trp Val Ala Leu Asp Trp Leu Glu
 210 215 220
 Asp Arg Leu Ser Thr Arg Arg Tyr Leu Met Gly Asp His Ile Thr Glu
 225 230 235 240
 Ala Asp Ile Arg Leu Tyr Pro Thr Leu Val Arg Phe Asp Ala Val Tyr
 245 250 255
 His Gly His Phe Lys Cys Gly Arg Asn Lys Ile Thr Glu Met Pro Asn
 260 265 270
 Leu Trp Gly Tyr Leu Arg Asp Leu Phe Gln Thr Pro Gly Phe Gly Asp
 275 280 285
 Thr Thr Asp Phe Thr Glu Ile Lys Gln His Tyr Tyr Ile Thr His Ala
 290 295 300
 Glu Ile Asn Pro Thr Arg Ile Val Pro Val Gly Pro Asp Leu Ser Gly
 305 310 315 320
 Phe Ala Thr Pro His Gly Arg Glu Lys Leu Gly Gly Ser Pro Phe Ala
 325 330 335
 Glu Gly Val Thr Leu Pro Gly Pro Ile Pro Ala Gly Glu Glu Val Lys
 340 345 350
 Asn Pro Glu Pro Phe Gln Lys
 355

<210> 741

<211> 1227

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1204)

<223> RXA00800

<400> 741

gactccgcag ggatggccta caagtacggt cacggactta atttctagat tgtaggtagt 60

 ctcgtgggca caactgaaat cttattgaaa aggagtgtcc atg agc act gta gtg 115
 Met Ser Thr Val Val

1

5

cct gga att gtc gca ctg tcc aag ggt gca ccg gta gaa aaa gta aac	163
Pro Gly Ile Val Ala Leu Ser Lys Gly Ala Pro Val Glu Lys Val Asn	
10 15 20	
ggt gtt gtc cct gat cca ggt gct aac gat gtc atc gtc aag att cag	211
Val Val Val Pro Asp Pro Gly Ala Asn Asp Val Ile Val Lys Ile Gln	
25 30 35	
gcc tgc ggt gtg tgc cac acc gac ttg gcc tac cgc gat ggc gat att	259
Ala Cys Gly Val Cys His Thr Asp Leu Ala Tyr Arg Asp Gly Asp Ile	
40 45 50	
tca gat gag ttc cct tac ctg ctg ggc cac gag gca gca ggc att gtt	307
Ser Asp Glu Phe Pro Tyr Leu Leu Gly His Glu Ala Ala Gly Ile Val	
55 60 65	
gag gag gta ggc gag tcc gtc acc cac gtt gag gtc ggc gat ttc gtc	355
Glu Glu Val Gly Glu Ser Val Thr His Val Glu Val Gly Asp Phe Val	
70 75 80 85	
atc ttg aac tgg cgt gca gtg tgc ggc gag tgc cgt gca tgt aag aag	403
Ile Leu Asn Trp Arg Ala Val Cys Gly Glu Cys Arg Ala Cys Lys Lys	
90 95 100	
ggc gag cca aag tac tgc ttt aac acc cac aac gcc tct aag aag atg	451
Gly Glu Pro Lys Tyr Cys Phe Asn Thr His Asn Ala Ser Lys Lys Met	
105 110 115	
acc ctg gaa gac ggc acc gag ctg tcc cca gca ctg ggt att ggc gcg	499
Thr Leu Glu Asp Gly Thr Glu Leu Ser Pro Ala Leu Gly Ile Gly Ala	
120 125 130	
ttc ttg gaa aag acc ctg gtc cac gaa ggc cag tgc acc aag gtt aac	547
Phe Leu Glu Lys Thr Leu Val His Glu Gly Gln Cys Thr Lys Val Asn	
135 140 145	
cct gag gaa gat cca gca gca gct ggc ctt ctg ggt tgt ggc atc atg	595
Pro Glu Glu Asp Pro Ala Ala Ala Gly Leu Leu Gly Cys Gly Ile Met	
150 155 160 165	
gca ggc ctt ggc gct gcg gtg aac acc ggt gat att aag cgt ggc gag	643
Ala Gly Leu Gly Ala Ala Val Asn Thr Gly Asp Ile Lys Arg Gly Glu	
170 175 180	
tcc gta gca gtc ttc ggc ctt ggt ggc gtg ggc atg gca gct att gct	691
Ser Val Ala Val Phe Gly Leu Gly Gly Val Gly Met Ala Ala Ile Ala	
185 190 195	
ggc gcc aag att gct ggc gct tcc aag atc att gct gtt gat atc gat	739
Gly Ala Lys Ile Ala Gly Ala Ser Lys Ile Ile Ala Val Asp Ile Asp	
200 205 210	
gag aag aag ctg gag tgg gcg aag gaa ttc ggc gca acc cac acc att	787
Glu Lys Lys Leu Glu Trp Ala Lys Glu Phe Gly Ala Thr His Thr Ile	
215 220 225	
aat tcc tct ggt ctt ggt ggc gaa ggt gat gcc tct gag gtc gtg gca	835
Asn Ser Ser Gly Leu Gly Gly Glu Gly Asp Ala Ser Glu Val Val Ala	
230 235 240 245	
aag gtt cgt gag ctg acc gat ggt ttc ggc acc gat gtc tcc atc gat	883

Lys Val Arg Glu Leu Thr Asp Gly Phe Gly Thr Asp Val Ser Ile Asp
 250 255 260

gcg gta ggc atc atg ccg acc tgg cag cag gcg ttt tac tcc cgt gac 931
 Ala Val Gly Ile Met Pro Thr Trp Gln Gln Ala Phe Tyr Ser Arg Asp
 265 270 275

cat gca ggc cgc atg gtg atg gtg ggc gtt cca aac ctg acg tct cgc 979
 His Ala Gly Arg Met Val Met Val Gly Val Pro Asn Leu Thr Ser Arg
 280 285 290

gta gat gtt cct gcg att gat ttt tac ggt cgc ggt gga tcc gtg cgc 1027
 Val Asp Val Pro Ala Ile Asp Phe Tyr Gly Arg Gly Gly Ser Val Arg
 295 300 305

cct gca tgg tac ggc gac tgc ctg cct gag cgt gat ttc cca act tat 1075
 Pro Ala Trp Tyr Gly Asp Cys Leu Pro Glu Arg Asp Phe Pro Thr Tyr
 310 315 320 325

gtg gat ctg cac ctg cag ggt cgt ttc cca ctg gat aag ttt gtt tct 1123
 Val Asp Leu His Leu Gln Gly Arg Phe Pro Leu Asp Lys Phe Val Ser
 330 335 340

gag cgt att ggt ctt gat gat gtt gaa gag gct ttc aac acc atg aag 1171
 Glu Arg Ile Gly Leu Asp Asp Val Glu Glu Ala Phe Asn Thr Met Lys
 345 350 355

gct ggc gac gtg ctg cgt tct gtg gtg gag atc taaatggctc acgacggatt 1224
 Ala Gly Asp Val Leu Arg Ser Val Val Glu Ile
 360 365

gcg 1227

<210> 742
 <211> 368
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 742
 Met Ser Thr Val Val Pro Gly Ile Val Ala Leu Ser Lys Gly Ala Pro
 1 5 10 15

Val Glu Lys Val Asn Val Val Val Pro Asp Pro Gly Ala Asn Asp Val
 20 25 30

Ile Val Lys Ile Gln Ala Cys Gly Val Cys His Thr Asp Leu Ala Tyr
 35 40 45

Arg Asp Gly Asp Ile Ser Asp Glu Phe Pro Tyr Leu Leu Gly His Glu
 50 55 60

Ala Ala Gly Ile Val Glu Glu Val Gly Glu Ser Val Thr His Val Glu
 65 70 75 80

Val Gly Asp Phe Val Ile Leu Asn Trp Arg Ala Val Cys Gly Glu Cys
 85 90 95

Arg Ala Cys Lys Lys Gly Glu Pro Lys Tyr Cys Phe Asn Thr His Asn
 100 105 110

```

Ala Ser Lys Lys Met Thr Leu Glu Asp Gly Thr Glu Leu Ser Pro Ala
    115                      120                      125

Leu Gly Ile Gly Ala Phe Leu Glu Lys Thr Leu Val His Glu Gly Gln
    130                      135                      140

Cys Thr Lys Val Asn Pro Glu Glu Asp Pro Ala Ala Ala Gly Leu Leu
    145                      150                      155                      160

Gly Cys Gly Ile Met Ala Gly Leu Gly Ala Ala Val Asn Thr Gly Asp
                      165                      170                      175

Ile Lys Arg Gly Glu Ser Val Ala Val Phe Gly Leu Gly Gly Val Gly
    180                      185                      190

Met Ala Ala Ile Ala Gly Ala Lys Ile Ala Gly Ala Ser Lys Ile Ile
    195                      200                      205

Ala Val Asp Ile Asp Glu Lys Lys Leu Glu Trp Ala Lys Glu Phe Gly
    210                      215                      220

Ala Thr His Thr Ile Asn Ser Ser Gly Leu Gly Gly Glu Gly Asp Ala
    225                      230                      235                      240

Ser Glu Val Val Ala Lys Val Arg Glu Leu Thr Asp Gly Phe Gly Thr
    245                      250                      255

Asp Val Ser Ile Asp Ala Val Gly Ile Met Pro Thr Trp Gln Gln Ala
    260                      265                      270

Phe Tyr Ser Arg Asp His Ala Gly Arg Met Val Met Val Gly Val Pro
    275                      280                      285

Asn Leu Thr Ser Arg Val Asp Val Pro Ala Ile Asp Phe Tyr Gly Arg
    290                      295                      300

Gly Gly Ser Val Arg Pro Ala Trp Tyr Gly Asp Cys Leu Pro Glu Arg
    305                      310                      315                      320

Asp Phe Pro Thr Tyr Val Asp Leu His Leu Gln Gly Arg Phe Pro Leu
    325                      330                      335

Asp Lys Phe Val Ser Glu Arg Ile Gly Leu Asp Asp Val Glu Glu Ala
    340                      345                      350

Phe Asn Thr Met Lys Ala Gly Asp Val Leu Arg Ser Val Val Glu Ile
    355                      360                      365

```

<210> 743

<211> 1011

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(988)

<223> RXA02143

<400> 743

tcttcatcac	tatttacttc	attcagtagg	cagtaaggaa	tcctcaacgt	tgttgaggtt	60
ccctatgccc	ttcacttcca	cagtcgagat	tcaaagggaa	atg atg gaa	acc aac	115
				Met Met	Glu Thr Asn	5
				1		
ccg cag acc cca gag gga aat agc atg gct aaa ccc tct gct aag aag	163					
Pro Gln Thr Pro Glu Gly Asn Ser Met Ala Lys Pro Ser Ala Lys Lys						
	10			15		20
gtc aag aat cgc cgc aag gtc cgg cgc acc gtc gca ggt gca ttg gct	211					
Val Lys Asn Arg Arg Lys Val Arg Arg Thr Val Ala Gly Ala Leu Ala						
	25			30		35
ctg acc att gga ctg agc gga gca gga atc ctc gca acc gcg atc act	259					
Leu Thr Ile Gly Leu Ser Gly Ala Gly Ile Leu Ala Thr Ala Ile Thr						
	40			45		50
cca gat gct caa gtt gct acc gct cag cgt gac gat cag gca ctt atc	307					
Pro Asp Ala Gln Val Ala Thr Ala Gln Arg Asp Asp Gln Ala Leu Ile						
	55			60		65
tcc gag ggt aaa gac ctc tac gat gtc gcc tgc atc acc tgc cac ggc	355					
Ser Glu Gly Lys Asp Leu Tyr Asp Val Ala Cys Ile Thr Cys His Gly						
	70			75		80
						85
gta aac ctc caa ggt gtt gag gac cgc ggt cct tcc ctc gta ggt gtt	403					
Val Asn Leu Gln Gly Val Glu Asp Arg Gly Pro Ser Leu Val Gly Val						
	90			95		100
ggc gaa ggc gca gtg tac ttc caa gtt cac tcc ggc cgt atg cca ata	451					
Gly Glu Gly Ala Val Tyr Phe Gln Val His Ser Gly Arg Met Pro Ile						
	105			110		115
ctg cgt aac gag gct cag gct gag cgc aag gct cct cgt tac acc gag	499					
Leu Arg Asn Glu Ala Gln Ala Glu Arg Lys Ala Pro Arg Tyr Thr Glu						
	120			125		130
gca cag acc ctt gcg atc gct gca tat gtt gca gct aat ggc ggt ggc	547					
Ala Gln Thr Leu Ala Ile Ala Ala Tyr Val Ala Ala Asn Gly Gly Gly						
	135			140		145
cca gga ctc gtt tac aac gag gac ggc acc ctc gcc atg gag gag ctc	595					
Pro Gly Leu Val Tyr Asn Glu Asp Gly Thr Leu Ala Met Glu Glu Leu						
	150			155		160
						165
cgt ggc gaa aac tac gac gga cag att acc tcc gcc gac gtc gct cgc	643					
Arg Gly Glu Asn Tyr Asp Gly Gln Ile Thr Ser Ala Asp Val Ala Arg						
	170			175		180
ggc gga gat ctg ttc cgc ctg aac tgt gca tcc tgc cac aac ttc act	691					
Gly Gly Asp Leu Phe Arg Leu Asn Cys Ala Ser Cys His Asn Phe Thr						
	185			190		195
ggc gga gat ctg ttc cgc ctg aac tgt gca tcc tgc cac aac ttc act	739					
Gly Gly Asp Leu Phe Arg Leu Asn Cys Ala Ser Cys His Asn Phe Thr						
	200			205		210
ggt cgt ggt ggc gca ctg tcc tct ggt aag tac gca cca aac ctg gat	787					
Gly Arg Gly Glu Ala Leu Ser Ser Gly Lys Tyr Ala Pro Asn Leu Asp						
	210			215		220
gct gca aac gag cag gaa atc tac cag gct atg ctt acc ggt cct cag						
	225			230		235

Ala Ala Asn Glu Gln Glu Ile Tyr Gln Ala Met Leu Thr Gly Pro Gln
 215 220 225

aac atg cct aag ttc tcc gat cgt cag ctc tcc gca gat gag aag aag 835
 Asn Met Pro Lys Phe Ser Asp Arg Gln Leu Ser Ala Asp Glu Lys Lys
 230 235 240 245

gac atc atc gcc ttc atc aag tcc acc aag gag act cca tca cct ggt 883
 Asp Ile Ile Ala Phe Ile Lys Ser Thr Lys Glu Thr Pro Ser Pro Gly
 250 255 260

ggt tac tca ctc ggt agc ttg ggc cca gtg gct gag ggt ctg ttc atg 931
 Gly Tyr Ser Leu Gly Ser Leu Gly Pro Val Ala Glu Gly Leu Phe Met
 265 270 275

tgg gta ttc ggc atc ttg gtc ctc gtg gcc gcc gct atg tgg att gga 979
 Trp Val Phe Gly Ile Leu Val Leu Val Ala Ala Ala Met Trp Ile Gly
 280 285 290

tca cgt tca tgagtaacaa caacgacaaaa cag 1011
 Ser Arg Ser
 295

<210> 744
 <211> 296
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 744
 Met Met Glu Thr Asn Pro Gln Thr Pro Glu Gly Asn Ser Met Ala Lys
 1 5 10 15

Pro Ser Ala Lys Lys Val Lys Asn Arg Arg Lys Val Arg Arg Thr Val
 20 25 30

Ala Gly Ala Leu Ala Leu Thr Ile Gly Leu Ser Gly Ala Gly Ile Leu
 35 40 45

Ala Thr Ala Ile Thr Pro Asp Ala Gln Val Ala Thr Ala Gln Arg Asp
 50 55 60

Asp Gln Ala Leu Ile Ser Glu Gly Lys Asp Leu Tyr Asp Val Ala Cys
 65 70 75 80

Ile Thr Cys His Gly Val Asn Leu Gln Gly Val Glu Asp Arg Gly Pro
 85 90 95

Ser Leu Val Gly Val Gly Glu Gly Ala Val Tyr Phe Gln Val His Ser
 100 105 110

Gly Arg Met Pro Ile Leu Arg Asn Glu Ala Gln Ala Glu Arg Lys Ala
 115 120 125

Pro Arg Tyr Thr Glu Ala Gln Thr Leu Ala Ile Ala Ala Tyr Val Ala
 130 135 140

Ala Asn Gly Gly Gly Pro Gly Leu Val Tyr Asn Glu Asp Gly Thr Leu
 145 150 155 160

Ala Met Glu Glu Leu Arg Gly Glu Asn Tyr Asp Gly Gln Ile Thr Ser

[illegible]

```
<210> 745
<211> 502
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101) .. (502)  
<223> RXN03096
```

<400> 745																
aagatcatgc	tcatcgaagc	cggcgcccga	agatggcagt	tggetggcat	gggtccttat	60										
cgcaggegcc	gttgtcacct	cactgctcac	cttgtacacc	atg	ggt	ctg	gtc	tgg	115							
				Met	Val	Leu	Val	Trp								
				1				5								
tcc	aag	gcc	ttc	tgg	cgc	gac	cgt	aaa	gac	gcc	ccc	gat	gga	gca	acc	163
Ser	Lys	Ala	Phe	Trp	Arg	Asp	Arg	Lys	Asp	Ala	Pro	Asp	Gly	Ala	Thr	
			10					15						20		
gca	cta	gca	aga	ccc	gca	cct	ttg	gta	gat	atc	caa	gac	gaa	gtc	gcc	211
Ala	Leu	Ala	Arg	Pro	Ala	Pro	Leu	Val	Asp	Ile	Gln	Asp	Glu	Val	Ala	
			25					30					35			
gtt	aaa	gac	cgc	aac	gat	gtc	gga	cgg	atg	cct	tgg	ggc	atg	gtc	ttc	259
Val	Lys	Asp	Arg	Asn	Asp	Val	Gly	Arg	Met	Pro	Trp	Gly	Met	Val	Phe	
		40					45					50				
tcc	act	gcc	ctg	ttg	gtt	tcc	gca	tcc	ctt	gct	gta	tcc	gtg	ctc	gca	307
Ser	Thr	Ala	Leu	Leu	Val	Ser	Ala	Ser	Leu	Ala	Val	Ser	Val	Leu	Ala	
	55					60					65					
gga	cca	ctg	tca	tct	att	act	gga	cgc	gcc	gcc	gaa	tcc	gca	caa	gat	355

Gly Pro Leu Ser Ser Ile Thr Gly Arg Ala Ala Glu Ser Ala Gln Asp
 70 75 80 85
 gtc aac atc tac cgc gcc gca gta ctc ggc cca act acc tcg acc cat 403
 Val Asn Ile Tyr Arg Ala Ala Val Leu Gly Pro Thr Thr Ser Thr His
 90 95 100
 cac gca cac tcg aga tgg agc gtt acg acg cca acc gcg atg aca tca 451
 His Ala His Ser Arg Trp Ser Val Thr Thr Pro Thr Ala Met Thr Ser
 105 110 115
 acc acc gcg tcg aca cca atg gaa cgg agg acc aac cat gat cag tgg 499
 Thr Thr Ala Ser Thr Pro Met Glu Arg Arg Thr Asn His Asp Gln Trp
 120 125 130
 att 502
 Ile

<210> 746
 <211> 134
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 746
 Met Val Leu Val Trp Ser Lys Ala Phe Trp Arg Asp Arg Lys Asp Ala
 1 5 10 15
 Pro Asp Gly Ala Thr Ala Leu Ala Arg Pro Ala Pro Leu Val Asp Ile
 20 25 30
 Gln Asp Glu Val Ala Val Lys Asp Arg Asn Asp Val Gly Arg Met Pro
 35 40 45
 Trp Gly Met Val Phe Ser Thr Ala Leu Leu Val Ser Ala Ser Leu Ala
 50 55 60
 Val Ser Val Leu Ala Gly Pro Leu Ser Ser Ile Thr Gly Arg Ala Ala
 65 70 75 80
 Glu Ser Ala Gln Asp Val Asn Ile Tyr Arg Ala Ala Val Leu Gly Pro
 85 90 95
 Thr Thr Ser Thr His His Ala His Ser Arg Trp Ser Val Thr Thr Pro
 100 105 110
 Thr Ala Met Thr Ser Thr Thr Ala Ser Thr Pro Met Glu Arg Arg Thr
 115 120 125
 Asn His Asp Gln Trp Ile
 130

<210> 747
 <211> 504
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS

<222> (101)..(481)

<223> RXN02036

<400> 747

ctaaaatgga aggcaatgga tacccgccgc atgaacctcc gccaatggaa aatcctcgtt 60

gccctcatct ctgctgcagt ggcggctctc ggaggggtggt gtg cat att cct ttt 115
 Val His Ile Pro Phe
 1 5

ggg cac ctc gcc gac acc gtc tcc tgg gac tgc ggg gga ggc agc tgc 163
 Gly His Leu Ala Asp Thr Val Ser Trp Asp Cys Gly Gly Gly Ser Cys
 10 15 20

gcc acc aac gat ttg gta tcc ctg ttc atg ccg gcc gcc ttc atg agt 211
 Ala Thr Asn Asp Leu Val Ser Leu Phe Met Pro Ala Ala Phe Met Ser
 25 30 35

acc ctc gcc gcc tgc gta ttt ggc gcg tgg gcc ata ggt ttg atc gct 259
 Thr Leu Ala Ala Cys Val Phe Gly Ala Trp Ala Ile Gly Leu Ile Ala
 40 45 50

ccc gca cta ttc atc gcg gtg act gcc tgg gca ttt cgc tcc ggc gtg 307
 Pro Ala Leu Phe Ile Ala Val Thr Ala Trp Ala Phe Arg Ser Gly Val
 55 60 65

cag gct gcg att gcc gac ggc tac acg tcc gcg act tcc gtc ggc ttc 355
 Gln Ala Ala Ile Ala Asp Gly Tyr Thr Ser Ala Thr Ser Val Gly Phe
 70 75 80 85

gaa atg act gtc tcg ctc att ctt ttc atc atc gca ggt ctg tgc ttt 403
 Glu Met Thr Val Ser Leu Ile Leu Phe Ile Ile Ala Gly Leu Cys Phe
 90 95 100

ctg ggc tgg atc ccc atg ttc atc aac aac cgc caa gtc gcg cgc aag 451
 Leu Gly Trp Ile Pro Met Phe Ile Asn Asn Arg Gln Val Ala Arg Lys
 105 110 115

gtc cgc gag agg gct gcg ggc ttg agc aat taggctctcg cttttcgacg 501
 Val Arg Glu Arg Ala Ala Gly Leu Ser Asn
 120 125

ttt 504

<210> 748

<211> 127

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 748

Val His Ile Pro Phe Gly His Leu Ala Asp Thr Val Ser Trp Asp Cys
 1 5 10 15

Gly Gly Gly Ser Cys Ala Thr Asn Asp Leu Val Ser Leu Phe Met Pro
 20 25 30

Ala Ala Phe Met Ser Thr Leu Ala Ala Cys Val Phe Gly Ala Trp Ala
 35 40 45

Ile Gly Leu Ile Ala Pro Ala Leu Phe Ile Ala Val Thr Ala Trp Ala

50	55	60
Phe Arg Ser Gly Val Gln Ala Ala Ile Ala Asp Gly Tyr Thr Ser Ala		
65	70	75 80
Thr Ser Val Gly Phe Glu Met Thr Val Ser Leu Ile Leu Phe Ile Ile		
	85	90 95
Ala Gly Leu Cys Phe Leu Gly Trp Ile Pro Met Phe Ile Asn Asn Arg		
	100	105 110
Gln Val Ala Arg Lys Val Arg Glu Arg Ala Ala Gly Leu Ser Asn		
	115	120 125

<210> 749
 <211> 882
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(859)
 <223> RXN02765

<400> 749
 tctgaacttt tccgcatcga cccagatgag gtttaccocg acgacgacgc cacctgcgaa 60
 ttcaacccat ggccgtatcc tcgcggattt taggagataa atg tct aat caa tta 115
 Met Ser Asn Gln Leu
 1 5
 ccc gat cac gtc cgc gac gcc ttc caa gta ggt gcg gga cct gcc gaa 163
 Pro Asp His Val Arg Asp Ala Phe Gln Val Gly Ala Gly Pro Ala Glu
 10 15 20
 caa ctc ggt caa gct tgg gac ttc gga ttc cgc gtc ggc aac act gtg 211
 Gln Leu Gly Gln Ala Trp Asp Phe Gly Phe Arg Val Gly Asn Thr Val
 25 30 35
 ttc gcc aaa gtg acg gcg ccg gaa gtg tcg ggc tgg tcg tcg aaa acc 259
 Phe Ala Lys Val Thr Ala Pro Glu Val Ser Gly Trp Ser Ser Lys Thr
 40 45 50
 cgc gaa acc ctg aaa cca gaa ggc gtg cgc gtc gta cga ccg atc cgc 307
 Arg Glu Thr Leu Lys Pro Glu Gly Val Arg Val Val Arg Pro Ile Arg
 55 60 65
 tcc acc gac ggc cga ttt gtg gtt gcg ggg tgg cgc gca tcg gtg ttc 355
 Ser Thr Asp Gly Arg Phe Val Val Ala Gly Trp Arg Ala Ser Val Phe
 70 75 80 85
 tct acg gga acg atc agc aag cga gtc gat gag acg gtc gtt gcg ggt 403
 Ser Thr Gly Thr Ile Ser Lys Arg Val Asp Glu Thr Val Val Ala Gly
 90 95 100
 ctt cgt ttg gca gat gca tta gtg gat acg cat gca ccg gaa cct gtg 451
 Leu Arg Leu Ala Asp Ala Leu Val Asp Thr His Ala Pro Glu Pro Val
 105 110 115
 gac aat gtg ttt aac cgt gct gat gtg cag gcc tgg gaa gag cag ccc 499

Asp Asn Val Phe Asn Arg Ala Asp Val Gln Ala Trp Glu Glu Gln Pro
 120 125 130
 ggt cga atc ggt gaa ttg ttg gag ccg att aat cgc gtg aac cag gtt 547
 Gly Arg Ile Gly Glu Leu Leu Glu Pro Ile Asn Arg Val Asn Gln Val
 135 140 145
 ggt cat gcg gat atg ttg gcg aca acg ctg tat gcg gga act cag cca 595
 Gly His Ala Asp Met Leu Ala Thr Thr Leu Tyr Ala Gly Thr Gln Pro
 150 155 160 165
 cct gca gtg acg gat ttg gtg cca gtg ctg cgt ccg cat ggt ttc act 643
 Pro Ala Val Thr Asp Leu Val Pro Val Leu Arg Pro His Gly Phe Thr
 170 175 180
 gcg gca ttg gtg atc gtt gat ggg ttg ctg ctg ggt gcg gtt gat gag 691
 Ala Ala Leu Val Ile Val Asp Gly Leu Leu Leu Gly Ala Val Asp Glu
 185 190 195
 gga att ctg cgg agg ttt tcg cat ttg ccg gaa att gag cag ctg gtt 739
 Gly Ile Leu Arg Arg Phe Ser His Leu Pro Glu Ile Glu Gln Leu Val
 200 205 210
 ttg agg gca ttt ttg ttc cgt cga aac ttg cag gag ttc tct gag aac 787
 Leu Arg Ala Phe Leu Phe Arg Arg Asn Leu Gln Glu Phe Ser Glu Asn
 215 220 225
 aac gat ccg aat gtt att tcg aac cta aac agg gtg gaa tcg aca ctc 835
 Asn Asp Pro Asn Val Ile Ser Asn Leu Asn Arg Val Glu Ser Thr Leu
 230 235 240 245
 gtg tcg tat gtt tct gac aag att tgaggtatgt cggaatacaa acc 882
 Val Ser Tyr Val Ser Asp Lys Ile
 250

<210> 750

<211> 253

<212> PRT

<213> Corynebacterium glutamicum

<400> 750

Met Ser Asn Gln Leu Pro Asp His Val Arg Asp Ala Phe Gln Val Gly
 1 5 10 15
 Ala Gly Pro Ala Glu Gln Leu Gly Gln Ala Trp Asp Phe Gly Phe Arg
 20 25 30
 Val Gly Asn Thr Val Phe Ala Lys Val Thr Ala Pro Glu Val Ser Gly
 35 40 45
 Trp Ser Ser Lys Thr Arg Glu Thr Leu Lys Pro Glu Gly Val Arg Val
 50 55 60
 Val Arg Pro Ile Arg Ser Thr Asp Gly Arg Phe Val Val Ala Gly Trp
 65 70 75 80
 Arg Ala Ser Val Phe Ser Thr Gly Thr Ile Ser Lys Arg Val Asp Glu
 85 90 95
 Thr Val Val Ala Gly Leu Arg Leu Ala Asp Ala Leu Val Asp Thr His

100					105					110					
Ala	Pro	Glu	Pro	Val	Asp	Asn	Val	Phe	Asn	Arg	Ala	Asp	Val	Gln	Ala
		115					120					125			
Trp	Glu	Glu	Gln	Pro	Gly	Arg	Ile	Gly	Glu	Leu	Leu	Glu	Pro	Ile	Asn
	130					135					140				
Arg	Val	Asn	Gln	Val	Gly	His	Ala	Asp	Met	Leu	Ala	Thr	Thr	Leu	Tyr
145					150					155					160
Ala	Gly	Thr	Gln	Pro	Pro	Ala	Val	Thr	Asp	Leu	Val	Pro	Val	Leu	Arg
				165					170					175	
Pro	His	Gly	Phe	Thr	Ala	Ala	Leu	Val	Ile	Val	Asp	Gly	Leu	Leu	Leu
			180						185				190		
Gly	Ala	Val	Asp	Glu	Gly	Ile	Leu	Arg	Arg	Phe	Ser	His	Leu	Pro	Glu
	195						200					205			
Ile	Glu	Gln	Leu	Val	Leu	Arg	Ala	Phe	Leu	Phe	Arg	Arg	Asn	Leu	Gln
	210					215					220				
Glu	Phe	Ser	Glu	Asn	Asn	Asp	Pro	Asn	Val	Ile	Ser	Asn	Leu	Asn	Arg
225				230						235					240
Val	Glu	Ser	Thr	Leu	Val	Ser	Tyr	Val	Ser	Asp	Lys	Ile			
				245						250					

<210> 751

<211> 1059

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1036)

<223> RXN02206

<400> 751

ggcaggatct gctgctgcgg ctaggagggt tatctcttca ttcacccgat ctaccgtact 60

accttatgac	ctcagtagtg	tggtgggcgt	gaaacagcga	atg	gtc	ggt	tca	agt	115
				Met	Val	Gly	Ser	Ser	
				1				5	

ggt	ttg	cgg	gta	tcc	agg	ctc	ggt	ttg	ggc	acc	tca	aca	tgg	ggc	tcg	163
Gly	Leu	Arg	Val	Ser	Arg	Leu	Gly	Leu	Gly	Thr	Ser	Thr	Trp	Gly	Ser	
			10					15						20		

ggc	acc	gag	ctg	gct	gag	gca	ggc	gat	atc	ttt	aag	gcg	ttc	atc	aat	211
Gly	Thr	Glu	Leu	Ala	Glu	Ala	Gly	Asp	Ile	Phe	Lys	Ala	Phe	Ile	Asn	
			25				30						35			

tct	ggt	ggc	acg	ctt	atc	gac	gtc	tcc	ccc	aac	tac	acc	acc	ggc	gtc	259
Ser	Gly	Gly	Thr	Leu	Ile	Asp	Val	Ser	Pro	Asn	Tyr	Thr	Thr	Gly	Val	
			40				45					50				

gcg	gaa	gaa	atg	ctc	ggc	acg	atg	ttg	gat	gcg	gaa	gtc	tct	cgt	tcg	307
Ala	Glu	Glu	Met	Leu	Gly	Thr	Met	Leu	Asp	Ala	Glu	Val	Ser	Arg	Ser	

55	60	65	
gct gtc gtc att tcc tcc agc gca ggt gtc aac ccc gct ctg ccg ctc Ala Val Val Ile Ser Ser Ser Ala Gly Val Asn Pro Ala Leu Pro Leu 70 75 80 85			355
ggc cga cgt gtg gat tgc tcc cgc cgc aat ttg att gcc caa tta gat Gly Arg Arg Val Asp Cys Ser Arg Arg Asn Leu Ile Ala Gln Leu Asp 90 95 100			403
gtc acc ctg cgg gca tta aac act gac tat ttg gat ttg tgg tct gtg Val Thr Leu Arg Ala Leu Asn Thr Asp Tyr Leu Asp Leu Trp Ser Val 105 110 115			451
ggc tat tgg gat gag ggc acc cca ccg cat gag gtg gcc gat act ttg Gly Tyr Trp Asp Glu Gly Thr Pro Pro His Glu Val Ala Asp Thr Leu 120 125 130			499
gat tac gcc gtg cgc acc ggc cga gtc cga tat gcc ggt gtc cga gga Asp Tyr Ala Val Arg Thr Gly Arg Val Arg Tyr Ala Gly Val Arg Gly 135 140 145			547
tat tcc ggt tgg cag tta gcg gtc acc cac gct gca tcc aat cat gca Tyr Ser Gly Trp Gln Leu Ala Val Thr His Ala Ala Ser Asn His Ala 150 155 160 165			595
gcg gcc tcc gcc cgc ccc gtg gtc gtt gca caa aat gaa tac agc ctg Ala Ala Ser Ala Arg Pro Val Val Val Ala Gln Asn Glu Tyr Ser Leu 170 175 180			643
ctg gaa cgc cgc gca gaa caa gaa ctc ctc cct gcc acc caa cac cta Leu Glu Arg Arg Ala Glu Gln Glu Leu Leu Pro Ala Thr Gln His Leu 185 190 195			691
ggt gtc gga ttc ttt gct ggc gct ccg ctg ggg caa ggc gtg ctg act Gly Val Gly Phe Phe Ala Gly Ala Pro Leu Gly Gln Gly Val Leu Thr 200 205 210			739
gct aaa tac cgc tcc gaa att ccc cat gat tcc aga gct gca tcc aca Ala Lys Tyr Arg Ser Glu Ile Pro His Asp Ser Arg Ala Ala Ser Thr 215 220 225			787
gga cgc gac gca gaa gtc caa agc tac cta gat aat cga ggc cgc atc Gly Arg Asp Ala Glu Val Gln Ser Tyr Leu Asp Asn Arg Gly Arg Ile 230 235 240 245			835
att gtc gat gct ctt gat act gca gcc aaa gga tta ggc att agc ccc Ile Val Asp Ala Leu Asp Thr Ala Ala Lys Gly Leu Gly Ile Ser Pro 250 255 260			883
gct gtc aca gcc acc acc tgg gtg cgt gat cgt ccc gga gtg aca gct Ala Val Thr Ala Thr Thr Trp Val Arg Asp Arg Pro Gly Val Thr Ala 265 270 275			931
gtc atc gtg ggc gct cgc aca cat gaa cag ctg tca cat ctt ctc aag Val Ile Val Gly Ala Arg Thr His Glu Gln Leu Ser His Leu Leu Lys 280 285 290			979
gcg gaa tcg gtg act ttg cca aca cca atc aca caa gcc ctt gat gat Ala Glu Ser Val Thr Leu Pro Thr Pro Ile Thr Gln Ala Leu Asp Asp 295 300 305			1027

gtc tcc ctg tgacttgggc caattacatt cac
 Val Ser Leu
 310

1059

<210> 752
 <211> 312
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 752
 Met Val Gly Ser Ser Gly Leu Arg Val Ser Arg Leu Gly Leu Gly Thr
 1 5 10 15
 Ser Thr Trp Gly Ser Gly Thr Glu Leu Ala Glu Ala Gly Asp Ile Phe
 20 25 30
 Lys Ala Phe Ile Asn Ser Gly Gly Thr Leu Ile Asp Val Ser Pro Asn
 35 40 45
 Tyr Thr Thr Gly Val Ala Glu Glu Met Leu Gly Thr Met Leu Asp Ala
 50 55 60
 Glu Val Ser Arg Ser Ala Val Val Ile Ser Ser Ser Ala Gly Val Asn
 65 70 75 80
 Pro Ala Leu Pro Leu Gly Arg Arg Val Asp Cys Ser Arg Arg Asn Leu
 85 90 95
 Ile Ala Gln Leu Asp Val Thr Leu Arg Ala Leu Asn Thr Asp Tyr Leu
 100 105 110
 Asp Leu Trp Ser Val Gly Tyr Trp Asp Glu Gly Thr Pro Pro His Glu
 115 120 125
 Val Ala Asp Thr Leu Asp Tyr Ala Val Arg Thr Gly Arg Val Arg Tyr
 130 135 140
 Ala Gly Val Arg Gly Tyr Ser Gly Trp Gln Leu Ala Val Thr His Ala
 145 150 155 160
 Ala Ser Asn His Ala Ala Ala Ser Ala Arg Pro Val Val Val Ala Gln
 165 170 175
 Asn Glu Tyr Ser Leu Leu Glu Arg Arg Ala Glu Gln Glu Leu Leu Pro
 180 185 190
 Ala Thr Gln His Leu Gly Val Gly Phe Phe Ala Gly Ala Pro Leu Gly
 195 200 205
 Gln Gly Val Leu Thr Ala Lys Tyr Arg Ser Glu Ile Pro His Asp Ser
 210 215 220
 Arg Ala Ala Ser Thr Gly Arg Asp Ala Glu Val Gln Ser Tyr Leu Asp
 225 230 235 240
 Asn Arg Gly Arg Ile Ile Val Asp Ala Leu Asp Thr Ala Ala Lys Gly
 245 250 255
 Leu Gly Ile Ser Pro Ala Val Thr Ala Thr Thr Trp Val Arg Asp Arg

260	265	270
Pro Gly Val Thr Ala Val Ile Val Gly Ala Arg Thr His Glu Gln Leu		
275	280	285
Ser His Leu Leu Lys Ala Glu Ser Val Thr Leu Pro Thr Pro Ile Thr		
290	295	300
Gln Ala Leu Asp Asp Val Ser Leu		
305	310	

<210> 753
 <211> 747
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(724)
 <223> RXN02554

<400> 753
 gcttttgaag tgtgtcgcgt gtgcggactg aaatagtttc cgcttcaact tggttgctaa 60
 ggataggctc cataaaaata accaaaggcg gaaaatttca atg tca cac act aag 115
 Met Ser His Thr Lys
 1 5
 cca tcc att gcc atc ctc ggt gct ggc cga gtg ggt tct tca ctt gcc 163
 Pro Ser Ile Ala Ile Leu Gly Ala Gly Arg Val Gly Ser Ser Leu Ala
 10 15 20
 agg tca gcg gtc gcc gca ggc tat gag gta aag gtt gct ggt tca ggt 211
 Arg Ser Ala Val Ala Ala Gly Tyr Glu Val Lys Val Ala Gly Ser Gly
 25 30 35
 gct gtg gac aaa atc gct ctt acc gct gag atc ctt atg ccc ggc gcg 259
 Ala Val Asp Lys Ile Ala Leu Thr Ala Glu Ile Leu Met Pro Gly Ala
 40 45 50
 gtt cca agc act gct gac cag gct gta aag gat gca gat att gtg ttc 307
 Val Pro Ser Thr Ala Asp Gln Ala Val Lys Asp Ala Asp Ile Val Phe
 55 60 65
 ttg gct gtt ccc ctg cat aaa ttc cgc agt gtc aat cca gcc act tta 355
 Leu Ala Val Pro Leu His Lys Phe Arg Ser Val Asn Pro Ala Thr Leu
 70 75 80 85
 gag ggc aag atc gtt att gac acg atg aac cac tgg gtt ccg gtc aat 403
 Glu Gly Lys Ile Val Ile Asp Thr Met Asn His Trp Val Pro Val Asn
 90 95 100
 ggt gag ttg gag gaa att gat cag gat ccg cgc agc act tcg gag att 451
 Gly Glu Leu Glu Glu Ile Asp Gln Asp Pro Arg Ser Thr Ser Glu Ile
 105 110 115
 att gcg gag ttt ttc gcg gga tca acc atg gtg aag tct ttt aac cac 499
 Ile Ala Glu Phe Phe Ala Gly Ser Thr Met Val Lys Ser Phe Asn His
 120 125 130

att ggt tat cac gag att gag cag gat gcg ggt acc ggg cgt gcg att 547
 Ile Gly Tyr His Glu Ile Glu Gln Asp Ala Gly Thr Gly Arg Ala Ile
 135 140 145

 gcg tat gcc acg gat gat gtg gat gca ggt gcc cag gtt gca cag cta 595
 Ala Tyr Ala Thr Asp Asp Val Asp Ala Gly Ala Gln Val Ala Gln Leu
 150 155 160 165

 att aag agt ttt ggg ttt gtt cct tta aat att ggc gca ttg gaa aac 643
 Ile Lys Ser Phe Gly Phe Val Pro Leu Asn Ile Gly Ala Leu Glu Asn
 170 175 180

 ggc cgt att ctg gaa cct ggc caa gaa gct ttc ggc gcg cac ctt aat 691
 Gly Arg Ile Leu Glu Pro Gly Gln Glu Ala Phe Gly Ala His Leu Asn
 185 190 195

 aaa gat tcg cgc cta gaa ctt gtt aat cag cgg tagtacctcg atcttcagcc 744
 Lys Asp Ser Arg Leu Glu Leu Val Asn Gln Arg
 200 205

 aac 747

<210> 754
 <211> 208
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 754

Met Ser His Thr Lys Pro Ser Ile Ala Ile Leu Gly Ala Gly Arg Val
 1 5 10 15

 Gly Ser Ser Leu Ala Arg Ser Ala Val Ala Ala Gly Tyr Glu Val Lys
 20 25 30

 Val Ala Gly Ser Gly Ala Val Asp Lys Ile Ala Leu Thr Ala Glu Ile
 35 40 45

 Leu Met Pro Gly Ala Val Pro Ser Thr Ala Asp Gln Ala Val Lys Asp
 50 55 60

 Ala Asp Ile Val Phe Leu Ala Val Pro Leu His Lys Phe Arg Ser Val
 65 70 75 80

 Asn Pro Ala Thr Leu Glu Gly Lys Ile Val Ile Asp Thr Met Asn His
 85 90 95

 Trp Val Pro Val Asn Gly Glu Leu Glu Glu Ile Asp Gln Asp Pro Arg
 100 105 110

 Ser Thr Ser Glu Ile Ile Ala Glu Phe Phe Ala Gly Ser Thr Met Val
 115 120 125

 Lys Ser Phe Asn His Ile Gly Tyr His Glu Ile Glu Gln Asp Ala Gly
 130 135 140

 Thr Gly Arg Ala Ile Ala Tyr Ala Thr Asp Asp Val Asp Ala Gly Ala
 145 150 155 160

 Gln Val Ala Gln Leu Ile Lys Ser Phe Gly Phe Val Pro Leu Asn Ile
 165 170 175

Gly Ala Leu Glu Asn Gly Arg Ile Leu Glu Pro Gly Gln Glu Ala Phe
 180 185 190

Gly Ala His Leu Asn Lys Asp Ser Arg Leu Glu Leu Val Asn Gln Arg
 195 200 205

<210> 755
 <211> 933
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(910)
 <223> RXN01204

<400> 755
 ttacagcgag tttttcagac gtccatcgca ccgtgcacaa caacatttca ggtgcacggc 60

ccgaacacgg gagagaacgc tgagcggttac aacactgtcc atg aag ggc gaa ttc 115
 Met Lys Gly Glu Phe
 1 5

cac gcc ccc gat ttg gac aaa gaa ttt ttc ccg ggg cac gta acc gat 163
 His Ala Pro Asp Leu Asp Lys Glu Phe Phe Pro Gly His Val Thr Asp
 10 15 20

agt ggt gaa gtc gtg aac atg ctg ttc acc gat ttc gct aat ggt tgg 211
 Ser Gly Glu Val Val Asn Met Leu Phe Thr Asp Phe Ala Asn Gly Trp
 25 30 35

ttc gca atg gac cgc atc gta ttg atc cgt ctt ctt atg acg gca gtc 259
 Phe Ala Met Asp Arg Ile Val Leu Ile Arg Leu Leu Met Thr Ala Val
 40 45 50

gtt gtg gtc ttc ttc ctt tgg gct atg cgc aag cca aag ctt gtt ccg 307
 Val Val Val Phe Phe Leu Trp Ala Met Arg Lys Pro Lys Leu Val Pro
 55 60 65

cat ggc gtc cag aat ttt gca gag tac gca ctc gat ttc gtt ggt att 355
 His Gly Val Gln Asn Phe Ala Glu Tyr Ala Leu Asp Phe Val Gly Ile
 70 75 80 85

cac atc gct gaa gac atc ctc gga aag aag aaa ggt cgt cgg ttc ctg 403
 His Ile Ala Glu Asp Ile Leu Gly Lys Lys Lys Gly Arg Arg Phe Leu
 90 95 100

ccg atc ctg gcc acc atc ttc ttc gcg gct ctg ttg atg aac ctt gca 451
 Pro Ile Leu Ala Thr Ile Phe Phe Ala Ala Leu Leu Met Asn Leu Ala
 105 110 115

acg atc atc ccg gga cta aac atc tcc tcc aac tca cgt att gca ttc 499
 Thr Ile Ile Pro Gly Leu Asn Ile Ser Ser Asn Ser Arg Ile Ala Phe
 120 125 130

cca atc gtg atg gcg gta gct ggt tac atc gcg ttt atc tac gca ggc 547

Pro Ile Val Met Ala Val Ala Gly Tyr Ile Ala Phe Ile Tyr Ala Gly
 135 140 145

tct aag cgt tac gga ttc ttc aaa tat gtg aag tct tct gtt gtg att 595
 Ser Lys Arg Tyr Gly Phe Phe Lys Tyr Val Lys Ser Ser Val Val Ile
 150 155 160 165

ccg aac att cca cca gca ctt cac gtc ttg gtg gtt cca att gag ttc 643
 Pro Asn Ile Pro Pro Ala Leu His Val Leu Val Val Pro Ile Glu Phe
 170 175 180

ttc tct aca ttc atc ttg agg cca gtc acc ctg gca ctg cgt ttg atg 691
 Phe Ser Thr Phe Ile Leu Arg Pro Val Thr Leu Ala Leu Arg Leu Met
 185 190 195

gcc aac ttc ctt gct ggc cac atc atc ctg gtt ctg ctt ttc tcc gca 739
 Ala Asn Phe Leu Ala Gly His Ile Ile Leu Val Leu Leu Phe Ser Ala
 200 205 210

acg aac ttc ttc ttc ttc cag ttc aac gga tgg aca gca atg tcc ggc 787
 Thr Asn Phe Phe Phe Phe Gln Phe Asn Gly Trp Thr Ala Met Ser Gly
 215 220 225

gta acc atc ttg atg gca gta ctc ttc acg gtt tac gag atc att gtt 835
 Val Thr Ile Leu Met Ala Val Leu Phe Thr Val Tyr Glu Ile Ile Val
 230 235 240 245

atc ttc ctg cag gca tac atc ttc gct ctg ctg gtc gct gta tac att 883
 Ile Phe Leu Gln Ala Tyr Ile Phe Ala Leu Leu Val Ala Val Tyr Ile
 250 255 260

gag ctt tca ctt cac gcg gat tct cac tagatgaaaa aggtcgctat 930
 Glu Leu Ser Leu His Ala Asp Ser His
 265 270

taa 933

<210> 756

<211> 270

<212> PRT

<213> Corynebacterium glutamicum

<400> 756

Met Lys Gly Glu Phe His Ala Pro Asp Leu Asp Lys Glu Phe Phe Pro
 1 5 10 15

Gly His Val Thr Asp Ser Gly Glu Val Val Asn Met Leu Phe Thr Asp
 20 25 30

Phe Ala Asn Gly Trp Phe Ala Met Asp Arg Ile Val Leu Ile Arg Leu
 35 40 45

Leu Met Thr Ala Val Val Val Val Phe Phe Leu Trp Ala Met Arg Lys
 50 55 60

Pro Lys Leu Val Pro His Gly Val Gln Asn Phe Ala Glu Tyr Ala Leu
 65 70 75 80

Asp Phe Val Gly Ile His Ile Ala Glu Asp Ile Leu Gly Lys Lys Lys
 85 90 95

Gly Arg Arg Phe Leu Pro Ile Leu Ala Thr Ile Phe Phe Ala Ala Leu
 100 105 110
 Leu Met Asn Leu Ala Thr Ile Ile Pro Gly Leu Asn Ile Ser Ser Asn
 115 120 125
 Ser Arg Ile Ala Phe Pro Ile Val Met Ala Val Ala Gly Tyr Ile Ala
 130 135 140
 Phe Ile Tyr Ala Gly Ser Lys Arg Tyr Gly Phe Phe Lys Tyr Val Lys
 145 150 155 160
 Ser Ser Val Val Ile Pro Asn Ile Pro Pro Ala Leu His Val Leu Val
 165 170 175
 Val Pro Ile Glu Phe Phe Ser Thr Phe Ile Leu Arg Pro Val Thr Leu
 180 185 190
 Ala Leu Arg Leu Met Ala Asn Phe Leu Ala Gly His Ile Ile Leu Val
 195 200 205
 Leu Leu Phe Ser Ala Thr Asn Phe Phe Phe Phe Gln Phe Asn Gly Trp
 210 215 220
 Thr Ala Met Ser Gly Val Thr Ile Leu Met Ala Val Leu Phe Thr Val
 225 230 235 240
 Tyr Glu Ile Ile Val Ile Phe Leu Gln Ala Tyr Ile Phe Ala Leu Leu
 245 250 255
 Val Ala Val Tyr Ile Glu Leu Ser Leu His Ala Asp Ser His
 260 265 270

<210> 757
 <211> 862
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(862)
 <223> FRXA01204

<400> 757
 ttacagcgag tttttcagac gtccatcgca ccgtgcacaa caacatttca ggtgcacggc 60
 ccgaacacgg gagagaacgc tgagcggttac aacactgtcc atg aag ggc gaa ttc 115
 Met Lys Gly Glu Phe
 1 5
 cac gcc ccc gat ttg gac aaa gaa ttt ttc ccg ggg cac gta acc gat 163
 His Ala Pro Asp Leu Asp Lys Glu Phe Phe Pro Gly His Val Thr Asp
 10 15 20
 agt ggt gaa gtc gtg aac atg ctg ttc acc gat ttc gct aat ggt tgg 211
 Ser Gly Glu Val Val Asn Met Leu Phe Thr Asp Phe Ala Asn Gly Trp
 25 30 35
 ttc gca atg gac cgc atc gta ttg atc cgt ctt ctt atg acg gca gtc 259

Phe	Ala	Met	Asp	Arg	Ile	Val	Leu	Ile	Arg	Leu	Leu	Met	Thr	Ala	Val	
	40						45					50				
gtt	gtg	gtc	ttc	ttc	ctt	tgg	gct	atg	cgc	aag	cca	aag	ctt	gtt	ccg	307
Val	Val	Val	Phe	Phe	Leu	Trp	Ala	Met	Arg	Lys	Pro	Lys	Leu	Val	Pro	
	55					60					65					
cat	ggc	gtc	cag	aat	ttt	gca	gag	tac	gca	ctc	gat	ttc	gtt	ggt	att	355
His	Gly	Val	Gln	Asn	Phe	Ala	Glu	Tyr	Ala	Leu	Asp	Phe	Val	Gly	Ile	
70					75					80					85	
cac	atc	gct	gaa	gac	atc	ctc	gga	aag	aag	aaa	ggt	cgt	cgg	ttc	ctg	403
His	Ile	Ala	Glu	Asp	Ile	Leu	Gly	Lys	Lys	Lys	Gly	Arg	Arg	Phe	Leu	
				90					95					100		
ccg	atc	ctg	gcc	acc	atc	ttc	ttc	gcg	gct	ctg	ttg	atg	aac	ctt	gca	451
Pro	Ile	Leu	Ala	Thr	Ile	Phe	Phe	Ala	Ala	Leu	Leu	Met	Asn	Leu	Ala	
			105					110					115			
acg	atc	atc	ccg	gga	cta	aac	atc	tcc	tcc	aac	tca	cgt	att	gca	ttc	499
Thr	Ile	Ile	Pro	Gly	Leu	Asn	Ile	Ser	Ser	Asn	Ser	Arg	Ile	Ala	Phe	
			120				125					130				
cca	atc	gtg	atg	gcg	gta	gct	ggt	tac	atc	gcg	ttt	atc	tac	gca	ggc	547
Pro	Ile	Val	Met	Ala	Val	Ala	Gly	Tyr	Ile	Ala	Phe	Ile	Tyr	Ala	Gly	
			135			140					145					
tct	aag	cgt	tac	gga	ttc	ttc	aaa	tat	gtg	aag	tct	tct	gtt	gtg	att	595
Ser	Lys	Arg	Tyr	Gly	Phe	Phe	Lys	Tyr	Val	Lys	Ser	Ser	Val	Val	Ile	
150					155					160					165	
ccg	aac	att	cca	cca	gca	ctt	cac	gtc	ttg	gtg	gtt	cca	att	gag	ttc	643
Pro	Asn	Ile	Pro	Pro	Ala	Leu	His	Val	Leu	Val	Val	Pro	Ile	Glu	Phe	
				170				175						180		
ttc	tct	aca	ttc	atc	ttg	agg	cca	gtc	acc	ctg	gca	ctg	cgt	ttg	atg	691
Phe	Ser	Thr	Phe	Ile	Leu	Arg	Pro	Val	Thr	Leu	Ala	Leu	Arg	Leu	Met	
			185				190						195			
gcc	aac	ttc	ctt	gct	ggc	cac	atc	atc	ctg	gtt	ctg	ctt	ttc	ttc	gca	739
Ala	Asn	Phe	Leu	Ala	Gly	His	Ile	Ile	Leu	Val	Leu	Leu	Phe	Phe	Ala	
			200				205					210				
acg	aac	ttc	ttc	ttc	ttc	cag	ttc	aac	gga	tgg	aca	gca	atg	tcc	ggc	787
Thr	Asn	Phe	Phe	Phe	Phe	Gln	Phe	Asn	Gly	Trp	Thr	Ala	Met	Ser	Gly	
			215			220					225					
gta	acc	atc	ttg	atg	gca	gta	ctc	ttc	acg	gtt	tac	gag	atc	att	gtt	835
Val	Thr	Ile	Leu	Met	Ala	Val	Leu	Phe	Thr	Val	Tyr	Glu	Ile	Ile	Val	
230					235				240						245	
atc	ttc	ctg	cag	gca	tac	atc	ttc	gct								862
Ile	Phe	Leu	Gln	Ala	Tyr	Ile	Phe	Ala								
				250												

<210> 758

<211> 254

<212> PRT

<213> Corynebacterium glutamicum

<400> 758

```

Met Lys Gly Glu Phe His Ala Pro Asp Leu Asp Lys Glu Phe Phe Pro
 1              5              10              15

Gly His Val Thr Asp Ser Gly Glu Val Val Asn Met Leu Phe Thr Asp
              20              25              30

Phe Ala Asn Gly Trp Phe Ala Met Asp Arg Ile Val Leu Ile Arg Leu
              35              40              45

Leu Met Thr Ala Val Val Val Val Phe Phe Leu Trp Ala Met Arg Lys
 50              55              60

Pro Lys Leu Val Pro His Gly Val Gln Asn Phe Ala Glu Tyr Ala Leu
 65              70              75              80

Asp Phe Val Gly Ile His Ile Ala Glu Asp Ile Leu Gly Lys Lys Lys
              85              90              95

Gly Arg Arg Phe Leu Pro Ile Leu Ala Thr Ile Phe Phe Ala Ala Leu
              100              105              110

Leu Met Asn Leu Ala Thr Ile Ile Pro Gly Leu Asn Ile Ser Ser Asn
              115              120              125

Ser Arg Ile Ala Phe Pro Ile Val Met Ala Val Ala Gly Tyr Ile Ala
              130              135              140

Phe Ile Tyr Ala Gly Ser Lys Arg Tyr Gly Phe Phe Lys Tyr Val Lys
              145              150              155              160

Ser Ser Val Val Ile Pro Asn Ile Pro Pro Ala Leu His Val Leu Val
              165              170              175

Val Pro Ile Glu Phe Phe Ser Thr Phe Ile Leu Arg Pro Val Thr Leu
              180              185              190

Ala Leu Arg Leu Met Ala Asn Phe Leu Ala Gly His Ile Ile Leu Val
              195              200              205

Leu Leu Phe Phe Ala Thr Asn Phe Phe Phe Phe Gln Phe Asn Gly Trp
              210              215              220

Thr Ala Met Ser Gly Val Thr Ile Leu Met Ala Val Leu Phe Thr Val
              225              230              235              240

Tyr Glu Ile Ile Val Ile Phe Leu Gln Ala Tyr Ile Phe Ala
              245              250

```

<210> 759

<211> 1764

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1741)

<223> RXA01201

<400> 759


```

tcgggcaaac tcgagcgtct gcgggcaagc ttgcataaa gacacgacga attagacaac 60
attagtaatg ctggaagaaa caaccgagag caggaagaac atg gcg gag ctg acg 115
                                         Met Ala Glu Leu Thr
                                         1           5

atc tcc tcc gat gag atc cgt agc gcg att gcg aac tac acc tcg agc 163
Ile Ser Ser Asp Glu Ile Arg Ser Ala Ile Ala Asn Tyr Thr Ser Ser
          10           15           20

tac tcc gcg gag gcc tcc cgt gag gag gtc gcc gtg gtt att tcg gcc 211
Tyr Ser Ala Glu Ala Ser Arg Glu Glu Val Gly Val Val Ile Ser Ala
          25           30           35

gct gac ggt atc gcc cag gtt tcg gcc ctc ccg tca gta atg gcg aat 259
Ala Asp Gly Ile Ala Gln Val Ser Gly Leu Pro Ser Val Met Ala Asn
          40           45           50

gag ctc ctc gaa ttc ccg gcc gcc gtc atc gcc gtc gca cag aac ctt 307
Glu Leu Leu Glu Phe Pro Gly Gly Val Ile Gly Val Ala Gln Asn Leu
          55           60           65

gaa gct gac cga gtc gcc gtc gtg gtc ctg ggt aac tac gag cta ctt 355
Glu Ala Asp Arg Val Gly Val Val Val Leu Gly Asn Tyr Glu Leu Leu
          70           75           80           85

aaa gaa gcc gac caa gtt cgt cgt act gga gac gtt ctg tct atc cca 403
Lys Glu Gly Asp Gln Val Arg Arg Thr Gly Asp Val Leu Ser Ile Pro
          90           95           100

gtc gcc gag gca ttc ctt gcc cgc gtt atc aac ccc ctt gcc cag cca 451
Val Gly Glu Ala Phe Leu Gly Arg Val Ile Asn Pro Leu Gly Gln Pro
          105           110           115

att gac gcc ctg gcc gaa att gca tcc gaa gag gac cgc gtc ctc gag 499
Ile Asp Gly Leu Gly Glu Ile Ala Ser Glu Glu Asp Arg Val Leu Glu
          120           125           130

ctt cag gca cca acc gtg ctt gag cgc cag cct gtc gag gag cct ttg 547
Leu Gln Ala Pro Thr Val Leu Glu Arg Gln Pro Val Glu Glu Pro Leu
          135           140           145

gca acc gcc atc aag gct atc gat gca atg acc cca atc gcc cgc ggt 595
Ala Thr Gly Ile Lys Ala Ile Asp Ala Met Thr Pro Ile Gly Arg Gly
          150           155           160           165

cag cgt cag ctg atc att ggt gac cgt aag act gcc aag acc gca gtc 643
Gln Arg Gln Leu Ile Ile Gly Asp Arg Lys Thr Gly Lys Thr Ala Val
          170           175           180

tgt gtc gat acc atc ctt aac cag aag gcc aac tgg gag acc gcc gac 691
Cys Val Asp Thr Ile Leu Asn Gln Lys Ala Asn Trp Glu Thr Gly Asp
          185           190           195

aag acc aag cag gtt cgc tgc atc tac gtc gca atc ggt cag aag gcc 739
Lys Thr Lys Gln Val Arg Cys Ile Tyr Val Ala Ile Gly Gln Lys Gly
          200           205           210

tcc acc att gca gcc ctg cgt aag acc ctc gag gag cag gcc gct ctc 787
Ser Thr Ile Ala Ala Leu Arg Lys Thr Leu Glu Glu Gln Gly Ala Leu
          215           220           225

```

gag tac acc acc atc gtg gct gca ccc gct tcc gat gct gca ggc ttc	835
Glu Tyr Thr Thr Ile Val Ala Ala Pro Ala Ser Asp Ala Ala Gly Phe	
230 235 240 245	
aag tgg ctt gca cca ttc gct ggc gct gct ctc gcc cag cac tgg atg	883
Lys Trp Leu Ala Pro Phe Ala Gly Ala Ala Leu Ala Gln His Trp Met	
250 255 260	
tac cag ggc aac cac gtc ctg gtc atc tac gat gat ctg acc aag cag	931
Tyr Gln Gly Asn His Val Leu Val Ile Tyr Asp Asp Leu Thr Lys Gln	
265 270 275	
gct gag gca tac cgt gct atc tcc ctg ctg ctg cgt cgc cca ccg ggc	979
Ala Glu Ala Tyr Arg Ala Ile Ser Leu Leu Leu Arg Arg Pro Pro Gly	
280 285 290	
cgc gaa gca tac cca ggt gac gtc ttc tac ctg cac tcc cgt ctg ctg	1027
Arg Glu Ala Tyr Pro Gly Asp Val Phe Tyr Leu His Ser Arg Leu Leu	
295 300 305	
gag cgc gct gcg aag ctg tcc gat gaa cta ggc gca ggt tct att aca	1075
Glu Arg Ala Ala Lys Leu Ser Asp Glu Leu Gly Ala Gly Ser Ile Thr	
310 315 320 325	
gca ctg cca atc att gag acc aag gct aat gac gtt tcc gcc ttc att	1123
Ala Leu Pro Ile Ile Glu Thr Lys Ala Asn Asp Val Ser Ala Phe Ile	
330 335 340	
cct acc aac gtg att tcc atc acc gac ggt cag gta ttc ctt gag tcc	1171
Pro Thr Asn Val Ile Ser Ile Thr Asp Gly Gln Val Phe Leu Glu Ser	
345 350 355	
gac ctg ttc aac cgt ggc gtt cgc ccg gcg atc aac gtc ggt gta tcc	1219
Asp Leu Phe Asn Arg Gly Val Arg Pro Ala Ile Asn Val Gly Val Ser	
360 365 370	
gtc tcc cgt gtc ggt ggc gca gct cag acc aag ggt atg aag aag gtt	1267
Val Ser Arg Val Gly Gly Ala Ala Gln Thr Lys Gly Met Lys Lys Val	
375 380 385	
gcc ggt tct ctc cgt ctg gat ctg gct gca ttc cgc gac ctg gaa gca	1315
Ala Gly Ser Leu Arg Leu Asp Leu Ala Ala Phe Arg Asp Leu Glu Ala	
390 395 400 405	
ttc gct acc ttc gca tct gac ttg gat gct gca tcc aag tct cag ctt	1363
Phe Ala Thr Phe Ala Ser Asp Leu Asp Ala Ala Ser Lys Ser Gln Leu	
410 415 420	
gag cgt ggc cag cgc ctc gtt cag ctg ttg att cag tct gag aac gca	1411
Glu Arg Gly Gln Arg Leu Val Gln Leu Leu Ile Gln Ser Glu Asn Ala	
425 430 435	
cct cag gct gtt gag tac cag atc att tct ctc tgg ctt gca ggc gaa	1459
Pro Gln Ala Val Glu Tyr Gln Ile Ile Ser Leu Trp Leu Ala Gly Glu	
440 445 450	
ggc gca ttc gac aac gtt cct gtt gaa gat gtt cgt cgc ttc gag tcc	1507
Gly Ala Phe Asp Asn Val Pro Val Glu Asp Val Arg Arg Phe Glu Ser	
455 460 465	

gaa ctg cac gag tac tta ggc tcc aac gct gca cag gtc tac gag cag 1555
 Glu Leu His Glu Tyr Leu Gly Ser Asn Ala Ala Gln Val Tyr Glu Gln
 470 475 480 485

 atc gct ggt gga gct cag ctt tcc gac gag tcc aag gaa acc ttg ctc 1603
 Ile Ala Gly Gly Ala Gln Leu Ser Asp Glu Ser Lys Glu Thr Leu Leu
 490 495 500

 aag gca acc gaa gat ttc aag agc gct ttc cag acc acc gat ggc acc 1651
 Lys Ala Thr Glu Asp Phe Lys Ser Ala Phe Gln Thr Thr Asp Gly Thr
 505 510 515

 cct gtc atc aac gag cct gag gtt gaa gca ctc gat gca ggc cag gtc 1699
 Pro Val Ile Asn Glu Pro Glu Val Glu Ala Leu Asp Ala Gly Gln Val
 520 525 530

 aag aaa gac cag ctc acc gtt tcc cgc aag gtc agc aag aag 1741
 Lys Lys Asp Gln Leu Thr Val Ser Arg Lys Val Ser Lys Lys
 535 540 545

 taaggcagcg agcctacact aaa 1764

<210> 760

<211> 547

<212> PRT

<213> Corynebacterium glutamicum

<400> 760

Met Ala Glu Leu Thr Ile Ser Ser Asp Glu Ile Arg Ser Ala Ile Ala
 1 5 10 15

 Asn Tyr Thr Ser Ser Tyr Ser Ala Glu Ala Ser Arg Glu Glu Val Gly
 20 25 30

 Val Val Ile Ser Ala Ala Asp Gly Ile Ala Gln Val Ser Gly Leu Pro
 35 40 45

 Ser Val Met Ala Asn Glu Leu Leu Glu Phe Pro Gly Gly Val Ile Gly
 50 55 60

 Val Ala Gln Asn Leu Glu Ala Asp Arg Val Gly Val Val Val Leu Gly
 65 70 75 80

 Asn Tyr Glu Leu Leu Lys Glu Gly Asp Gln Val Arg Arg Thr Gly Asp
 85 90 95

 Val Leu Ser Ile Pro Val Gly Glu Ala Phe Leu Gly Arg Val Ile Asn
 100 105 110

 Pro Leu Gly Gln Pro Ile Asp Gly Leu Gly Glu Ile Ala Ser Glu Glu
 115 120 125

 Asp Arg Val Leu Glu Leu Gln Ala Pro Thr Val Leu Glu Arg Gln Pro
 130 135 140

 Val Glu Glu Pro Leu Ala Thr Gly Ile Lys Ala Ile Asp Ala Met Thr
 145 150 155 160

 Pro Ile Gly Arg Gly Gln Arg Gln Leu Ile Ile Gly Asp Arg Lys Thr
 165 170 175

Gly Lys Thr Ala Val Cys Val Asp Thr Ile Leu Asn Gln Lys Ala Asn
 180 185 190
 Trp Glu Thr Gly Asp Lys Thr Lys Gln Val Arg Cys Ile Tyr Val Ala
 195 200 205
 Ile Gly Gln Lys Gly Ser Thr Ile Ala Ala Leu Arg Lys Thr Leu Glu
 210 215 220
 Glu Gln Gly Ala Leu Glu Tyr Thr Thr Ile Val Ala Ala Pro Ala Ser
 225 230 235 240
 Asp Ala Ala Gly Phe Lys Trp Leu Ala Pro Phe Ala Gly Ala Ala Leu
 245 250 255
 Ala Gln His Trp Met Tyr Gln Gly Asn His Val Leu Val Ile Tyr Asp
 260 265 270
 Asp Leu Thr Lys Gln Ala Glu Ala Tyr Arg Ala Ile Ser Leu Leu Leu
 275 280 285
 Arg Arg Pro Pro Gly Arg Glu Ala Tyr Pro Gly Asp Val Phe Tyr Leu
 290 295 300
 His Ser Arg Leu Leu Glu Arg Ala Ala Lys Leu Ser Asp Glu Leu Gly
 305 310 315 320
 Ala Gly Ser Ile Thr Ala Leu Pro Ile Ile Glu Thr Lys Ala Asn Asp
 325 330 335
 Val Ser Ala Phe Ile Pro Thr Asn Val Ile Ser Ile Thr Asp Gly Gln
 340 345 350
 Val Phe Leu Glu Ser Asp Leu Phe Asn Arg Gly Val Arg Pro Ala Ile
 355 360 365
 Asn Val Gly Val Ser Val Ser Arg Val Gly Gly Ala Ala Gln Thr Lys
 370 375 380
 Gly Met Lys Lys Val Ala Gly Ser Leu Arg Leu Asp Leu Ala Ala Phe
 385 390 395 400
 Arg Asp Leu Glu Ala Phe Ala Thr Phe Ala Ser Asp Leu Asp Ala Ala
 405 410 415
 Ser Lys Ser Gln Leu Glu Arg Gly Gln Arg Leu Val Gln Leu Leu Ile
 420 425 430
 Gln Ser Glu Asn Ala Pro Gln Ala Val Glu Tyr Gln Ile Ile Ser Leu
 435 440 445
 Trp Leu Ala Gly Glu Gly Ala Phe Asp Asn Val Pro Val Glu Asp Val
 450 455 460
 Arg Arg Phe Glu Ser Glu Leu His Glu Tyr Leu Gly Ser Asn Ala Ala
 465 470 475 480
 Gln Val Tyr Glu Gln Ile Ala Gly Gly Ala Gln Leu Ser Asp Glu Ser
 485 490 495

Lys Glu Thr Leu Leu Lys Ala Thr Glu Asp Phe Lys Ser Ala Phe Gln
 500 505 510

Thr Thr Asp Gly Thr Pro Val Ile Asn Glu Pro Glu Val Glu Ala Leu
 515 520 525

Asp Ala Gly Gln Val Lys Lys Asp Gln Leu Thr Val Ser Arg Lys Val
 530 535 540

Ser Lys Lys
 545

<210> 761
 <211> 1572
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1549)
 <223> RXN01193

<400> 761
 gtgtggccaa ccaggcacgt caggcacaga tcacccagga aatcacagag attgttggtg 60

gcgcaggcgc gctcgccgac agcggagaaaa gtgactaatt atg act aca gct ctt 115
 Met Thr Thr Ala Leu
 1 5

gaa gag cag aac gca cag cag gca gcc act gcc ggc cgt gtc gtg cgt 163
 Glu Glu Gln Asn Ala Gln Gln Ala Ala Thr Ala Gly Arg Val Val Arg
 10 15 20

gtc att ggt gcg gtc gtc gac gtg gag ttt ccc cgc ggc gag ctg cca 211
 Val Ile Gly Ala Val Val Asp Val Glu Phe Pro Arg Gly Glu Leu Pro
 25 30 35

gca ctg tac aac gca ctt act gta gag gta acc ctc gaa tca gtt aag 259
 Ala Leu Tyr Asn Ala Leu Thr Val Glu Val Thr Leu Glu Ser Val Lys
 40 45 50

aag acc gtt gtt ctc gag gtt gct cag cac ctc ggc gac aac ctc atc 307
 Lys Thr Val Val Leu Glu Val Ala Gln His Leu Gly Asp Asn Leu Ile
 55 60 65

cgc acc atc gct atg gca cca acc gac gga ctt gtc cgc ggt gct gct 355
 Arg Thr Ile Ala Met Ala Pro Thr Asp Gly Leu Val Arg Gly Ala Ala
 70 75 80 85

gta acc gat act gca cgc cca att tcc gta cca gtg ggc gat gtt gtt 403
 Val Thr Asp Thr Ala Arg Pro Ile Ser Val Pro Val Gly Asp Val Val
 90 95 100

aag ggc cac gta ttc aac gct ttg ggc gac tgc cta gac gac gtt tcc 451
 Lys Gly His Val Phe Asn Ala Leu Gly Asp Cys Leu Asp Asp Val Ser
 105 110 115

ctg aac aac aac cca gag atc gag cgt tgg ggc atc cac cgc gag cca 499
 Leu Asn Asn Asn Pro Glu Ile Glu Arg Trp Gly Ile His Arg Glu Pro
 120 125 130

cca tca ttc gat cag ctt gag ggt aag acc gag atc ctg gaa aca ggc	547
Pro Ser Phe Asp Gln Leu Glu Gly Lys Thr Glu Ile Leu Glu Thr Gly	
135 140 145	
atc aag gtt atc gac ctt ctc acc cct tac gtt aag ggt gga aag atc	595
Ile Lys Val Ile Asp Leu Leu Thr Pro Tyr Val Lys Gly Gly Lys Ile	
150 155 160 165	
ggc ctc ttc ggt ggt gca ggt gtg ggt aag acc gtt ctt atc cag gaa	643
Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr Val Leu Ile Gln Glu	
170 175 180	
atg atc acc cgt att gca cgt gag ttc tcc ggt act tcc gtg ttc gca	691
Met Ile Thr Arg Ile Ala Arg Glu Phe Ser Gly Thr Ser Val Phe Ala	
185 190 195	
ggt gtt ggt gag cgt acc cgt gag ggc acc gac ctc ttc ctc gaa atg	739
Gly Val Gly Glu Arg Thr Arg Glu Gly Thr Asp Leu Phe Leu Glu Met	
200 205 210	
gaa gaa atg ggc gtt ctc cag gac acc gcc ctg gtg ttc ggt cag atg	787
Glu Glu Met Gly Val Leu Gln Asp Thr Ala Leu Val Phe Gly Gln Met	
215 220 225	
gat gag cca cca gga gtc ggt atg cgc gtg gct ctg tcc ggc ctg acc	835
Asp Glu Pro Pro Gly Val Gly Met Arg Val Ala Leu Ser Gly Leu Thr	
230 235 240 245	
atg gcg gag tac ttc cgc gat gtt cag aac cag gac gtg ctg ctg ttc	883
Met Ala Glu Tyr Phe Arg Asp Val Gln Asn Gln Asp Val Leu Leu Phe	
250 255 260	
atc gac aac atc ttc cgt ttc acc cag gca ggt tct gag gtt tcc acc	931
Ile Asp Asn Ile Phe Arg Phe Thr Gln Ala Gly Ser Glu Val Ser Thr	
265 270 275	
ctt ctg ggt cgt atg cct tcc gcc gtg ggt tac cag cca acc ctg gct	979
Leu Leu Gly Arg Met Pro Ser Ala Val Gly Tyr Gln Pro Thr Leu Ala	
280 285 290	
gac gag atg ggt gtt ctc cag gag cgc att acc tcc acc aag ggc cgt	1027
Asp Glu Met Gly Val Leu Gln Glu Arg Ile Thr Ser Thr Lys Gly Arg	
295 300 305	
tcg att acc tct ctg cag gcc gtt tac gtt cct gcc gat gac tac acc	1075
Ser Ile Thr Ser Leu Gln Ala Val Tyr Val Pro Ala Asp Asp Tyr Thr	
310 315 320 325	
gac ccg gct cca gcg acc acc ttc gct cac ttg gat gca acc acc gag	1123
Asp Pro Ala Pro Ala Thr Thr Phe Ala His Leu Asp Ala Thr Thr Glu	
330 335 340	
ctt gac cgc tcc att gct tcc aag ggt att tac cca gca gtg aac cca	1171
Leu Asp Arg Ser Ile Ala Ser Lys Gly Ile Tyr Pro Ala Val Asn Pro	
345 350 355	
ctg acc tcc acc tct cgt att ctc gag cca gca atc gtt ggt gag cgt	1219
Leu Thr Ser Thr Ser Arg Ile Leu Glu Pro Ala Ile Val Gly Glu Arg	
360 365 370	

cac tac gag gtt tct cag cgt gtc atc ggc att ctg cag aag aac aag 1267
 His Tyr Glu Val Ser Gln Arg Val Ile Gly Ile Leu Gln Lys Asn Lys
 375 380 385

 gaa ctt cag gac atc atc gcc atc ctt ggt atg gac gag ctt tct gaa 1315
 Glu Leu Gln Asp Ile Ile Ala Ile Leu Gly Met Asp Glu Leu Ser Glu
 390 395 400 405

 gag gac aag atc acc gtt gca cgt gcg cgt cgc atc gag cgc ttc ctg 1363
 Glu Asp Lys Ile Thr Val Ala Arg Ala Arg Arg Ile Glu Arg Phe Leu
 410 415 420

 ggt cag aac ttc ttc gtt gca gag aag ttc acc ggt ctt cct ggc tcc 1411
 Gly Gln Asn Phe Phe Val Ala Glu Lys Phe Thr Gly Leu Pro Gly Ser
 425 430 435

 tac gtg cca ctg acc gac acc gtc gac gct ttc gag cgt att tgc aac 1459
 Tyr Val Pro Leu Thr Asp Thr Val Asp Ala Phe Glu Arg Ile Cys Asn
 440 445 450

 ggc gac ttc gac cac tac cca gag cag gct ttc aac ggc ctc ggt ggt 1507
 Gly Asp Phe Asp His Tyr Pro Glu Gln Ala Phe Asn Gly Leu Gly Gly
 455 460 465

 ttg gac gat gtc gaa gct gca tac aag aag ctg acc gga aag 1549
 Leu Asp Asp Val Glu Ala Ala Tyr Lys Lys Leu Thr Gly Lys
 470 475 480

 taaggtagag acacatggct gaa 1572

<210> 762

<211> 483

<212> PRT

<213> Corynebacterium glutamicum

<400> 762

Met Thr Thr Ala Leu Glu Glu Gln Asn Ala Gln Gln Ala Ala Thr Ala
 1 5 10 15

 Gly Arg Val Val Arg Val Ile Gly Ala Val Val Asp Val Glu Phe Pro
 20 25 30

 Arg Gly Glu Leu Pro Ala Leu Tyr Asn Ala Leu Thr Val Glu Val Thr
 35 40 45

 Leu Glu Ser Val Lys Lys Thr Val Val Leu Glu Val Ala Gln His Leu
 50 55 60

 Gly Asp Asn Leu Ile Arg Thr Ile Ala Met Ala Pro Thr Asp Gly Leu
 65 70 75 80

 Val Arg Gly Ala Ala Val Thr Asp Thr Ala Arg Pro Ile Ser Val Pro
 85 90 95

 Val Gly Asp Val Val Lys Gly His Val Phe Asn Ala Leu Gly Asp Cys
 100 105 110

 Leu Asp Asp Val Ser Leu Asn Asn Asn Pro Glu Ile Glu Arg Trp Gly
 115 120 125

Ile His Arg Glu Pro Pro Ser Phe Asp Gln Leu Glu Gly Lys Thr Glu
 130 135 140
 Ile Leu Glu Thr Gly Ile Lys Val Ile Asp Leu Leu Thr Pro Tyr Val
 145 150 155 160
 Lys Gly Gly Lys Ile Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr
 165 170 175
 Val Leu Ile Gln Glu Met Ile Thr Arg Ile Ala Arg Glu Phe Ser Gly
 180 185 190
 Thr Ser Val Phe Ala Gly Val Gly Glu Arg Thr Arg Glu Gly Thr Asp
 195 200 205
 Leu Phe Leu Glu Met Glu Glu Met Gly Val Leu Gln Asp Thr Ala Leu
 210 215 220
 Val Phe Gly Gln Met Asp Glu Pro Pro Gly Val Gly Met Arg Val Ala
 225 230 235 240
 Leu Ser Gly Leu Thr Met Ala Glu Tyr Phe Arg Asp Val Gln Asn Gln
 245 250 255
 Asp Val Leu Leu Phe Ile Asp Asn Ile Phe Arg Phe Thr Gln Ala Gly
 260 265 270
 Ser Glu Val Ser Thr Leu Leu Gly Arg Met Pro Ser Ala Val Gly Tyr
 275 280 285
 Gln Pro Thr Leu Ala Asp Glu Met Gly Val Leu Gln Glu Arg Ile Thr
 290 295 300
 Ser Thr Lys Gly Arg Ser Ile Thr Ser Leu Gln Ala Val Tyr Val Pro
 305 310 315 320
 Ala Asp Asp Tyr Thr Asp Pro Ala Pro Ala Thr Thr Phe Ala His Leu
 325 330 335
 Asp Ala Thr Thr Glu Leu Asp Arg Ser Ile Ala Ser Lys Gly Ile Tyr
 340 345 350
 Pro Ala Val Asn Pro Leu Thr Ser Thr Ser Arg Ile Leu Glu Pro Ala
 355 360 365
 Ile Val Gly Glu Arg His Tyr Glu Val Ser Gln Arg Val Ile Gly Ile
 370 375 380
 Leu Gln Lys Asn Lys Glu Leu Gln Asp Ile Ile Ala Ile Leu Gly Met
 385 390 395 400
 Asp Glu Leu Ser Glu Glu Asp Lys Ile Thr Val Ala Arg Ala Arg Arg
 405 410 415
 Ile Glu Arg Phe Leu Gly Gln Asn Phe Phe Val Ala Glu Lys Phe Thr
 420 425 430
 Gly Leu Pro Gly Ser Tyr Val Pro Leu Thr Asp Thr Val Asp Ala Phe
 435 440 445
 Glu Arg Ile Cys Asn Gly Asp Phe Asp His Tyr Pro Glu Gln Ala Phe

450	455	460	
Asn Gly Leu Gly Gly Leu Asp Asp Val Glu Ala Ala Tyr Lys Lys Leu			
465	470	475	480
Thr Gly Lys			
<210> 763			
<211> 778			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (15) .. (755)			
<223> FRXA01193			
<400> 763			
caccaggagt	cggtatg	cgc	gtg gct ctg tcc ggc ctg acc atg gcg gag 50
	Met Arg Val Ala Leu Ser Gly Leu Thr Met Ala Glu		
	1	5	10
tac ttc cgc gat gtt cag aac cag gac gtg ctg ctg ttc atc gac aac 98			
Tyr Phe Arg Asp Val Gln Asn Gln Asp Val Leu Leu Phe Ile Asp Asn			
	15	20	25
atc ttc cgt ttc acc cag gca ggt tct gag gtt tcc acc ctt ctg ggt 146			
Ile Phe Arg Phe Thr Gln Ala Gly Ser Glu Val Ser Thr Leu Leu Gly			
	30	35	40
cgt atg cct tcc gcc gtg ggt tac cag cca acc ctg gct gac gag atg 194			
Arg Met Pro Ser Ala Val Gly Tyr Gln Pro Thr Leu Ala Asp Glu Met			
	45	50	55 60
ggg gtt ctc cag gag cgc att acc tcc acc aag ggc cgt tcg att acc 242			
Gly Val Leu Gln Glu Arg Ile Thr Ser Thr Lys Gly Arg Ser Ile Thr			
	65	70	75
tct ctg cag gcc gtt tac gtt cct gcc gat gac tac acc gac ccg gct 290			
Ser Leu Gln Ala Val Tyr Val Pro Ala Asp Asp Tyr Thr Asp Pro Ala			
	80	85	90
cca gcg acc acc ttc gct cac ttg gat gca acc acc gag ctt gac cgc 338			
Pro Ala Thr Thr Phe Ala His Leu Asp Ala Thr Thr Glu Leu Asp Arg			
	95	100	105
tcc att gct tcc aag ggt att tac cca gca gtg aac cca ctg acc tcc 386			
Ser Ile Ala Ser Lys Gly Ile Tyr Pro Ala Val Asn Pro Leu Thr Ser			
	110	115	120
acc tct cgt att ctc gag cca gca atc gtt ggt gag cgt cac tac gag 434			
Thr Ser Arg Ile Leu Glu Pro Ala Ile Val Gly Glu Arg His Tyr Glu			
	125	130	135 140
gtt tct cag cgt gtc atc ggc att ctg cag aag aac aag gaa ctt cag 482			
Val Ser Gln Arg Val Ile Gly Ile Leu Gln Lys Asn Lys Glu Leu Gln			
	145	150	155
gac atc atc gcc atc ctt ggt atg gac gag gct tct gaa gag gac aag 530			

Asp Ile Ile Ala Ile Leu Gly Met Asp Glu Leu Ser Glu Glu Asp Lys
 160 165 170
 atc acc gtt gca cgt gcg cgt cgc atc gag cgc ttc ctg ggt cag aac 578
 Ile Thr Val Ala Arg Ala Arg Arg Ile Glu Arg Phe Leu Gly Gln Asn
 175 180 185
 ttc ttc gtt gca gag aag ttc acc ggt ctt cct ggc tcc tac gtg cca 626
 Phe Phe Val Ala Glu Lys Phe Thr Gly Leu Pro Gly Ser Tyr Val Pro
 190 195 200
 ctg acc gac acc gtc gac gct ttc gag cgt att tgc aac ggc gac ttc 674
 Leu Thr Asp Thr Val Asp Ala Phe Glu Arg Ile Cys Asn Gly Asp Phe
 205 210 215 220
 gac cac tac cca gag cag gct ttc aac ggc ctc ggt ggt ttg gac gat 722
 Asp His Tyr Pro Glu Gln Ala Phe Asn Gly Leu Gly Gly Leu Asp Asp
 225 230 235
 gtc gaa gct gca tac aag aag ctg acc gga aag taaggtagag acacatggct 775
 Val Glu Ala Ala Tyr Lys Lys Leu Thr Gly Lys
 240 245
 gaa 778

<210> 764

<211> 247

<212> PRT

<213> Corynebacterium glutamicum

<400> 764

Met Arg Val Ala Leu Ser Gly Leu Thr Met Ala Glu Tyr Phe Arg Asp
 1 5 10 15
 Val Gln Asn Gln Asp Val Leu Leu Phe Ile Asp Asn Ile Phe Arg Phe
 20 25 30
 Thr Gln Ala Gly Ser Glu Val Ser Thr Leu Leu Gly Arg Met Pro Ser
 35 40 45
 Ala Val Gly Tyr Gln Pro Thr Leu Ala Asp Glu Met Gly Val Leu Gln
 50 55 60
 Glu Arg Ile Thr Ser Thr Lys Gly Arg Ser Ile Thr Ser Leu Gln Ala
 65 70 75 80
 Val Tyr Val Pro Ala Asp Asp Tyr Thr Asp Pro Ala Pro Ala Thr Thr
 85 90 95
 Phe Ala His Leu Asp Ala Thr Thr Glu Leu Asp Arg Ser Ile Ala Ser
 100 105 110
 Lys Gly Ile Tyr Pro Ala Val Asn Pro Leu Thr Ser Thr Ser Arg Ile
 115 120 125
 Leu Glu Pro Ala Ile Val Gly Glu Arg His Tyr Glu Val Ser Gln Arg
 130 135 140
 Val Ile Gly Ile Leu Gln Lys Asn Lys Glu Leu Gln Asp Ile Ile Ala
 145 150 155 160

Ile Leu Gly Met Asp Glu Leu Ser Glu Glu Asp Lys Ile Thr Val Ala
 165 170 175

Arg Ala Arg Arg Ile Glu Arg Phe Leu Gly Gln Asn Phe Phe Val Ala
 180 185 190

Glu Lys Phe Thr Gly Leu Pro Gly Ser Tyr Val Pro Leu Thr Asp Thr
 195 200 205

Val Asp Ala Phe Glu Arg Ile Cys Asn Gly Asp Phe Asp His Tyr Pro
 210 215 220

Glu Gln Ala Phe Asn Gly Leu Gly Gly Leu Asp Asp Val Glu Ala Ala
 225 230 235 240

Tyr Lys Lys Leu Thr Gly Lys
 245

<210> 765
 <211> 739
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(739)
 <223> FRXA01203

<400> 765
 gtgtggccaa ccaggcacgt caggcacaga tcacccagga aatcacagag attgttggtg 60

gcgcaggcgc gctcgccgac agcggagaaa gtgactaatt atg act aca gct ctt 115
 Met Thr Thr Ala Leu
 1 5

gaa gag cag aac gca cag cag gca gcc act gcc ggc cgt gtc gtg cgt 163
 Glu Glu Gln Asn Ala Gln Gln Ala Ala Thr Ala Gly Arg Val Val Arg
 10 15 20

gtc att ggt gcg gtc gtc gac gtg gag ttt ccc cgc ggc gag ctg cca 211
 Val Ile Gly Ala Val Val Asp Val Glu Phe Pro Arg Gly Glu Leu Pro
 25 30 35

gca ctg tac aac gca ctt act gta gag gta acc ctc gaa tca gtt aag 259
 Ala Leu Tyr Asn Ala Leu Thr Val Glu Val Thr Leu Glu Ser Val Lys
 40 45 50

aag acc gtt gtt ctc gag gtt gct cag cac ctc ggc gac aac ctc atc 307
 Lys Thr Val Val Leu Glu Val Ala Gln His Leu Gly Asp Asn Leu Ile
 55 60 65

cgc acc atc gct atg gca cca acc gac gga ctt gtc cgc ggt gct gct 355
 Arg Thr Ile Ala Met Ala Pro Thr Asp Gly Leu Val Arg Gly Ala Ala
 70 75 80 85

gta acc gat act gca cgc cca att tcc gta cca gtg ggc gat gtt gtt 403
 Val Thr Asp Thr Ala Arg Pro Ile Ser Val Pro Val Gly Asp Val Val
 90 95 100

aag ggc cac gta ttc aac gct ttg ggc gac tgc cta gac gac gtt tcc 451
 Lys Gly His Val Phe Asn Ala Leu Gly Asp Cys Leu Asp Asp Val Ser
 105 110 115

ctg aac aac aac cca gag atc gag cgt tgg ggc atc cac cgc gag cca 499
 Leu Asn Asn Asn Pro Glu Ile Glu Arg Trp Gly Ile His Arg Glu Pro
 120 125 130

cca tca ttc gat cag ctt gag ggt aag acc gag atc ctg gaa aca ggc 547
 Pro Ser Phe Asp Gln Leu Glu Gly Lys Thr Glu Ile Leu Glu Thr Gly
 135 140 145

atc aag gtt atc gac ctt ctc acc cct tac gtt aag ggt gga aag atc 595
 Ile Lys Val Ile Asp Leu Leu Thr Pro Tyr Val Lys Gly Gly Lys Ile
 150 155 160 165

ggc ctc ttc ggt ggt gca ggt gtg ggt aag acc gtt ctt atc cag gaa 643
 Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr Val Leu Ile Gln Glu
 170 175 180

atg atc acc cgt att gca cgt gag ttc tcc ggt act tcc gtg ttc gca 691
 Met Ile Thr Arg Ile Ala Arg Glu Phe Ser Gly Thr Ser Val Phe Ala
 185 190 195

ggt gtt ggt aag cgt acc cgt gag ggc acc gac ctc ttc ctc gaa atg 739
 Gly Val Gly Lys Arg Thr Arg Glu Gly Thr Asp Leu Phe Leu Glu Met
 200 205 210

<210> 766
 <211> 213
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 766
 Met Thr Thr Ala Leu Glu Glu Gln Asn Ala Gln Gln Ala Ala Thr Ala
 1 5 10 15
 Gly Arg Val Val Arg Val Ile Gly Ala Val Val Asp Val Glu Phe Pro
 20 25 30
 Arg Gly Glu Leu Pro Ala Leu Tyr Asn Ala Leu Thr Val Glu Val Thr
 35 40 45
 Leu Glu Ser Val Lys Lys Thr Val Val Leu Glu Val Ala Gln His Leu
 50 55 60
 Gly Asp Asn Leu Ile Arg Thr Ile Ala Met Ala Pro Thr Asp Gly Leu
 65 70 75 80
 Val Arg Gly Ala Ala Val Thr Asp Thr Ala Arg Pro Ile Ser Val Pro
 85 90 95
 Val Gly Asp Val Val Lys Gly His Val Phe Asn Ala Leu Gly Asp Cys
 100 105 110
 Leu Asp Asp Val Ser Leu Asn Asn Asn Pro Glu Ile Glu Arg Trp Gly
 115 120 125
 Ile His Arg Glu Pro Pro Ser Phe Asp Gln Leu Glu Gly Lys Thr Glu
 130 135 140

Ile Leu Glu Thr Gly Ile Lys Val Ile Asp Leu Leu Thr Pro Tyr Val
 145 150 155 160

Lys Gly Gly Lys Ile Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr
 165 170 175

Val Leu Ile Gln Glu Met Ile Thr Arg Ile Ala Arg Glu Phe Ser Gly
 180 185 190

Thr Ser Val Phe Ala Gly Val Gly Lys Arg Thr Arg Glu Gly Thr Asp
 195 200 205

Leu Phe Leu Glu Met
 210

<210> 767
 <211> 363
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(340)
 <223> RXN02821

<400> 767
 aagtcgccca gatagcgagc ggaccactcg gtcaactgaa taaccccact aaacacttca 60

cagcccgaac acacgggcac cagaaaggga acgacacctc atg aac gag atc atc 115
 Met Asn Glu Ile Ile
 1 5

ctg gca cag gac gca acc gag tcc acc atc acc gga ctt ggc gct gtc 163
 Leu Ala Gln Asp Ala Thr Glu Ser Thr Ile Thr Gly Leu Gly Ala Val
 10 15 20

ggc tac ggc atc gca acc atc gga cct ggc ctc ggc atc ggc atc ctg 211
 Gly Tyr Gly Ile Ala Thr Ile Gly Pro Gly Leu Gly Ile Gly Ile Leu
 25 30 35

gtt ggt aag gct ctc gag ggt atg gca cgt cag cct gag atg gct gga 259
 Val Gly Lys Ala Leu Glu Gly Met Ala Arg Gln Pro Glu Met Ala Gly
 40 45 50

cag ctc cgt acc acc atg ttc ctg ggc atc gcc ttc gtt gag gcc ctg 307
 Gln Leu Arg Thr Thr Met Phe Leu Gly Ile Ala Phe Val Glu Ala Leu
 55 60 65

gca ctg atc ggc ctt gtt gct ggc ttc ctg ttc taatcagcta acttaaccga 360
 Ala Leu Ile Gly Leu Val Ala Gly Phe Leu Phe
 70 75 80

aag 363

<210> 768
 <211> 80
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 768

Met Asn Glu Ile Ile Leu Ala Gln Asp Ala Thr Glu Ser Thr Ile Thr
 1 5 10 15
 Gly Leu Gly Ala Val Gly Tyr Gly Ile Ala Thr Ile Gly Pro Gly Leu
 20 25 30
 Gly Ile Gly Ile Leu Val Gly Lys Ala Leu Glu Gly Met Ala Arg Gln
 35 40 45
 Pro Glu Met Ala Gly Gln Leu Arg Thr Thr Met Phe Leu Gly Ile Ala
 50 55 60
 Phe Val Glu Ala Leu Ala Leu Ile Gly Leu Val Ala Gly Phe Leu Phe
 65 70 75 80

<210> 769

<211> 303

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(280)

<223> FRXA02821

<400> 769

agcccgaaca cacgggcacc agaaaggga cgacacctca tgaacgagat catcttggca 60
 caggacgcaa ccgagtccac catcaccgga ccttggcgct gtg ggc tac ggc atc 115
 Val Gly Tyr Gly Ile
 1 5
 gca acc atc gga cct ggc ctc ggc atc ggc atc ttg gtt ggt aag gct 163
 Ala Thr Ile Gly Pro Gly Leu Gly Ile Gly Ile Leu Val Gly Lys Ala
 10 15 20
 ctc gag ggt atg gca cgt cag cct gag atg gct gga cag ctc cgt acc 211
 Leu Glu Gly Met Ala Arg Gln Pro Glu Met Ala Gly Gln Leu Arg Thr
 25 30 35
 acc atg ttc ctg ggc atc gcc ttc gtt gag gcc ctg gca ctg atc ggc 259
 Thr Met Phe Leu Gly Ile Ala Phe Val Glu Ala Leu Ala Leu Ile Gly
 40 45 50
 ctt gtt gct ggc ttc ctg ttc taatcagcta acttaaccga aag 303
 Leu Val Ala Gly Phe Leu Phe
 55 60

<210> 770

<211> 60

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 770

Val Gly Tyr Gly Ile Ala Thr Ile Gly Pro Gly Leu Gly Ile Gly Ile
 1 5 10 15
 Leu Val Gly Lys Ala Leu Glu Gly Met Ala Arg Gln Pro Glu Met Ala
 20 25 30
 Gly Gln Leu Arg Thr Thr Met Phe Leu Gly Ile Ala Phe Val Glu Ala
 35 40 45
 Leu Ala Leu Ile Gly Leu Val Ala Gly Phe Leu Phe
 50 55 60

<210> 771

<211> 632

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(609)

<223> RXA01200

<400> 771

ggc tgt ctt cgg tgg aaa agt gag cca tct gtt ctc gaa gtc ctc aag 48
 Gly Cys Leu Arg Trp Lys Ser Glu Pro Ser Val Leu Glu Val Leu Lys
 1 5 10 15
 gac gcc gca gag cag acc tgg tcc act cca cgc gag ttc cgc gct gga 96
 Asp Ala Ala Glu Gln Thr Trp Ser Thr Pro Arg Glu Phe Arg Ala Gly
 20 25 30
 cta gtc caa ctt ggc cgt cgc gcc ctt ctt cgc tct gcg gag aaa cag 144
 Leu Val Gln Leu Gly Arg Arg Ala Leu Leu Arg Ser Ala Glu Lys Gln
 35 40 45
 ggt cag ctt ggt cag gtg gaa gat gaa ctg ttc cga ctc agc cga atc 192
 Gly Gln Leu Gly Gln Val Glu Asp Glu Leu Phe Arg Leu Ser Arg Ile
 50 55 60
 ctg gat cgc gaa agc aag ctg act cag ctt ctt tca gat cgc act cag 240
 Leu Asp Arg Glu Ser Lys Leu Thr Gln Leu Leu Ser Asp Arg Thr Gln
 65 70 75 80
 gaa att ggc ggt cga cgt gac ctc ctg gct aag gtg ctc tac ggc aag 288
 Glu Ile Gly Gly Arg Arg Asp Leu Leu Ala Lys Val Leu Tyr Gly Lys
 85 90 95
 gta act gct gtt acc gaa gcc ctc gca ctg cag gct att ggt cgc cct 336
 Val Thr Ala Val Thr Glu Ala Leu Ala Leu Gln Ala Ile Gly Arg Pro
 100 105 110
 gag cac aac cca att gac gat atc gca gct ttg gct ggc gct gta gca 384
 Glu His Asn Pro Ile Asp Asp Ile Ala Ala Leu Ala Gly Ala Val Ala
 115 120 125
 gag cta cag ggt cgt tcc gtt gca cat gtc gtt acc gca gtt gaa ctc 432
 Glu Leu Gln Gly Arg Ser Val Ala His Val Val Thr Ala Val Glu Leu
 130 135 140
 aac gag gga cag caa caa gcg cta gct gaa aag ctg gga cgt att tat 480

Asn Glu Gly Gln Gln Gln Ala Leu Ala Glu Lys Leu Gly Arg Ile Tyr
 145 150 155 160
 ggt cgt gcg atg agc atc cac tcc gag gtt gat acc agc ctc ctc ggt 528
 Gly Arg Ala Met Ser Ile His Ser Glu Val Asp Thr Ser Leu Leu Gly
 165 170 175
 gga atg atc atc cgc gtc gga gac gaa gta att gac ggc agc acc tcg 576
 Gly Met Ile Ile Arg Val Gly Asp Glu Val Ile Asp Gly Ser Thr Ser
 180 185 190
 ggc aaa ctc gag cgt ctg cgg gca agc ttc gca taaagacacg acgaattaga 629
 Gly Lys Leu Glu Arg Leu Arg Ala Ser Phe Ala
 195 200
 caa 632
 <210> 772
 <211> 203
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 772
 Gly Cys Leu Arg Trp Lys Ser Glu Pro Ser Val Leu Glu Val Leu Lys
 1 5 10 15
 Asp Ala Ala Glu Gln Thr Trp Ser Thr Pro Arg Glu Phe Arg Ala Gly
 20 25 30
 Leu Val Gln Leu Gly Arg Arg Ala Leu Leu Arg Ser Ala Glu Lys Gln
 35 40 45
 Gly Gln Leu Gly Gln Val Glu Asp Glu Leu Phe Arg Leu Ser Arg Ile
 50 55 60
 Leu Asp Arg Glu Ser Lys Leu Thr Gln Leu Leu Ser Asp Arg Thr Gln
 65 70 75 80
 Glu Ile Gly Gly Arg Arg Asp Leu Leu Ala Lys Val Leu Tyr Gly Lys
 85 90 95
 Val Thr Ala Val Thr Glu Ala Leu Ala Leu Gln Ala Ile Gly Arg Pro
 100 105 110
 Glu His Asn Pro Ile Asp Asp Ile Ala Ala Leu Ala Gly Ala Val Ala
 115 120 125
 Glu Leu Gln Gly Arg Ser Val Ala His Val Val Thr Ala Val Glu Leu
 130 135 140
 Asn Glu Gly Gln Gln Gln Ala Leu Ala Glu Lys Leu Gly Arg Ile Tyr
 145 150 155 160
 Gly Arg Ala Met Ser Ile His Ser Glu Val Asp Thr Ser Leu Leu Gly
 165 170 175
 Gly Met Ile Ile Arg Val Gly Asp Glu Val Ile Asp Gly Ser Thr Ser
 180 185 190
 Gly Lys Leu Glu Arg Leu Arg Ala Ser Phe Ala

200

```
<220>  
<221> CDS  
<222> (101)..(472)  
<223> RXA01194
```

```
<210> 774
<211> 124
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 774
Met Ala Glu Ile Thr Val Glu Leu Val Ser Val Glu Arg Met Leu Trp
1 5 10 15

Ala	Gly	Gln	Ala	Ser	Ile	Val	Thr	Ala	Gln	Thr	Thr	Glu	Gly	Glu	Ile
20								25				30			
Gly	Val	Leu	Pro	Asp	His	Glu	Pro	Leu	Leu	Gly	Gln	Leu	Val	Glu	Asn
35								40				45			
Gly	Val	Val	Thr	Ile	Gln	Pro	Ile	Asp	Gly	Glu	Lys	Leu	Ile	Ala	Gly
50								55				60			
Val	Ser	Asp	Gly	Phe	Leu	Ser	Val	Ser	Lys	Glu	Lys	Val	Thr	Ile	Leu
65								70				75			
Ala	Asp	Phe	Ala	Val	Trp	Ala	Asn	Glu	Val	Asp	Thr	Ala	Ser	Ala	Glu
				85								90			
Ala	Asp	Leu	Asn	Ser	Asp	Asp	Glu	Leu	Ala	Lys	Ala	His	Ala	Glu	Ala
100								105				110			
Gly	Leu	Arg	Ala	Val	Arg	Arg	Ser	Ser	Glu	Gly	Leu				
115								120							

```
<210> 775
<211> 1098
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(1075)  
<223> RXA01202
```

<400> 775																	
agaaagacca gctcaccgtt tcccgcgaagg tcagcaagaa gtaaggcagc gagcctacac																	60
taaagtactg tccaagcaac tgaagggagg cgtgtgaacc atg gca aca att cgt																	115
Met Ala Thr Ile Arg																	
1 5																	
gaa ttg cgt gac cga att cgt tcg gtt aac tca acc aag aag atc acc																	163
Glu Leu Arg Asp Arg Ile Arg Ser Val Asn Ser Thr Lys Lys Ile Thr																	
10 15 20																	
aag gct caa gag ctc atc gcc acc tct cgc atc acc aag gca cag ggt																	211
Lys Ala Gln Glu Leu Ile Ala Thr Ser Arg Ile Thr Lys Ala Gln Gly																	
25 30 35																	
cgc gtc gcg gca gct gcg ccg tac gcc gag gaa atc cag cgc gtg ctg																	259
Arg Val Ala Ala Ala Ala Pro Tyr Ala Glu Glu Ile Gln Arg Val Leu																	
40 45 50																	
gag cgc ctc gcg tcg gca agc tcc cta gac cac cca atg ctg cgt gag																	307
Glu Arg Leu Ala Ser Ala Ser Ser Leu Asp His Pro Met Leu Arg Glu																	
55 60 65																	
cgt gaa ggc ggc aag cga gcc gcc gtg ctc gtg gtt act tct gac cgc																	355
Arg Glu Gly Gly Lys Arg Ala Ala Val Leu Val Val Thr Ser Asp Arg																	
70 75 80 85																	
ggc atg gct ggt ggc tac aac cac aac gtt ctg aaa aag gca gcg gag																	403

Gly	Met	Ala	Gly	Gly	Tyr	Asn	His	Asn	Val	Leu	Lys	Lys	Ala	Ala	Glu	
				90					95						100	
ctg	gaa	aag	ctt	ctt	gct	gaa	agt	gga	tac	gaa	gtg	gtt	cgt	tat	gtc	451
Leu	Glu	Lys	Leu	Leu	Ala	Glu	Ser	Gly	Tyr	Glu	Val	Val	Arg	Tyr	Val	
			105					110					115			
acc	ggc	aaa	aag	ggc	gtc	gac	tac	tac	aag	ttc	cgc	gct	gaa	gat	gtg	499
Thr	Gly	Lys	Lys	Gly	Val	Asp	Tyr	Tyr	Lys	Phe	Arg	Ala	Glu	Asp	Val	
			120				125					130				
gct	ggc	acc	tgg	act	gga	ttc	tca	cag	gat	cca	gac	tgg	gca	gct	acc	547
Ala	Gly	Thr	Trp	Thr	Gly	Phe	Ser	Gln	Asp	Pro	Asp	Trp	Ala	Ala	Thr	
			135			140						145				
cac	aac	gtg	cgc	cgt	cac	ctc	att	gat	ggc	ttc	acc	gcc	agc	tct	gaa	595
His	Asn	Val	Arg	Arg	His	Leu	Ile	Asp	Gly	Phe	Thr	Ala	Ser	Ser	Glu	
					155					160					165	
ggc	gaa	gct	gca	tgg	cgc	gag	gga	ctg	aac	cta	cca	gaa	ggc	cag	gat	643
Gly	Glu	Ala	Ala	Trp	Arg	Glu	Gly	Leu	Asn	Leu	Pro	Glu	Gly	Gln	Asp	
				170					175					180		
atc	cag	ggc	ttc	gac	cag	gtt	cac	gtg	gtc	tac	acc	gag	ttc	atc	tcc	691
Ile	Gln	Gly	Phe	Asp	Gln	Val	His	Val	Val	Tyr	Thr	Glu	Phe	Ile	Ser	
			185					190					195			
atg	ctg	act	caa	aac	cca	gta	gtg	cac	caa	ctg	ctg	cct	gtt	gag	cca	739
Met	Leu	Thr	Gln	Asn	Pro	Val	Val	His	Gln	Leu	Leu	Pro	Val	Glu	Pro	
			200				205					210				
gtc	atc	gaa	gat	gaa	att	ttc	gaa	aaa	ggc	gag	gat	ctg	ctg	tcc	tct	787
Val	Ile	Glu	Asp	Glu	Ile	Phe	Glu	Lys	Gly	Glu	Asp	Leu	Leu	Ser	Ser	
			215			220					225					
tcc	ggc	gaa	gtc	gaa	ccc	gac	tac	gag	ttc	gag	ccg	gat	gca	gac	act	835
Ser	Gly	Glu	Val	Glu	Pro	Asp	Tyr	Glu	Phe	Glu	Pro	Asp	Ala	Asp	Thr	
					235					240					245	
ctg	ctt	gag	gca	ctg	ctt	ccg	cag	tac	gtc	tct	cgt	agg	ctg	ttc	tcc	883
Leu	Leu	Glu	Ala	Leu	Leu	Pro	Gln	Tyr	Val	Ser	Arg	Arg	Leu	Phe	Ser	
				250					255					260		
atc	ttc	ttg	gag	gct	gca	gct	gca	gag	tcc	gct	tca	cgt	cga	aac	gcg	931
Ile	Phe	Leu	Glu	Ala	Ala	Ala	Ala	Glu	Ser	Ala	Ser	Arg	Arg	Asn	Ala	
			265					270					275			
atg	aag	tct	gcg	act	gac	aac	gct	acg	gaa	ctg	gtc	aag	gac	ctg	tcc	979
Met	Lys	Ser	Ala	Thr	Asp	Asn	Ala	Thr	Glu	Leu	Val	Lys	Asp	Leu	Ser	
			280				285					290				
cgt	gtg	gcc	aac	cag	gca	cgt	cag	gca	cag	atc	acc	cag	gaa	atc	aca	1027
Arg	Val	Ala	Asn	Gln	Ala	Arg	Gln	Ala	Gln	Ile	Thr	Gln	Glu	Ile	Thr	
			295			300					305					
gag	att	gtt	ggt	ggc	gca	ggc	gcg	ctc	gcc	gac	agc	gga	gaa	agt	gac	1075
Glu	Ile	Val	Gly	Gly	Ala	Gly	Ala	Leu	Ala	Asp	Ser	Gly	Glu	Ser	Asp	
			310			315				320					325	
taattatgac	tacagctctt	gaa														1098

<210> 776

<211> 325

<212> PRT

<213> Corynebacterium glutamicum

<400> 776

Met Ala Thr Ile Arg Glu Leu Arg Asp Arg Ile Arg Ser Val Asn Ser
 1 5 10 15

Thr Lys Lys Ile Thr Lys Ala Gln Glu Leu Ile Ala Thr Ser Arg Ile
 20 25 30

Thr Lys Ala Gln Gly Arg Val Ala Ala Ala Pro Tyr Ala Glu Glu
 35 40 45

Ile Gln Arg Val Leu Glu Arg Leu Ala Ser Ala Ser Ser Leu Asp His
 50 55 60

Pro Met Leu Arg Glu Arg Glu Gly Gly Lys Arg Ala Ala Val Leu Val
 65 70 75 80

Val Thr Ser Asp Arg Gly Met Ala Gly Gly Tyr Asn His Asn Val Leu
 85 90 95

Lys Lys Ala Ala Glu Leu Glu Lys Leu Leu Ala Glu Ser Gly Tyr Glu
 100 105 110

Val Val Arg Tyr Val Thr Gly Lys Lys Gly Val Asp Tyr Tyr Lys Phe
 115 120 125

Arg Ala Glu Asp Val Ala Gly Thr Trp Thr Gly Phe Ser Gln Asp Pro
 130 135 140

Asp Trp Ala Ala Thr His Asn Val Arg Arg His Leu Ile Asp Gly Phe
 145 150 155 160

Thr Ala Ser Ser Glu Gly Glu Ala Ala Trp Arg Glu Gly Leu Asn Leu
 165 170 175

Pro Glu Gly Gln Asp Ile Gln Gly Phe Asp Gln Val His Val Val Tyr
 180 185 190

Thr Glu Phe Ile Ser Met Leu Thr Gln Asn Pro Val Val His Gln Leu
 195 200 205

Leu Pro Val Glu Pro Val Ile Glu Asp Glu Ile Phe Glu Lys Gly Glu
 210 215 220

Asp Leu Leu Ser Ser Ser Gly Glu Val Glu Pro Asp Tyr Glu Phe Glu
 225 230 235 240

Pro Asp Ala Asp Thr Leu Leu Glu Ala Leu Leu Pro Gln Tyr Val Ser
 245 250 255

Arg Arg Leu Phe Ser Ile Phe Leu Glu Ala Ala Ala Ala Glu Ser Ala
 260 265 270

Ser Arg Arg Asn Ala Met Lys Ser Ala Thr Asp Asn Ala Thr Glu Leu
 275 280 285

Val Lys Asp Leu Ser Arg Val Ala Asn Gln Ala Arg Gln Ala Gln Ile
 290 295 300

Thr Gln Glu Ile Thr Glu Ile Val Gly Gly Ala Gly Ala Leu Ala Asp
 305 310 315 320

Ser Gly Glu Ser Asp
 325

<210> 777
 <211> 1773
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1750)
 <223> RXN02434

<400> 777
 cttcaatagt caaaaccagc aaactaatTT tttaagtttt acgtaactgg cccaccgct 60

tgtggcaggc cttgcgTTTT gacattgaag gaccctTTTT atg cgc act ttt gcc 115
 Met Arg Thr Phe Ala
 1 5

gct tat att gcc att gat ggc ctc agc ttt tcc tac ccc aac acc cac 163
 Ala Tyr Ile Ala Ile Asp Gly Leu Ser Phe Ser Tyr Pro Asn Thr His
 10 15 20

gtt tta agc gat att tcg ctc acc gtt gcc aat ggc gat atc gcc gga 211
 Val Leu Ser Asp Ile Ser Leu Thr Val Ala Asn Gly Asp Ile Ala Gly
 25 30 35

ctg att ggt gaa aac ggc gca gga aaa tcc acc ctg ctc agc ctc atc 259
 Leu Ile Gly Glu Asn Gly Ala Gly Lys Ser Thr Leu Leu Ser Leu Ile
 40 45 50

gct ggc gtc atg gaa ccc gac cag ggc agg att tac ctc ccc gaa cgc 307
 Ala Gly Val Met Glu Pro Asp Gln Gly Arg Ile Tyr Leu Pro Glu Arg
 55 60 65

acc gga ttc atc gcc caa gaa aca gac tta ccg ttt gaa caa ccc gtg 355
 Thr Gly Phe Ile Ala Gln Glu Thr Asp Leu Pro Phe Glu Gln Pro Val
 70 75 80 85

cag tcg ctt atc gac gcc gcc gtc gcc cca gtg cgc gcg gtc gat gcc 403
 Gln Ser Leu Ile Asp Ala Ala Val Ala Pro Val Arg Ala Val Asp Ala
 90 95 100

gcg att aca gat ttg tcc acc aag ctt ggc gac gcc tcc ctc agc gcc 451
 Ala Ile Thr Asp Leu Ser Thr Lys Leu Gly Asp Ala Ser Leu Ser Ala
 105 110 115

gaa gag cag gcg caa gtc gcc aca gat ttc gat gca gcg cta ggc gct 499
 Glu Glu Gln Ala Gln Val Ala Thr Asp Phe Asp Ala Ala Leu Gly Ala
 120 125 130

gca gaa gaa ctc gga ctg tgg gaa tta gat gca cgt att gaa acc atc 547
 Ala Glu Glu Leu Gly Leu Trp Glu Leu Asp Ala Arg Ile Glu Thr Ile

135	140	145	
gtc gcg ggt ctc ggc ctt gcc gag gtg gat cgc agc act ccc att ggt 595 Val Ala Gly Leu Gly Leu Ala Glu Val Asp Arg Ser Thr Pro Ile Gly 165 150 155 160			
gag ctt tcc ggc ggt cag cgc cgc aga ttc gca ttg gca gcg ctg ctg 643 Glu Leu Ser Gly Gly Gln Arg Arg Arg Phe Ala Leu Ala Ala Leu Leu 180 170 175			
ttg gaa cca cac gat gct ctg att ttc gat gag ccc acc aac cac ctc 691 Leu Glu Pro His Asp Ala Leu Ile Phe Asp Glu Pro Thr Asn His Leu 195 185 190			
gac gac aca gcc gta gat ttc ctc atc tcg gag att tcc cgt ttc aaa 739 Asp Asp Thr Ala Val Asp Phe Leu Ile Ser Glu Ile Ser Arg Phe Lys 210 200 205			
ggt cca gtg ctg atc gcc agc cac gat cgc ttc ttc ctc gac tcc gtc 787 Gly Pro Val Leu Ile Ala Ser His Asp Arg Phe Phe Leu Asp Ser Val 225 215 220			
tgt acc gag tta atc gac ctc gat cct gca ctt gga cct gag ggc gga 835 Cys Thr Glu Leu Ile Asp Leu Asp Pro Ala Leu Gly Pro Glu Gly Gly 245 230 235 240			
tcc ggc gaa gaa gta aaa caa gcc gtg tct ttt ggt ggt gga ttt tct 883 Ser Gly Glu Glu Val Lys Gln Ala Val Ser Phe Gly Gly Gly Phe Ser 260 250 255			
gaa tac atc aaa gaa cgc gag acc cgc cgc acc cgc tgg gct cag ttg 931 Glu Tyr Ile Lys Glu Arg Glu Thr Arg Arg Thr Arg Trp Ala Gln Leu 275 265 270			
tac acc gca caa gaa acc gag cgg gaa aaa ctc gaa gaa acc acc ggc 979 Tyr Thr Ala Gln Glu Thr Glu Arg Glu Lys Leu Glu Glu Thr Thr Gly 290 280 285 290			
acc acc gaa tcg gat att ttc cac agc tcg gtt tcc aaa tcg gaa gct 1027 Thr Thr Glu Ser Asp Ile Phe His Ser Ser Val Ser Lys Ser Glu Ala 305 295 300 305			
aaa atc acc gcg aaa ttt tac gca gac cgg gca gct aaa act caa ggc 1075 Lys Ile Thr Ala Lys Phe Tyr Ala Asp Arg Ala Ala Lys Thr Gln Gly 325 310 315 320			
aac cgc gtc cgc tcc gcc aaa aac cgc ctg aag gaa ttg gaa cgc tat 1123 Asn Arg Val Arg Ser Ala Lys Asn Arg Leu Lys Glu Leu Glu Arg Tyr 340 330 335 340			
gaa atc cca gca cct cca aag cca ctg gaa ttc caa ggc atc cca gaa 1171 Glu Ile Pro Ala Pro Pro Lys Pro Leu Glu Phe Gln Gly Ile Pro Glu 355 345 350 355			
gcc tcc gga aac ggt cac ggt gaa aca cta gaa gtg cgg gct att gct 1219 Ala Ser Gly Asn Gly His Gly Glu Thr Leu Glu Val Arg Ala Ile Ala 370 360 365 370			
gtg gaa aac agg ctt caa ccc ttg act ttc cac atc gat ccc ggc gac 1267 Val Glu Asn Arg Leu Gln Pro Leu Thr Phe His Ile Asp Pro Gly Asp 385 375 380 385			

cac atc ctg gtc gaa ggc ccc aac ggt gtc ggt aaa tcc acc ctg ctg 1315
 His Ile Leu Val Glu Gly Pro Asn Gly Val Gly Lys Ser Thr Leu Leu
 390 395 400 405
 agc gtt ctg gaa ggc gtg ctt gaa cca acc gaa ggt gaa ttg atc gtc 1363
 Ser Val Leu Glu Gly Val Leu Glu Pro Thr Glu Gly Glu Leu Ile Val
 410 415 420
 ccc gaa ggg ctg aaa gtt gcg cgc ctg aaa cag gac gat cag tgg acg 1411
 Pro Glu Gly Leu Lys Val Ala Arg Leu Lys Gln Asp Asp Gln Trp Thr
 425 430 435
 gaa aag cag ttg aac acc ccc gtc gac gaa ctg ttc gcc gcc cta tcg 1459
 Glu Lys Gln Leu Asn Thr Pro Val Asp Glu Leu Phe Ala Ala Leu Ser
 440 445 450
 aaa ggt ccg gtc gga ctc aac ctc gtg gag atg ggg ctg ttg agg gag 1507
 Lys Gly Pro Val Gly Leu Asn Leu Val Glu Met Gly Leu Leu Arg Glu
 455 460 465
 acg tcg caa agc agc ccg cta cgg gcc cta tcg ctc ggc caa cgc cgg 1555
 Thr Ser Gln Ser Ser Pro Leu Arg Ala Leu Ser Leu Gly Gln Arg Arg
 470 475 480 485
 cgc gtc tcg ctc ggg ctc atc ctg gcg agc cca cca gat ctt ttg ctt 1603
 Arg Val Ser Leu Gly Leu Ile Leu Ala Ser Pro Pro Asp Leu Leu Leu
 490 495 500
 ctt gac gag ccc acc aac cac ctc tcc ctc gcg ctg agc gaa gaa ctc 1651
 Leu Asp Glu Pro Thr Asn His Leu Ser Leu Ala Leu Ser Glu Glu Leu
 505 510 515
 gag tcg gcg ata gaa aaa ttc ccc ggt cgc gtt att ctg gcc agc cac 1699
 Glu Ser Ala Ile Glu Lys Phe Pro Gly Arg Val Ile Leu Ala Ser His
 520 525 530
 gat agg tgg atc aga aaa cgt tgg acg ggg aag aaa atc agc ctg agc 1747
 Asp Arg Trp Ile Arg Lys Arg Trp Thr Gly Lys Lys Ile Ser Leu Ser
 535 540 545
 cgt taaaccctac tgaacaggaa cct 1773
 Arg
 550

<210> 778

<211> 550

<212> PRT

<213> Corynebacterium glutamicum

<400> 778

Met Arg Thr Phe Ala Ala Tyr Ile Ala Ile Asp Gly Leu Ser Phe Ser
 1 5 10 15

Tyr Pro Asn Thr His Val Leu Ser Asp Ile Ser Leu Thr Val Ala Asn
 20 25 30

Gly Asp Ile Ala Gly Leu Ile Gly Glu Asn Gly Ala Gly Lys Ser Thr
 35 40 45

Leu Leu Ser Leu Ile Ala Gly Val Met Glu Pro Asp Gln Gly Arg Ile
 50 55 60
 Tyr Leu Pro Glu Arg Thr Gly Phe Ile Ala Gln Glu Thr Asp Leu Pro
 65 70 75 80
 Phe Glu Gln Pro Val Gln Ser Leu Ile Asp Ala Ala Val Ala Pro Val
 85 90 95
 Arg Ala Val Asp Ala Ala Ile Thr Asp Leu Ser Thr Lys Leu Gly Asp
 100 105 110
 Ala Ser Leu Ser Ala Glu Glu Gln Ala Gln Val Ala Thr Asp Phe Asp
 115 120 125
 Ala Ala Leu Gly Ala Ala Glu Glu Leu Gly Leu Trp Glu Leu Asp Ala
 130 135 140
 Arg Ile Glu Thr Ile Val Ala Gly Leu Gly Leu Ala Glu Val Asp Arg
 145 150 155 160
 Ser Thr Pro Ile Gly Glu Leu Ser Gly Gly Gln Arg Arg Arg Phe Ala
 165 170 175
 Leu Ala Ala Leu Leu Leu Glu Pro His Asp Ala Leu Ile Phe Asp Glu
 180 185 190
 Pro Thr Asn His Leu Asp Asp Thr Ala Val Asp Phe Leu Ile Ser Glu
 195 200 205
 Ile Ser Arg Phe Lys Gly Pro Val Leu Ile Ala Ser His Asp Arg Phe
 210 215 220
 Phe Leu Asp Ser Val Cys Thr Glu Leu Ile Asp Leu Asp Pro Ala Leu
 225 230 235 240
 Gly Pro Glu Gly Gly Ser Gly Glu Glu Val Lys Gln Ala Val Ser Phe
 245 250 255
 Gly Gly Gly Phe Ser Glu Tyr Ile Lys Glu Arg Glu Thr Arg Arg Thr
 260 265 270
 Arg Trp Ala Gln Leu Tyr Thr Ala Gln Glu Thr Glu Arg Glu Lys Leu
 275 280 285
 Glu Glu Thr Thr Gly Thr Thr Glu Ser Asp Ile Phe His Ser Ser Val
 290 295 300
 Ser Lys Ser Glu Ala Lys Ile Thr Ala Lys Phe Tyr Ala Asp Arg Ala
 305 310 315 320
 Ala Lys Thr Gln Gly Asn Arg Val Arg Ser Ala Lys Asn Arg Leu Lys
 325 330 335
 Glu Leu Glu Arg Tyr Glu Ile Pro Ala Pro Pro Lys Pro Leu Glu Phe
 340 345 350
 Gln Gly Ile Pro Glu Ala Ser Gly Asn Gly His Gly Glu Thr Leu Glu
 355 360 365
 Val Arg Ala Ile Ala Val Glu Asn Arg Leu Gln Pro Leu Thr Phe His

370 375 380
 Ile Asp Pro Gly Asp His Ile Leu Val Glu Gly Pro Asn Gly Val Gly
 385 390 395 400
 Lys Ser Thr Leu Leu Ser Val Leu Glu Gly Val Leu Glu Pro Thr Glu
 405 410 415
 Gly Glu Leu Ile Val Pro Glu Gly Leu Lys Val Ala Arg Leu Lys Gln
 420 425 430
 Asp Asp Gln Trp Thr Glu Lys Gln Leu Asn Thr Pro Val Asp Glu Leu
 435 440 445
 Phe Ala Ala Leu Ser Lys Gly Pro Val Gly Leu Asn Leu Val Glu Met
 450 455 460
 Gly Leu Leu Arg Glu Thr Ser Gln Ser Ser Pro Leu Arg Ala Leu Ser
 465 470 475 480
 Leu Gly Gln Arg Arg Arg Val Ser Leu Gly Leu Ile Leu Ala Ser Pro
 485 490 495
 Pro Asp Leu Leu Leu Leu Asp Glu Pro Thr Asn His Leu Ser Leu Ala
 500 505 510
 Leu Ser Glu Glu Leu Glu Ser Ala Ile Glu Lys Phe Pro Gly Arg Val
 515 520 525
 Ile Leu Ala Ser His Asp Arg Trp Ile Arg Lys Arg Trp Thr Gly Lys
 530 535 540
 Lys Ile Ser Leu Ser Arg
 545 550

<210> 779
 <211> 1407
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1384)
 <223> RXN00684

<400> 779
 agtcacacct aaaagtgata gccatcacga atcttttagga aaagtgattc aaacttcact 60
 gtgatcggct toggccacac acaagtgatca ggagatgaca atg act tcc cag act 115
 Met Thr Ser Gln Thr
 1 5
 tcc caa caa tcc acc tca acc ggt gga tgc cca ttc ggg cac aca tca 163
 Ser Gln Gln Ser Thr Ser Thr Gly Gly Cys Pro Phe Gly His Thr Ser
 10 15 20
 gag tcc acc agc cat cac ggc tac cag cct ttc gat atg cac aac ccg 211
 Glu Ser Thr Ser His His Gly Tyr Gln Pro Phe Asp Met His Asn Pro
 25 30 35

ttt cct gca tat aaa gaa ctc cgt cag gaa gag cca gtg atg ttc gat	259
Phe Pro Ala Tyr Lys Glu Leu Arg Gln Glu Glu Pro Val Met Phe Asp	
40 45 50	
gag cgc atc ggc tac tgg gtg gta acc aaa tat gac gac atc aaa acc	307
Glu Arg Ile Gly Tyr Trp Val Val Thr Lys Tyr Asp Asp Ile Lys Thr	
55 60 65	
acc ttt gat gac tgg gaa aca ttc tcc tct gaa aat gca caa gcc cca	355
Thr Phe Asp Asp Trp Glu Thr Phe Ser Ser Glu Asn Ala Gln Ala Pro	
70 75 80 85	
gtc cgc aag cgt gga cct cag gca acc caa atc atg acc gat ggc ggc	403
Val Arg Lys Arg Gly Pro Gln Ala Thr Gln Ile Met Thr Asp Gly Gly	
90 95 100	
ttc act gca tac tcc gga tta tca gct cgt att cca cca gag cac acc	451
Phe Thr Ala Tyr Ser Gly Leu Ser Ala Arg Ile Pro Pro Glu His Thr	
105 110 115	
cgc atc cgc gca atc gca caa aag gcc ttc acg cca cgc cgc tat aaa	499
Arg Ile Arg Ala Ile Ala Gln Lys Ala Phe Thr Pro Arg Arg Tyr Lys	
120 125 130	
gca ctc gaa cca gat atc cga gca atg gtg att gat cgt gtg gag aaa	547
Ala Leu Glu Pro Asp Ile Arg Ala Met Val Ile Asp Arg Val Glu Lys	
135 140 145	
atg ttg gcg aat gat caa cac gtc ggc gat atg gtg tca gat ctt gcc	595
Met Leu Ala Asn Asp Gln His Val Gly Asp Met Val Ser Asp Leu Ala	
150 155 160 165	
tac gac att cca acc atc acg atc ctg acg ctg atc ggt gca gat att	643
Tyr Asp Ile Pro Thr Ile Thr Ile Leu Thr Leu Ile Gly Ala Asp Ile	
170 175 180	
ttc atg gtg gtc acc tac aag cgg tgg tca gat tcc cgt gcg gcc atg	691
Phe Met Val Val Thr Tyr Lys Arg Trp Ser Asp Ser Arg Ala Ala Met	
185 190 195	
acc tgg ggc gat ctt agt gat gaa gag cag atc cca cac gca cac aat	739
Thr Trp Gly Asp Leu Ser Asp Glu Glu Gln Ile Pro His Ala His Asn	
200 205 210	
ttg gtt gag tac tgg cag gaa tgc caa cgc atg gta gct gat gca cat	787
Leu Val Glu Tyr Trp Gln Glu Cys Gln Arg Met Val Ala Asp Ala His	
215 220 225	
gca cac ggt ggc gac aac ctc acc gct gat cta gtg cga gca cag caa	835
Ala His Gly Gly Asp Asn Leu Thr Ala Asp Leu Val Arg Ala Gln Gln	
230 235 240 245	
gag ggt caa gaa atc acc gat cat gag att gct tct ttg ctg tac tcc	883
Glu Gly Gln Glu Ile Thr Asp His Glu Ile Ala Ser Leu Leu Tyr Ser	
250 255 260	
ctg ctt ttt gcg ggg cac gaa aca acc acc acg ttg atc tcc aat tgt	931
Leu Leu Phe Ala Gly His Glu Thr Thr Thr Thr Leu Ile Ser Asn Cys	
265 270 275	
ttc cga gtt ctc ctc gat cat cca gag cag tgg caa gcc att cta gag	979

Phe Arg Val Leu Leu Asp His Pro Glu Gln Trp Gln Ala Ile Leu Glu
 280 285 290
 aat cca aaa ctg att cct gcg gca gtg gat gag gtc ttg cgg tac tcc 1027
 Asn Pro Lys Leu Ile Pro Ala Ala Val Asp Glu Val Leu Arg Tyr Ser
 295 300 305
 ggc tcg atc gtg ggg tgg cgt cga aaa gca tta aaa gac acc gag atc 1075
 Gly Ser Ile Val Gly Trp Arg Arg Lys Ala Leu Lys Asp Thr Glu Ile
 310 315 320 325
 ggc ggc gtt gcc att aag gaa ggc gat ggt gtt ctg ctg ctc atg ggt 1123
 Gly Gly Val Ala Ile Lys Glu Gly Asp Gly Val Leu Leu Leu Met Gly
 330 335 340
 tcc gcg aac cgc gat gaa gct cgc ttt gaa aat ggc gag gaa ttc gat 1171
 Ser Ala Asn Arg Asp Glu Ala Arg Phe Glu Asn Gly Glu Glu Phe Asp
 345 350 355
 atc agc cgc gct aat gcg cgc gag cac ctg tct ttt ggt ttc ggc atc 1219
 Ile Ser Arg Ala Asn Ala Arg Glu His Leu Ser Phe Gly Phe Gly Ile
 360 365 370
 cac tat tgc cta gga aac atg ctg gcc aaa ctt caa gcc aag atc tgt 1267
 His Tyr Cys Leu Gly Asn Met Leu Ala Lys Leu Gln Ala Lys Ile Cys
 375 380 385
 ctc gag gaa gtc acc agg ctt gtt cct tcc ctg cac ttg gtt gcg gac 1315
 Leu Glu Glu Val Thr Arg Leu Val Pro Ser Leu His Leu Val Ala Asp
 390 395 400 405
 aaa gct atc ggg ttc cgg gag aac ctc tcc ttc cgc gtc ccc act tct 1363
 Lys Ala Ile Gly Phe Arg Glu Asn Leu Ser Phe Arg Val Pro Thr Ser
 410 415 420
 gtt ccc gtg act tgg aac gct taacgcttta ttaaataagg aga 1407
 Val Pro Val Thr Trp Asn Ala
 425

<210> 780

<211> 428

<212> PRT

<213> Corynebacterium glutamicum

<400> 780

Met Thr Ser Gln Thr Ser Gln Gln Ser Thr Ser Thr Gly Gly Cys Pro
 1 5 10 15
 Phe Gly His Thr Ser Glu Ser Thr Ser His His Gly Tyr Gln Pro Phe
 20 25 30
 Asp Met His Asn Pro Phe Pro Ala Tyr Lys Glu Leu Arg Gln Glu Glu
 35 40 45
 Pro Val Met Phe Asp Glu Arg Ile Gly Tyr Trp Val Val Thr Lys Tyr
 50 55 60
 Asp Asp Ile Lys Thr Thr Phe Asp Asp Trp Glu Thr Phe Ser Ser Glu
 65 70 75 80

Asn Ala Gln Ala Pro Val Arg Lys Arg Gly Pro Gln Ala Thr Gln Ile
 85 90 95
 Met Thr Asp Gly Gly Phe Thr Ala Tyr Ser Gly Leu Ser Ala Arg Ile
 100 105 110
 Pro Pro Glu His Thr Arg Ile Arg Ala Ile Ala Gln Lys Ala Phe Thr
 115 120 125
 Pro Arg Arg Tyr Lys Ala Leu Glu Pro Asp Ile Arg Ala Met Val Ile
 130 135 140
 Asp Arg Val Glu Lys Met Leu Ala Asn Asp Gln His Val Gly Asp Met
 145 150 155 160
 Val Ser Asp Leu Ala Tyr Asp Ile Pro Thr Ile Thr Ile Leu Thr Leu
 165 170 175
 Ile Gly Ala Asp Ile Phe Met Val Val Thr Tyr Lys Arg Trp Ser Asp
 180 185 190
 Ser Arg Ala Ala Met Thr Trp Gly Asp Leu Ser Asp Glu Glu Gln Ile
 195 200 205
 Pro His Ala His Asn Leu Val Glu Tyr Trp Gln Glu Cys Gln Arg Met
 210 215 220
 Val Ala Asp Ala His Ala His Gly Gly Asp Asn Leu Thr Ala Asp Leu
 225 230 235 240
 Val Arg Ala Gln Gln Glu Gly Gln Glu Ile Thr Asp His Glu Ile Ala
 245 250 255
 Ser Leu Leu Tyr Ser Leu Leu Phe Ala Gly His Glu Thr Thr Thr Thr
 260 265 270
 Leu Ile Ser Asn Cys Phe Arg Val Leu Leu Asp His Pro Glu Gln Trp
 275 280 285
 Gln Ala Ile Leu Glu Asn Pro Lys Leu Ile Pro Ala Ala Val Asp Glu
 290 295 300
 Val Leu Arg Tyr Ser Gly Ser Ile Val Gly Trp Arg Arg Lys Ala Leu
 305 310 315 320
 Lys Asp Thr Glu Ile Gly Gly Val Ala Ile Lys Glu Gly Asp Gly Val
 325 330 335
 Leu Leu Leu Met Gly Ser Ala Asn Arg Asp Glu Ala Arg Phe Glu Asn
 340 345 350
 Gly Glu Glu Phe Asp Ile Ser Arg Ala Asn Ala Arg Glu His Leu Ser
 355 360 365
 Phe Gly Phe Gly Ile His Tyr Cys Leu Gly Asn Met Leu Ala Lys Leu
 370 375 380
 Gln Ala Lys Ile Cys Leu Glu Glu Val Thr Arg Leu Val Pro Ser Leu
 385 390 395 400
 His Leu Val Ala Asp Lys Ala Ile Gly Phe Arg Glu Asn Leu Ser Phe

405

410

415

Arg Val Pro Thr Ser Val Pro Val Thr Trp Asn Ala
420 425

<210> 781

<211> 978

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(955)

<223> RXN00387

<400> 781

ttccgcgcgcg gcgccaactt cgacggcacc gggctgacca ctttctgctt tgaagcgcac 60

gatttctccg ccgactacct cgccaacggg ccaggccgag atg ttc cgc tcg aat 115
Met Phe Arg Ser Asn
1 5

att tcc tac gca gtc ggc gac gac atc caa aac gac cca gaa acc tgg 163
Ile Ser Tyr Ala Val Gly Asp Asp Ile Gln Asn Asp Pro Glu Thr Trp
10 15 20

gaa gac tac gaa ctt cgc gtc aac cac cca ctg cgc atc gaa ggc gac 211
Glu Asp Tyr Glu Leu Arg Val Asn His Pro Leu Arg Ile Glu Gly Asp
25 30 35

cgc gtc tac ctt cag ggc cac ggc ttc gcc cca aca ttc acc gtg acc 259
Arg Val Tyr Leu Gln Gly His Gly Phe Ala Pro Thr Phe Thr Val Thr
40 45 50

tgg cca aat ggc gag acc cgc acc cag acc gtg cag tgg cgc cca gac 307
Trp Pro Asn Gly Glu Thr Arg Thr Gln Thr Val Gln Trp Arg Pro Asp
55 60 65

gac ccg acc ttc ttc ctg tcc tca ggc gtg gtc cgt ttc gat cca ccc 355
Asp Pro Thr Phe Phe Leu Ser Ser Gly Val Val Arg Phe Asp Pro Pro
70 75 80 85

gcc ggc atg tac cca gac ctt tac gag cgc cgc caa aac cag ttg gcc 403
Ala Gly Met Tyr Pro Asp Leu Tyr Glu Arg Arg Gln Asn Gln Leu Ala
90 95 100

atc cag gga ctt ttc gca ccg acc gcg gaa tgg gaa ggc gac aac aac 451
Ile Gln Gly Leu Phe Ala Pro Thr Ala Glu Trp Glu Gly Asp Asn Asn
105 110 115

gaa ctg ctg acc tcc tcc tac ccg gcg atg cgt gac cca gcc gtg gcg 499
Glu Leu Leu Thr Ser Ser Tyr Pro Ala Met Arg Asp Pro Ala Val Ala
120 125 130

atc gat att tac cgc ggc gac aat ggc ctc gat acc ggc atc gga cag 547
Ile Asp Ile Tyr Arg Gly Asp Asn Gly Leu Asp Thr Gly Ile Gly Gln
135 140 145

tca ttg ttc agc ctg gac tct agt ctc atg cac agc ggc gtg ctg caa 595
Ser Leu Phe Ser Leu Asp Ser Ser Leu Met His Ser Gly Val Leu Gln

150	155	160	165	
aaa att gag cgc gtc	aac ctc caa atc	ggc gac acc gtc	acc ctg gat	643
Lys Ile Glu Arg Val	Asn Leu Gln Ile	Gly Asp Thr Val	Thr Leu Asp	
	170	175	180	
gat ggc acc acc gtc	tcc ttc gac ggc	gcg tca gaa ttt	gcc aac tac	691
Asp Gly Thr Thr Val	Ser Phe Asp Gly	Ala Ser Glu Phe	Ala Asn Tyr	
	185	190	195	
cag atc agc cgc gac	ccc aca caa aac	tgg gtg ctg gtc	acc acc gtg	739
Gln Ile Ser Arg Asp	Pro Thr Gln Asn	Trp Val Leu Val	Thr Thr Val	
	200	205	210	
att tcg ctg gtc tcc	ctg gtt gga tcc	ctg atg atc cga	cgc cgc cgc	787
Ile Ser Leu Val Ser	Leu Val Gly Ser	Leu Met Ile Arg	Arg Arg Arg	
	215	220	225	
att tgg gtg cgt ttc	tat cca caa gaa	aac gga acc acc	cgc gtg gaa	835
Ile Trp Val Arg Phe	Tyr Pro Gln Glu	Asn Gly Thr Thr	Arg Val Glu	
	230	235	240	245
acc ggc gga ctt gcc	cgc acc gac cgc	gca ggc tgg ggt	ggc gaa tac	883
Thr Gly Gly Leu Ala	Arg Thr Asp Arg	Ala Gly Trp Gly	Gly Glu Tyr	
	250	255	260	
gag aaa ttc cac cgc	gaa ctg ctg ggt	ctg aag gag gaa	gat gaa gac	931
Glu Lys Phe His Arg	Glu Leu Leu Gly	Leu Lys Glu Glu	Asp Glu Asp	
	265	270	275	
gaa gag tac ttc gac	cac gac gac taacaccgca	atttaaaggc ttt		978
Glu Glu Tyr Phe Asp	His Asp Asp			
	280	285		

<210> 782

<211> 285

<212> PRT

<213> Corynebacterium glutamicum

<400> 782

Met Phe Arg Ser Asn	Ile Ser Tyr Ala	Val Gly Asp Asp	Ile Gln Asn
1	5	10	15
Asp Pro Glu Thr Trp	Glu Asp Tyr Glu	Leu Arg Val Asn	His Pro Leu
	20	25	30
Arg Ile Glu Gly Asp	Arg Val Tyr Leu	Gln Gly His Gly	Phe Ala Pro
	35	40	45
Thr Phe Thr Val Thr	Trp Pro Asn Gly	Glu Thr Arg Thr	Gln Thr Val
	50	55	60
Gln Trp Arg Pro Asp	Asp Pro Thr Phe	Phe Leu Ser Ser	Gly Val Val
	65	70	75
Arg Phe Asp Pro Pro	Ala Gly Met Tyr	Pro Asp Leu Tyr	Glu Arg Arg
	85	90	95
Gln Asn Gln Leu Ala	Ile Gln Gly Leu	Phe Ala Pro Thr	Ala Glu Trp
	100	105	110

Glu Gly Asp Asn Asn Glu Leu Leu Thr Ser Ser Tyr Pro Ala Met Arg
 115 120 125
 Asp Pro Ala Val Ala Ile Asp Ile Tyr Arg Gly Asp Asn Gly Leu Asp
 130 135 140
 Thr Gly Ile Gly Gln Ser Leu Phe Ser Leu Asp Ser Ser Leu Met His
 145 150 155 160
 Ser Gly Val Leu Gln Lys Ile Glu Arg Val Asn Leu Gln Ile Gly Asp
 165 170 175
 Thr Val Thr Leu Asp Asp Gly Thr Thr Val Ser Phe Asp Gly Ala Ser
 180 185 190
 Glu Phe Ala Asn Tyr Gln Ile Ser Arg Asp Pro Thr Gln Asn Trp Val
 195 200 205
 Leu Val Thr Thr Val Ile Ser Leu Val Ser Leu Val Gly Ser Leu Met
 210 215 220
 Ile Arg Arg Arg Arg Ile Trp Val Arg Phe Tyr Pro Gln Glu Asn Gly
 225 230 235 240
 Thr Thr Arg Val Glu Thr Gly Gly Leu Ala Arg Thr Asp Arg Ala Gly
 245 250 255
 Trp Gly Gly Glu Tyr Glu Lys Phe His Arg Glu Leu Leu Gly Leu Lys
 260 265 270
 Glu Glu Asp Glu Asp Glu Glu Tyr Phe Asp His Asp Asp
 275 280 285

BGI-126CPPC - 6 -

BGI-126CPPC - 19 -